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1001

501 GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGCcg actTTCTTcc
 551 ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CatcgTACAT
 601 ACCCTcgtCT TTTTcgTTtt cAAACTACTg taa

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

g627.pep
 1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FVLISILKAG EAGALGGVVS LVHDTAGHPI
 101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
 201 TLVFFVFKLL *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

m627.seq
 1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
 51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
 101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
 151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTCC TCGGCATCTT
 201 CATCACCATC TTTCCCGTCC TGAGCATCTT GAAAGCAGGC GAGGCAGGCG
 251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
 301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
 351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GCGGGGCGGC GATGCCCAAG
 401 CCTTGATGAC GGGTACCCTG TTTCATTTCG TGCTGGCGGT TTCTATGGGT
 451 TCGGTATTC A TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
 501 GGTC AAGGCC ATGCGCGAAC AGCGCGGCGT ACCGATGCCG ACTTCTTTCG
 551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
 601 ACCCTTATCT TTTTCGTTT CAAACTGCTG TAA

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

m627.pep
 1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FVLISILKAG EAGALGGVVS LVHDTAGHPI
 101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
 201 TLIFFVFKLL *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
g627	MSGLWKPEHPGFEILGSRYALQNLVRDVILITLTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60

1002

	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVS LVHDTAGHPINVMYFWMSGILSAFLDNAPT					
g627	KLFLGIFITIFPVLSILKAGEAGALGGVVS LVHDTAGHPINTMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
g627	YLVFFNMAGGDAQALMTGPLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627.seq
1  ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT
201 CATCACCATC TTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTTCCTCG TTTCATTTCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAGGCC ATTGCCGAAC AGCGCGCGCT ACCGATGCCG ACTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCTCTG CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

a627.pep	1	MSG	LWK	PEHP	GFE	ILG	SRYA	LQN	LVR	DVIL	IAL	TAV	SMAI	TPK	QVR	AGNE
	51	FNFE	PIAE	VG	KLFL	GIFIT	IFPV	LSIL	KAG	EAG	ALGG	VVS	LVH	D	TAG	HP
	101	NVM	YFW	MSG	LSA	FLDN	APT	YLV	FFNM	AGG	DAQ	ALMT	GSL	FHS	LLAV	SMG
	151	SVFM	GALTY	GNAP	NFM	VKA	IAE	QRG	VMP	TFF	GYMM	WSV	AFL	TPV	FIV	H
	201	TLIF	FVFK	LL	*											

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSG LWK PEHP GFE ILG SRYA LQN LVR DVIL IAL TAV SMAI TPK QVR AGNE FNFE PIAE VG					
a627	MSG LWK PEHP GFE ILG SRYA LQN LVR DVIL IAL TAV SMAI TPK QVR AGNE FNFE PIAE VG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVS LVHDTAGHPINVMYFWMSGILSAFLDNAPT					
a627	KLFLGIFITIFPVLSILKAGEAGALGGVVS LVHDTAGHPINVMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					

a627 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX
 190 200 210

g628.seq

```
1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGCCCGCAA ATTCATGTGT
51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTTAC
101 ACACATAGGT TTTACGTTTC GTTCAGCGGC TCAATACCAA CAGGCCGCGT
151 TTGAAGTCTT CGCGCGCTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA
251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT
301 GATTGAATCA GGTTCGGCGC CACTTTTTTC CTGCTCAATT TTGCCAGCGC
351 TTCAGGTacg TAG
```

g628.pep
1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VVRLNTNRPR
51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
101 D*IRLRRTFS LLNFASASGT *

```
m628.seq
  1  ATGTGCGTGC  CACTCAAACC  GGCAGGATGC  GGCCCGCCGA  ATTCATGTGT
51  TTCGATGTTG  GCAGCATTTT  CAGACGGCAC  GTCTGCGCCA  GCTGCCTTAC
101 AAACATGGAT  TTTGCGTTCG  GTCAAACGGC  TCAATACCAA  CAGGCCCGGT
151 TTGAATCCT  CGCGGGCTTC  TTTGATAATG  ACCGTAGGGT  CGGCAGCCAG
201 CGGATTGGTG  TCCATCGCAT  TGACGAAGAT  GGCGAACGGC  TCGGCATCGA
251 CGGCAGGAAT  TTTGCTGAAC  GGACGGGTGC  GCAGCGCAGT  CCACAAACCG
301 GATTGGATCA  GGTTCGGGCG  CACTTCTTCG  CCGCTTAAGT  TTGCCAGCGC
351 TTCAGGTGCG  TAG
```

m628.pep

1	MCVPLKPAGC	GPPNSCVSML	AAFSDGTSAP	AAQTWILRS	VKRLNTNRP
51	LKSSAASLIM	TVGSAASGLV	SIALTKMANG	SASTAGILLN	GRVRSVHKP
101	DWIRLRTSS	PLKFASASGA	*		

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLA	AFSDGTSAPAALQ	TWILRSVKRLNTNR	PRLKSSAAS	LIM	
g628	MCVPLKPAGCGPPNSCVSILA	AFSDGTSAPAALHT	WILRSVRR	LNTNR	PRLKSSAAS	LIMM
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALT	KMANGSASTAGILL	NGRVRS	AVHKPDWIR	LRTSSPLKF	ASASGA
g628	TVGSAASGLVSIALT	KMANGSASTAGILL	NGRVRS	AVHKPD	XIRLRT	FSLLNFASAGT
	70	80	90	100	110	120

q628 X

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2019>:

1004

```

a628.seq
1   ATGTGCGTGC CACTCAAACC GGCCGGATGC GGGCCGCCGA ATTCATGTGT
51  TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
101 ACACATGGAT TTTACGCTCG GTCAAACGGC TCAATACCAG CAAACCTCGT
151 CTGAAATCCT CGGCGGCTTC TTTGATCACA ACCACAGGGT CTGCCGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
251 CGGCAGGGAT TTTGCTGAAC GGACGGGTAC GCAGCGCAGT CCACAAACCG
301 GATTGGATCA GATTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAACGC
351 TTCGGGCGCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

```

a628.pep
1   MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALHTWILRS VKRLNTSKPR
51  LKSSAASLIT TTGSAASGLV SIALTKMANG SASTAGILLN GRVRSVAVHKP
101 DWIRLRTSS PLKFANASGA *

```

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQ	TWILRSVKRLN	TNRPR	LKSSAAS	LIM
a628	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALHTWILRSVKRLN	TSKPR	LKSSAAS	LIT	
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLV	SIALTKMANGSASTAGILLN	GRVRSVAVHKPDWIRL	RRTSSPLKFASASGA		
a628	TTGSAASGLV	SIALTKMANGSASTAGILLN	GRVRSVAVHKPDWIRL	RRTSSPLKFANASGA		
	70	80	90	100	110	120

m628.pep	X
a628	X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

```

g629.seq
1   ATGACTGcca aacCTTTTTC CCTCAACCTG GCcaaCCTCC TGCTGCCggc
51  ggtatTGTTT GCCGTcAGcc tGtcgTcGG cattgccgaT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCC GACAGCCAGC AAGTGATGTT CATCAGCCGC
151 CTGCCCGCca CGTTTGcgaT TGTGTGACG GGCgcgtcga tagcgGtggc
201 gGGGAtgatt atgcagATTC TGATGCGCAA CcgtTTTGTC GAGCCTtcta
251 tggcgGGTGC GGGCCAAAGt gcgGCTTTGG GTttgcttct gAtgtccctg
301 ctgctgcctg CcgGcgcgt gccggtcaAA ATGTCGGtag Ccgccgttgc
351 CGCGCTGATC GGGATGTTGG tctTtatgct gctaataccgC Cgcctgccac
401 cgacggcgca gctgatgGTg ccgCTGGTGG Gg.ttATTTT CGGCGGCGTG
451 GttgaGGCGG TGGCGACGTT TGTCGCGTAT GAGTTTGAGA TGCTGCAAAAT
501 GTTGGGCGTG TGGCAGCAGG GCGACTTTTC AAGCGTGCTG CTGGGGCGGT
551 ACGAGCTGCT TTGGATTACG GGCGGTTTGG CGGTGTGTTGC CTACCTGATT
601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAGACGGTGA GCGTGAATTT
651 GGGTTTGAAC CGGACGGCGG TGTGTGTTGC GGGTTTGATT ATTGTGGCAC
701 TGATTACATC GCTGGTCATT GTAACGTCG GCAATATTC GTTTATCGGG
751 CTGGTCGTGC CGAATATCGT CAGCCGCCTG ATGGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTCGCCC TCTGGGCGC GTCTTTGTTT TTATTGTGCG
851 ACATTATCGG ACGCATGATT GTGTTTCCGT TTGAAATTC GGTCTCCACG
901 GTTTTGGTG TGTTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
951 ACCCGCTAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

```

g629.pep
1   MTAKPFSLNL ANLLLPAVLf AVLSVGIAD FRWSDVFSLS DSQQVMFISR
51  LPRTFAIVLT GASIAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLLSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGXIFGGV

```

1005

```

151 VEAVATFVAY EFEMQLMLGV WQQDFSSVL LGRYELLWIT GGLAVFAYLI
201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
251 LVVPNIISRL MGDRLRQSLP AVALLGASLV LLCIDIIRMI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAY AV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2023>:

```

m629.seq
1 ATGACTGCCA AACCTTTTTC CCTCAACCTG ACCAACCTGC TGCTGCTGGC
51 GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CTGATGTGTT TTCCTGTGCC GACAGCCAGC AGGTCATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCGAT TGTGCTGACG GGCGCGTCGA TGGCGGTGGC
201 CGGCATGATT ATGCAGATTT TGATGCGCAA CCGTTTGTGC GAACCGTCGA
251 TGGTGGGCGC AAGCCAAAGC GCGGCTTTAG GTTTGCTGCT GATGACCCTG
301 CTGCTGCCGG CCGCGCCGCT GCCGCGGAAA ATGTCGGTTG CCGCCGTTGC
351 CGCGCTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC
401 CGACCGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGTGTG
451 ATTGAGGCGG TAGCCACCTT TATCGCGTAT GAAAACGAAA TGCTGCAAAAT
501 GCTCGGCGTG TGGCAGCAGG GCGATTTTTC GAGCGTGCTG CTGGGGCGGT
551 ACGAGCTGCT TTGGATTACG GCGGCTTTGG CCGTGTGTTG CTATCTGATT
601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAAACGGTAA GCGTGAATTT
651 GGGTTTGAAC CGGACGCGCG TGTTGTGGTC GGGTTTGATT ATTGTGGCTT
701 TGATTACGTC GCTGTTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCCTG ATGGGCGACA GGTTCGCCCA
801 AAGCCTGCCT GCGGTGGCCT TGCTGGGCGC ATCTTTGGTG TTGCTGTGCG
851 ACATTATCGG ACGCGTGATT GTGTTCCCGT TTGAAATTCC GGTCTCTACG
901 GTTTTGGTG TATTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
951 ACCCGCCTAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2024; ORF 629>:

```

m629.pep
1 MTAKPFSNLN LNLLLLAVLF AVSLVGVAD FRWSDVFSLS DSQQVMFISR
51 LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMVGASQS AALGLLMLTL
101 LLPAAPLPAK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGIIFGGV
151 IEAVATFIAY ENEMQLMLGV WQQDFSSVL LGRYELLWIT GGLAVFAYLI
201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
251 LVVPNIISRL MGDRLRQSLP AVALLGASLV LLCIDIIRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAY AV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m629/g629 95.7% identity in 322 aa overlap

	10	20	30	40	50	60
m629.pep	MTAKPFSNLNLTNLLLLAVLFAVSLVGVADFRWSDVFSLSDSQQVMFISR					
	: : : : : : : : :					
g629	MTAKPFSNLNLANLLPAVLFAVSLVGVADFRWSDVFSLSDSQQVMFISR					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m629.pep	GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLMLTLLPAAPLPAKMSVAAVAALI					
	: : : : : : : :					
g629	GASIAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLMSLLPAAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
	130 140 150 160 170 180					
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMQLMLGVWQQDFSSVL					
	: : : : : : : :					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVVEAVATFVAYEFEMQLMLGVWQQDFSSVL					
	130	140	150	160	170	180
	190 200 210 220 230 240					
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
	: : : : : : : :					

1006

```

g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           190      200      210      220      230      240
           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVFNIIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VTVGNIPFIGLVVFNIVSRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
           250      260      270      280      290      300
           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VFGVLGTALFLWLLLRKPAYAVX
           310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```

a629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51 GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCGAT TGTGTTGACG GGCGCGTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTG TGATGCGTAA CCGTTTTGTC GAGCCTTCTA
251 TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTGCTTCTG GATGTCCCTG
301 CTGCTGCTCG CCGCGCCGCT GCGCGTCAAA ATGTCGGTTG CCGCCGTTGC
351 CGCGTTAATC GGGATGTTGG TGTTTATGAT GCTTATCCGC CGCCTGCCGC
401 CGACGGCGCA ACTGATGGTG CTTTGGTTCG GGATTATTTT CGGCGGCGTG
451 GTTGAGGCGG TGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAT
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTG CTCGGACGGT
551 ATGAACGTG GTGGGCAACG GGGATTTTGG CTTTGTGTTG CTATTTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA CCGTGAACCT
651 GGGGCTGAAC CGGACGGCGA TTCTGTGGTC GGGGCTGATT ATTGTGGCTT
701 TGATTACGTC GCTGTTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCTG ATAGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTCCGT TTGAAATCC GGTATCGACC
901 GTCTTCGCG TATTGGGTAC GCGTTGTTT TTATGGCTT TGTTAAGGAA
951 ACCTGCTCAT GCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```

a629.pep
1  MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
51 LPRTFAIVLT GASMAGMI MQILMRNFV EPSMAGAGQS AALGLLMSL
101 LLPAAPLPVK MSVAVAALI GMLVFMMLIR RLPPTAQLMV PLVGIIIFGV
151 VEAVATFIAY ENEMQLMGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251 LVVFNIIISRL IGDRLRQSLP AVALLGASLV LLCIDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAH AV*

```

m629/a629 95.7% identity in 322 aa overlap

```

           10      20      30      40      50      60
m629.pep  MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISR
           10      20      30      40      50      60
           70      80      90      100     110     120
m629.pep  GASMAGMIMQILMRNFVEPSMVGASQSAALGLLMTLLLPAPLPKMSVAVAALI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      GASMAGMIMQILMRNFVEPSMAGAGQSAALGLLMSLLLPAPLPVKMSVAVAALI
           70      80      90      100     110     120
           130     140     150     160     170     180
m629.pep  GMLVFMMLIRRLPPTAQLMVPLVGIIIFGGVIEAVATFIAYENEMQLMGVWQQGDFSSVL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

1007

```

a629      GMLVFMMLIRRLPPTAQLMVPLVGIIFGGVVEAVATFIAZENMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180

           190      200      210      220      230      240
m629.pep  LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||
a629      VFGVLGTALFLWLLLRKPAHAVX
           310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATT  TGGTGTGGCT  ggctttgttt  ccccccattgt  tttacggcat
51  gtacaacgtc  GGCGCACAGG  CATTTCGGTGC  CTTAACGCCC  Gatttgcgtgc
101 aacaaagcat  cgcccacgac  ggcaattacg  ccctcgccaa  cgctttgggc
151 atcaatatgt  cccccgaaGc  gggcgtgtTg  ggcaaaatgc  tgttcgGCGC
201 GATttacttc  ctgccgattt  acgcgaccgt  aTTTATTGTG  GGcggcttct
251 ggGaaagtCTT  GTTCGCATC  gtACGCAAAC  ACGAAATCAA  CGAAGGTTTC
301 TTCGTTACTT  CGATTCTGTT  TGCCTTAATC  GTTCCGCCCA  CGCTGCCGCT
351 GTGGCAGGCG  GCTTTGGGTA  TTTCTTTCGG  CGTTGTGGTT  GCGAAAGAAG
401 TATTCGGCGG  TACAGGTAAA  AACTTCATGA  ACCCTGCGCT  GGCAGGCCGC
451 GCCTTCCTGT  TCTTCGCCTA  CCCCGCCAAC  TTGAGCGGCG  ATGCGGTTTG
501 GACGGCGGTT  GACGGCTATT  CCGGCGCAAC  CGCGCTGGCG  CAATGGGCGG
551 CACACGGTGC  AGACGGCCTG  AAAACGCCG  TAACCGGTCA  AACCATCACT
601 TGGATGGACG  CGTTTATCGG  CAAACTGCCC  GGCTCCATCG  GCGAAGTCTC
651 CACTTTGGCA  CTCTTAATCG  GCGGCGCGTT  TATCGTGTTT  GCCCGCATCG
701 CTtcttgGCG  CATTATTGCC  ggCGTGATGA  TCGGTatGat  tGcgatgtCT
751 tcgctgatta  acttcatCGg  ttctgacacc  aaagctatgt  ttgctatgca
801 cttggtacat  ggcacttggt  GGAaagatGa  ttAtcactca  ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pop
1  MMILVWLALF  PPMFYGMYNV  GAQAFGALTP  DLLQOSIAHD  GNYALANALG
51  INMSPEAGVL  GKMLFGAIYF  LPIYATVFIV  GGFWEVLFAS  VRKHEINEGE
101 FVTSILFALI  VPPTLPLWQA  ALGISFGVVV  AKEVFGGTGK  NFMNPALAGR
151 AFLFFAYPAN  LSGDAVWTAV  DGYSGATALA  QWAHAGADGL  KNAVGTQIT
201 WMDAFIGKLP  GSIGEVSTLA  LLIGGAFIVE  ARIASWRIIA  GVMIGMIAMS
251 SLINFIGSDT  KAMFAMHLVH  GTWWKDDYHS  LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATT  TGGTGTGGCT  GGCTTTGTTC  CCTGCCATGT  TCTACGGTAT
51  GTACAACGTC  GGCGCGCAGG  CATTTCGGTGC  GTTAACGCCT  GATTTGCTGC
101 AACAAAACAT  CGCCACGAC  TGGCATTACG  CCTTTGCCAA  CGCTTTGGGC
151 ATCAATATGT  CGTCTGAAGC  GGGCGTGTCG  GACAAAATGC  TGTTTGGCGC
201 GATTTACTTC  CTGCCGATT  ACGCGACTGT  ATTTGTTGTG  GGCGGTTTCT
251 GGGAAAGTTT  GTTCGCCACC  GTGCGCAAAC  ACGAAATCAA  CGAAGGTTTC
301 TTCGTTACTT  CGATTCTGTT  TGCCTTAATC  GTTCCGCCCA  CGCTGCCGCT
351 GTGGCAGGCG  GCTTTGGGTA  TTTCTTTCGG  CGTTGTGGTT  GCGAAAGAAG
401 TATTCGGCGG  TACAGGTAAA  AACTTCATGA  ACCCTGCGCT  GGCAGGCCGT
451 GCTTTCCTGT  TCTTCGCCTA  CCCTGCCAAC  TTGAGCGGCG  ATGCGGTTTG
501 GACGGCGGTT  GACGGCTATT  CCGGCGCAAC  CGCACTGGCG  CAATGGGCGG
551 CACACGGTGC  AGACGGCCTG  AAAACGCCG  TAACCGGTCA  AACCATCACT
601 TGGATGGACG  CGTTTATCGG  CAAACTGCCC  GGCTCCATTG  GCGAAGTCTC
651 CACTTTGGCA  CTCTTAATCG  GCGGCGCGTT  TATCGTGTTT  GCCCGCATCG
701 CTTCTTGCGG  CATTATTGCC  GCGGTGATGA  TCGGTATGAT  TGCGATGTCT
751 TCGCTGTTCA  ACTTCATCGG  TTCGGACACC  AACGCTATGT  TTGCTATGCC

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1008

801 TTGGTACTGG CACTTGGTGG TCGGGGGCTT CGCCATCGGT ATGCTGTTTA
 851 TGGCGACCGA CCCTGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
 901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
 951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGCC AACCTGTTTG
 1001 CCCCATTTC CGACTATTTC GTCGCACAG CGAACATCA ACGCAGAAAG
 1051 GCGCGCAGCA ATGGCTAA

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

m630.pep
 1 MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQONIAND WHYAFANALG
 51 INMSSEAGVS DKMLFGAIYF LPIYATVFV VGGFWEVL FAT VRKHEINEGF
 101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMN PALAGR
 151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAV TGQTIT
 201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
 251 SLFNFIGSDT NAMFAMPWYH HLVG GFAIG MLF MATDPVS ASFTNVGKWW
 301 YGALIGVMCV LIRVVPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
 351 ARSNG*

m630/g630 93.5% identity in 275 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALF	PAMFYGMYNV	GAQAFGALTP	DLLQONIAND	WHYAFANALG	INMSSEAGVS
g630	MMILVWLALF	PMPFYGMYNV	GAQAFGALTP	PDLLQOSIAH	DGNALANALG	INMSPEAGVL
	10	20	30	40	50	60
	70	80	90	100	110	120
m630.pep	DKMLFGAIYF	LPIYATVFV	VGGFWEVL	FATVRKHEINEG	FFVTSILFALI	VPPTLPLWQA
g630	GKMLFGAIYF	LPIYATVFIV	GFGFWEVL	FASVRKHEINEG	FFVTSILFALI	VPPTLPLWQA
	70	80	90	100	110	120
	130	140	150	160	170	180
m630.pep	ALGISFGVVV	AKEVFGGTG	KNFMN PALAGR	AEFFAYPAN	LSGDAVWTAV	DGYSGATALA
g630	ALGISFGVVV	AKEVFGGTG	KNFMN PALAGR	AEFFAYPAN	LSGDAVWTAV	DGYSGATALA
	130	140	150	160	170	180
	190	200	210	220	230	240
m630.pep	QWAAHGADGL	KNAV TGQTIT	WMDAFIGKLP	GSIGEVSTLA	LALLIGGAFIV	FARIASWRIIA
g630	QWAAHGADGL	KNAV TGQTIT	WMDAFIGKLP	GSIGEVSTLA	LALLIGGAFIV	FARIASWRIIA
	190	200	210	220	230	240
	250	260	270	280	290	300
m630.pep	GVMIGMIAMSS	LFNFIGSDT	NAMFAMPWYH	HLVG GFAIG	MLF MATDPVS	ASFTNVGKWW
g630	GVMIGMIAMSS	LFNFIGSDT	KAMFAM	HLVHGTW	KDDYHSLYIK	
	250	260	270	280		
	310	320	330	340	350	
m630.pep	YGALIGVMCV	LIRVVPAYP	EGMMLAILFA	NLFAPIFDYF	VAQANIKRRK	ARSNGX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

a630.seq
 1 ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
 51 GTACAACGTC GGCACACAGG CATTGCGTGC GTTAACGCCC GATTGTGCTGC
 101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
 151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GGCAAAATGC TGTTCCGCGC
 201 GATTACTTTC CTGCCGATTT ACGCGACCGT ATTTATTGTC GGCGGTTTCT
 251 GGGAAGTTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGGTTTC
 301 TTTGTTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
 351 GTGGCAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
 401 TATTCGGCGG TACAGGTAAG AACTTCATGA ACCCTGCGCT GGCAGGCCGT
 451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
 501 GACGCGGTT GACGGCTATT CCGCGCAAC CGCGTGGCG CAATGGCGCG
 551 CACACGGTGC AGACGGCCTG AAAACGCCA TAACCGGTCA AACCATCACT
 601 TGGATGGATG CGTTTATCGG CAACTGCCC GGCTCCATCG GCGAAGTCTC
 651 CACTTTGGCA CTCTTAATCG GCGCGCGT TATCGTGT TCCCCATCG

1009

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701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGGTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCCTTTCC GCTTCCTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGCC AACCTGTTTG
1001 CCCCATTTC CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

```

a630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQOSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPFALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
351 ARSNG*

```

m630/a630 98.3% identity in 355 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIAN	WHYAFANALGINMSSEAGVS				
a630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQOSIAND	WHYALANALGINMSSEAGVL				
	10	20	30	40	50	60
m630.pep	DKMLFGAIYFLPIYATVFVVGGFWEVLFATVRKHEINEG	FFVTSILFALIVPPTLPLWQA				
a630	GKMLFGAIYFLPIYATVFIVGGFWEVLFATVRKHEINEG	FFVTSILFALIVPPTLPLWQA				
	70	80	90	100	110	120
m630.pep	ALGISFGVVVAKEVFGGTGKNFMNPFALAGRAFLFFAYPAN	LSGDAVWTAVDGYSGATALA				
a630	ALGISFGVVVAKEVFGGTGKNFMNPFALAGRAFLFFAYPAN	LSGDAVWTAVDGYSGATALA				
	130	140	150	160	170	180
m630.pep	QWAAHGADGLKNAVTGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
a630	QWAAHGADGLKNAITGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
	190	200	210	220	230	240
m630.pep	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIG	MLFMATDPVSASFTNVGKWW				
a630	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIG	MLFMATDPVSASFTNVGKWW				
	250	260	270	280	290	300
m630.pep	YGALIGVMCVLIRVVNPAYPEGMMLAILFANL	FAPIFDYFVAQANIKRRKARSNGX				
a630	YGALIGVMCVLIRVVNPAYPEGMMLAILFANL	FAPIFDYFVAQANIKRRKARSNGX				
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

```

g635.seq
1  ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTTGCGGT ATTTCAGATA CACGATGACG
101 GGGATTTTCA ACTGCGCGAG CTGTTCGAAA GACAGGGCAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTTT CTTACCCAGT TTTTCCAACA CTCTCTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGAG

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301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCCGCCGC GCTTTCCAAC
351 TCTGCAATTT GATTTTTCG TAAACAACAG GATTATCGTT AAACATCGGT
401 GCAGCATTCA AACGATAAGA CAAGGGTCTG TACCAGATTA G

g635.pap

1 MTRRRVGKQN RIAIHSQYR KMOVFAVFI HDDGDFQLRE LFERQGIAGR
51 LKTQIGHNAP HILKRAHLF LTQFFQHFF RQLLPVKIVQ KRRHRSRPAG
101 KIOILLYNIE IPPREPTLOF DFSVNNRIIV KHRCSTQIR QGSVPD*

m635. seq

1	ATGACCCAGG	GACGGGTCCG	CAAGCAAAAC	CGTATTGC	TCTATACCG
51	GCAATACCGA	GAAATGATCA	TCCTTCCAGT	ATTTCAGATA	CACGATGACG
101	GGGATTTCGA	TCTGTGCAAG	TCTGTGCGAA	GACAGGGCAT	AGCCTTCGCG
151	TTCAAAACCC	AAATCAGCGA	TAATGCGCGC	CATATCTCTA	AACACGCGGG
201	CGATCTGCTC	CTTATCCAGT	TTTTTAAAC	CGCTCTTTC	CGTCACTTT
251	TGCCCGTAAA	AATTGTTCAA	AAGCGTCACC	ACCGAAGCCG	CCCCGCGAGGA
301	AAAATCAAAA	TCTGTGTTTA	CAATATGAA	ATCGCGCTT	TCTTTCCAAC
351	TCTGCATCTT	TGCTTTTCCA	TAAGCAACAG	GATTATATGT	GATTAA

m635.pcp

```

1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIAPR
51 FKTQIRHNAP HILKRRGHLL LIQFF*HVLF RQLLPVKIVQ KRHHRSRPAG
101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

```

m635/q635 80.0% identity in 130 aa overlap

		10	20	30	40	50	60
m635.pep		MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFCKTQIRHNAP					
g635		MTARRVGKQNRRIAHSAQYRKMMVFAVFQIHDDGDFQLRELFERQGIARFLKLTQIGHNAP					
		10	20	30	40	50	60
		70	80	90	100	110	120
m635.pep		HILKRRGHLILLIQFFXHVLFQRLLPVKIVQKRHRHSRPAAGKIQILLYNIEIAPFFPTLHF					
g635		HILKRRRAHLFLTQFFQHFFFRQLLPVKIVQKRHRHSRPAAGKIQILLYNIEIPPRFFPTLQF					
		70	80	90	100	110	120
		130					
m635.pep		DFSISNRIIVDX					
g635		DFSVNNRIIVKHRCISIQTIRQGSVPDX					
		130	140				

a635.seq

1	ATGACCCAGC	GACGGGTCGG	CAAGCAAAAC	CGTATTGCCG	TCTATACCGC
51	GCAATATCCGA	GAAATGATCA	TCCTTGCGGT	ATTTCAGATA	CACGATAGCG
101	GGGATTTCGA	ACTGTGCAGG	CTGCTCGAA	GACAGGGCAT	AGCCTTTCCG
151	CTCAAAACCC	AAATCAGGCA	TGATGCGCCG	CATATCCTCA	AACGACGCGC
201	GCATCTGCTC	CTTATCCAGC	TTTTTCAACA	CGTCCTCTTC	CGTCAGCTTT
251	TGCCCGTGAA	AATTTGTTAA	AAGCGTCGCG	ACCGAAGCGT	CCCCGACAGGA
301	AAAATCCAAA	TCTTGCTTTA	CAATATTGAA	ATCGCGCCTT	TCTTTCCAAC
351	TCGTCACTTT	GATTTTTCCTA	TAAGCAACAG	GATTATAGTG	GATTAA

a635.ppt

1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIQAFR
51 LKTQIRHDAP HILKRRRAHL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG
101 KIOILLYNIE IAPFPTLHF DESISNRIIV D*

m635/a635 95.4% identity in 131 aa overlap

10 20 30 40 50 60

1011

```

m635.pep    MTQRRVKGQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHNAP
a635        MTQRRVKGQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHDAP
              10      20      30      40      50      60

              70      80      90      100     110     120
m635.pep    HILKRRGHLLLIQFFXHVLFRLQLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
a635        HILKRRHLLLIQLFQHVLFRLQLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
              70      80      90      100     110     120

              130
m635.pep    DFSISNRRIIVDX
a635        DFSISNRRIIVDX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGttgGc atTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcCCACGG
201 AAATATTGCC GCTGacttcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCgcccgg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTACAG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTGTGTGT
501 CAACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGGCAGCG TCATACCGGA ACGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGCG CCTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 GGCGCGGGCA AAAATTTCCG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 CGGCTGCCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCAGC
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCGGTAT GGCCGAACAA AATAAAGCAT CATTCAAATG TGCTGTGTTT
951 TATACGGAAA CCGCTGAAA CGGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVRAG
101 IGKNVVPFPG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 RTMKVYAERI IKNIIVFNQG ARGGFFEINT GIHCWQAHNT TGNGQVAERY
201 VRRVYGYGTP ALVPFDGCGT VGRPFNRNRF VDIKFLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSVWPNKIKH HSNVPVFIK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCCCTGCCTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTGAGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACACGG
201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAAT CGCTGAAGCG GTTGTTTTTG TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCGGG TGCGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTGTGTGT
501 CAATCAGGGC GCGCGGGGCA GTTCTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCCTGTGC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCATGTGA
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```


1012

This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

```

m638.pep
1  MIGEKFIIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVIH VDGETQIAEA VVFIGVVRAG
101 IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
151 RTMQIYADRI IQNIVVFNQG ARGSFPEINT GIHCGQAHTG TNGGQVAERY
201 VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
251 GAGKCGIPIS IIGS*

m638/g638 88.2% identity in 254 aa overlap

      10      20      30      40      50      60
m638.pep  MIGEKFIIVVGIIIGKYALACLVDNVVNIGIVDIVEHNALIAAADGDIVEYFEPLGKHQHI
g638      MIGGQFIIVVGIVGKNALARFVDNIVVNIGIVDIVEHDALIAAADGDIVEHFEPFGKHQHI
      10      20      30      40      50      60

      70      80      90     100     110     120
m638.pep  AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFIGVVRAGIGKNAVPPFGNVVADDLRTG
g638      AHIVAHGNIAADFAVVGVIHVDGETQVAEAVVFIGVVRAGIGKNAVPPFGNVVADDLRAG
      70      80      90     100     110     120

      130     140     150     160     170     180
m638.pep  CVPNGNAVAAALVHAQSRVADDFILAHHRIGRTMQIYADRIIQNIVVFNQARGSFPEINT
g638      RVPNGNAIAALIHQAQRIADDFILAHHRIGRTMKVYAEIRIKNIVVFNQARGGFFEINT
      130     140     150     160     170     180

      190     200     210     220     230     240
m638.pep  GIHCGQAHTGTNGGQVAERYVRRVYGYGTPAPVAFDGCCTVGRPFNRNRFVNVKFGFIYA
g638      GIHCWQAHTGTNGGQVAERYVRRVYGYGTPALVPFDGCCTVGRPFNRNRFVDIKFGLIYA
      190     200     210     220     230     240

      250     260
m638.pep  GSQFERIARPGAGKCGIPISIIGSX
g638      GSQFDRIARPGAGKNFGKVVLRGNVDDGCRCLKNAAGGKYQHGLQPYTERGCVHSVPLF
      250     260     270     280     290     300

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

```

a638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTAGCATGA TGCCTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCGG
201 AAATATTGCC GCTGATTTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAGAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
351 GCGCGCCGGG CGCGTTCCTA ACGGTAACGC CATTGCCGCG CTCGTTACAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
451 AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTCTGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGTAACGC GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCCTGTCT CCTTCGATGG
651 TTGCAGAACG GTCGCGAGGC CTTCAATCG TAATCGGTTT GTCGATGTGA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GCGCGGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

```

a638.pep
1  MIGGQFIIVVG IVGKNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVKH
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVIH VDGETQIAEA VVFIGVVRAG
101 IGKNAVPPFG NIVADDLRAG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
151 RTMQIDADRI IQNIIIVFNQG ARGSFPEINT GIHCGQAHTG TNGGQVAERY
201 VRRVYGYGTP APVSFDGCRT VGRPFNRNRF VDVKFGLIYA GSQFERIARP

```

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251 GAGKCGIPIS IIDSW*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGIIGKYALACLDVNVVNVNIGIVDIVEHNALIAAADGDIVEYFEPLGKHQHI					
a638	MIGGQFIVVGIVGKNALARFVNVVNVNIGIVDIVEHDALVAAADGDIVKHFEPLGKHQHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m638.pep	AHIVAHGNIAADFVVGHVHVDGETQIAEAVVFGVVVRAGIGKNAVPPFGNVVADDLRTG					
a638	AHIVAHGNIAADFVVGHVHVDGETQIAEAVVFIGVVVRAGIGKNAVPPFGNIVADDLRTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m638.pep	CVPNGNAVALVHAQSRVADDFILAHHRIGRTMQIYADRIIQNIIVFNQGARGSFEEINT					
a638	RVPNGNAIALVHAQSRVADDFILPHHRIGRTMQIDADRIIQNIIVFNQGARGSFEEINT					
	130	140	150	160	170	180
	190	200	210	220	230	240
m638.pep	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCCTVGRPFNRNRFVNVKFGFIYA					
a638	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVSFDGCRTVGRPFNRNRFVNVKFGFIYA					
	190	200	210	220	230	240
	250	260				
m638.pep	GSQFERIARPGAGKCGIPISIIGSX					
a638	GSQFERIARPGAGKCGIPISIIDSX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACAAAC CCTATAAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCGGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTCACG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTAGTA CGCGCTTCTT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTGAA CCGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGGCAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SCLRFAVHYM YTNDSEVSGN ISVGNMNGYV LMFSERLKVF DNIAVGSRD*
151 GIMLVNPNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201 AIEGTSLDHN SFINNGSQVK YVSTRFLDWS EGGHGNYSW SDNSPFDLNGDG
251 FGDSAYRPDG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLKEAET ROSEGRGAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1014

m639-1.seq

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTCCCCC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGAA
201 CGCACCCGGT GCGCAGGTGC TCGGCAACGA CATTTCACAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACT CCTACAAAAA CAACCGCTTC
301 AGCGATTGTC GTTTCGCGCT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCC GATATTCACG ACAACATTAT
501 CAACAAGGCA GGCAAGTGCG TATTGCTTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAAT TCCTTTATCA ACAACGAAAG
651 CAGCGTCAAA TACGTACGCA CGCGCTTCT CGATTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG CCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGGCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATGGGC GCAGGCGCAG TTTCCGCGC TTCTGCCTGG CGGCGTGGTG
901 GACAGCAAC CGCTGATGAA GCCTTATGCC CCCAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAACG CGGCAGTCGG
1001 AATGGGCGAG GCGGAAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

m639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSSEISG ISVGNMGGYV LMFSERLKVF DNIAVGSRDQ
151 GIMLNYYVYS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLDHN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPNQ IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEKETV RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFDNSFGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
	70	80	90	100	110	120
g639-1.pep	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEVSGN					
m639-1	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
	130	140	150	160	170	180
g639-1.pep	ISVGNMGGYVLMFSERLKVF DNIAVGSRDQXGIMLNYYVYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGGYVLMFSERLKVF DNIAVGSRDQXGIMLNYYVYS DIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
	190	200	210	220	230	240
g639-1.pep	YDKLSANHFENCQIGMHFTA AIEGTSLDHNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTA AIEGTSLDHNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
	250	260	270	280	290	300
g639-1.pep	NSPFDLNGDGFSDSAYRPNQIIDQIIWRAPVSRLLMNSPAISIVKWAQAF FPAVLPGGVV					
m639-1	NSAFDLNGDGFSDSAYRPNQIIDQIIWRAPVSRLLMNSPAISIVKWAQAF FPAVLPGGVV					
	250	260	270	280	290	300
	310	320	330	340		
g639-1.pep	DSKPLMKPYAPKIQTRYQAMKDELLKEAETRQSERGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

a639-1.seq

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```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAC TGCCCC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTCTG GTCGGCGTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 GCGCGCCGGC GCGCAGGTCG TCGGCAACGA TATTTCCAAA GGGCGGGACG
251 GCATTTTTTC CAATACCAAG ACGCACAACA CCTATAAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAACATTAT
501 CAACAAAGCG GGCAAGTGGC TTTTTCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAAA TACGTCAGCA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCACCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAA TTTCCGCGC TTTTGCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATC AAACCGTTA
951 TCAGGCGATG AAGGACGGGC TGCTCAAAA AGTCGAAACG CGGCAGTTGG
1001 AATGGGGCAG GCGGAAAAC GGTTCCTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSISGN ISVGNMNGYV LMFSERLKVF DNIAVGSRDQ
151 GIMLNYNVYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTSLDHN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPNQ IIDQIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

```

a639-1/m639-1 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
a639-1.pep	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
a639-1.pep	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
m639-1	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
a639-1.pep	ISVGNMNGYVLMFSERLKVFDNIAVGSRDQGIMLNYNYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMNGYVLMFSERLKVFDNIAVGSRDQGIMLNYNYS DIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
a639-1.pep	YDKLSANHFENCQIGIHFTA AIEGTSLDHNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTA AIEGTSLDHNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
a639-1.pep	NSAFDLNGDGFSDSAYRPNQIIDQIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
m639-1	NSAFDLNGDGFSDSAYRPNQIIDQIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
	250	260	270	280	290	300
a639-1.pep	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

1016

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
1  ATGATTCATA TAATATCAAT ATTAAGAGT ATCGGTATAT CGGGGATAGC
51  TATGTCCTGT TTTTCAATCC GGCGTATGTC TCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151 GcggAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201 TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251 GCgtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATCGATA CGCTGATGGC
351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCAGC
401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGTGCA TAAGTTCATC
451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCGAGCGT
501 GCGCGCCGGC GACATCATCA GcggTGCgAC TgttaCACTG ATGGTGGTTA
551 ACGACAGCAT CCAGCGTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
601 GGTTCGACGA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651 CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCCGACAAGC
701 AGGATATTTT GTCTTGGGAC GAACTTTGA AACAAAAGGC CGTCGGCCAT
751 CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
801 GGCCGGCGTG GCCGATCAGC CCGAACAGGG CGATCCTGAC GATACCTTTA
851 TTGATTTGTA TGTTCGCTTG GTCAGCCAGC CTTCATCGG TAAAAGCCTG
901 CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACCCGGGCA
951 GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCCG
1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCG TCAGAGCTGC
1101 TGCCGCCGAT GCGCCGCGTT TTAAAGAAGT TTCTTGGTTT ACCATCCCTG
1151 AAGGCGTAGC GTTGACGGT GCGGAGCCGT GCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
1  MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151 DKYIGLNFIL NPPTPSVAPG DIISGATVTL MVVNSIQRS YKVIANQYRL
201 GSDKALQTAS ASDVREAPA SETPRRMAN PDKQDILSWD ELLKQKAVGH
251 LHITLDQINK LFEKGGKAGV ADHAEQGDPD DTFIDLYVAL VSQPSIGKSL
301 LGEDGWAHLQ KRLKPGQAV LVAGEGRYSW KSGYVRGGI FDRIEMIQE
351 NSFRFTDAQH ERVELSAAD APREKESWF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201 TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGT
351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCAGC
401 AACCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
1  MIHIISILKS IGISGIVMSC FSIKMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

	10	20	30	40	50	60
m640.pep	MIHIISILKSIGISGIVMSCFSIKMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK					
g640	MIHIISILKSIGISGIAMSCFSIRMSAFRARITAFFTAFVFLTAALPAYAERLPDFLAK					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITDDAVNTRGYSSKPIDTLMVLAN
                ||||||||||||||||||||||||||||||||||||||||||||
g640          IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITDDAVNTRGYSSKPIDTLMALAN
                70      80      90      100     110     120

                130     140
m640.pep      DGTIAGAKLV DHHEPIMLIGIPH
                ||||||||||||||||
g640          DGTIAGAKLV DHHEPIMLIGIPQSRVDKFIDKYIGLNFIFKNPPTPSVAPGDIISGATVTL
                130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
1  ATGATTTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51 CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTT TCGCGCCTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCCTGATT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGT GATCACCATG
401 AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51 AERLPDFLAK IQPSEIVPGA DRYSKPEGK PMVARVYKGE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

                10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
                ||||||||||||||||||||||||||||||||||||||||||||
a640          MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
                10      20      30      40      50      60

                70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITDDAVNTRGYSSKPIDTLMVLAN
                ||||| |||||:|||||||||||||||||||||||||||||||:|:
a640          IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITDDAVNTRGYSSKPIDTLMALAK
                70      80      90      100     110     120

                130     140
m640.pep      DGTIAGAKLV DHHEPIMLIGIPH
                ||||||||||||
a640          DGTIAGAKLV DHHEPIMLIGIPH
                130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
1  ATGCGGTATC CGCCGCAATC GCGGTTTTG CAGAATGCCG CGCGTTGCCT
51 TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTTGCCCG CTATCCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGTCTTCG TGTTCTCTCT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201 TGCCGATGAA GACTTTTTGC AGGGCGCAGG CGTCGGTCAG GGTGTGTTC
251 TGCAGGAAGC TCGGATGTC TTCGGGCAAA GCGTAgtCgc gGGCAACGGC
301 GGcaaagcgc ACatcggtTT Gcacggcgtc gagCAGGGtt tggTTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTTCTTCGG CGGTGGCGCG GACGAACTGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451 GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAC
501 CCTTCGCGCC CAAGAGTTTT TGCAACATTT GCGCGGCGgc gTAAGTGAT
551 TCCGTGGCGa ggGTTTTGAc gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggGCGgcgcg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTTCG
651 AAACCTGATG GCGGCGTTGG ATTCGCGGC GTTCGTAATC GACGAATCTG

```

1018

```

701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCAGGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCACGGCG
851 GTTGCAGGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTCGCGAGCG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgC Cgtttttgcg ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCCTGCCAGT ATTTTCGCGGC
1051 GttgACGTAA ATGGTttgtt cgtcgggtata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAT cgCcgcgccg .gaggtTtcgg gttcggtaAc gccccaaacgg
1151 cggcttttcgc ctTTGAAAAA CATGTCCAAA CCTTGTGCGA CTTGCgcttc
1201 gccgcccgaac tCTTGACAGAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

```

g642.pep
1 MRYPPQSAVL QNAARCLLRR PKSACRRICP LSAISAVQYI FADVVOQEGC
51 GVVFVFLLYED KKS GDDFADE DFLQAGVGVQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLVFLVQLN ACFFFFGGGA DELVVNFGIK HIVRAFKNRE
151 GADIDGDIAG WWSAFKTLRA QEFLLQHLRGG VSVFRGEGFD DVRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFNH
251 AVRHADQLQA AADKDVLER AQTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVCFGDEQOV DDFGEFAVFA LFGGNEEVA LRIALPVFRG
351 VDVGLEFVGI FVAGLHFACN RRAGGFGFGN AQTAFAFEN HVQTLCDLRF
401 AEELLQRLQH QRAFDAGTQR NGHAVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

```

m642.seq (partial)
1 GCCTGCCGCC GTATTTGCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
51 CTTTGGCGAT GTCGTTCAGC AGGAAGGCTG CGGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTTC
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTT CTGCAGGAAG CTGCGGATGT
201 CTTACGCAA AGTGTAAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACCTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TGCGCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTGCG CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGGCGCGCG
601 GATTTTCGCG CGTTCGTAAT CGACGAATTT GATGTCGTTG CGGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTTCGCTC TGGGAGAGTT TCATCACGGC GGTTGCAGGC ATTTCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTGGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGCG GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCTGCCAG TATTTTCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGACTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTTC GGTTCGGTAA CACCCAAACC GCCGCCCTCG CCTTTGAAAA
1101 TCATCTCCAA ACCTTGCGCG ACTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

```

m642.pep (partial)
1 ACRRICPLFA ISAVQYIFAD VVQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADVSFQI FKDVFNHNAVR HADQLQAAAD KDVLERAGTG
251 SVALGEFHNG GCRHFGIDAV DGVTGDAQAF GCEGFAADVC FGDEQQVDDF
301 GEFAVFALEF GNEEEVALRV ALPVFRGVDV NGLSVDIFVV GLHFACNRRR
351 GGFVFGNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHQRA FDAGTQRNGH
401 AVMPRNP

```

1019

m642/g642 90.4% identity in 407 aa overlap

m642.pep				10	20	30	
				ACRRICPLPAISAVQYIFADV	VVQEGCGVFVFR	LYED	
g642	MRYPPQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADV	VVQEGCGVFVFL	LYED				
	10	20	30	40	50	60	
m642.pep	40	50	60	70	80	90	
	KESGDDFADKDFLQAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLV	FVQLH					
g642	KKSGDDFADEDFLQAGVGQGVFLQEAADVFRQSVVAGNGGKADIGLH	VEQGLV	FVQLN				
	70	80	90	100	110	120	
m642.pep	100	110	120	130	140	150	
	ACFFFFGGGADKLVNFGIKHIVRAFKNREGADVDS	DIAGGVSAFKTL	RTQEF	LQHL	RG		
g642	ACFFFFGGGADELVNFGIKHIVRAFKNREGADIDG	DIAGVWSAFKTL	RAQEF	LQHL	RG		
	130	140	150	160	170	180	
m642.pep	160	170	180	190	200	210	
	VSVFRGEGFDDVRLHQLMGDGGNRRNGMADVAVK	NLGNLMAAPDFAAF	VIDE	F	VDV	ADV	
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVK	DFGNLMAALDFAAF	VIDES	D	I	V	
	190	200	210	220	230	240	
m642.pep	220	230	240	250	260	270	
	FQIFKDVFNHNAVRHADQLQAAADKDVLERAQ	TGSVALGEFHHGGCRH	FGIDA	V	D	G	
g642	VQVVKDVFNHNAVRHADQLQAAADKDVLERAQ	TGSVAPGEFHHGGCRH	FGIDA	V	D	G	
	250	260	270	280	290	300	
m642.pep	280	290	300	310	320	330	
	QAFGCEGFAADVCFGDEQQVDDFGEFAVFAL	FGNNEEVALR	VALPVFR	G	V	D	
g642	QAFGCEGFAADVCFGDEQQVDDFGEFAVFAL	FGNNEEVALRI	ALPVFR	G	V	D	
	310	320	330	340	350	360	
m642.pep	340	350	360	370	380	390	
	FVVGHLHFACNRRAGGFGFGNTQTAALAFENH	LQTLRDLRFIAE	LQWLQ	HQRA	F	D	
g642	FVAGLHFACNRRAGGFGFGNAQTAALAFENH	VQTLCDLRFIAE	LQWLQ	HQRA	F	D	
	370	380	390	400	410	420	
m642.pep	400						
	NGHAVMPRNP						
g642	NGHAVMPRNPX						
	430						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

```

1 GCCTGCCGCC GTATTTGCC GCTATCCGCA ATATCGGCAG TCCAATATGT
51 CTTTGCGGAT GTCGTTTCAGC AGGAAGGCTG CGGTGTCTTC GTGTTCGCC
101 TGTACGAAGA CAAAGAGTCG GCGATGATT TTGCCGATAA AGACTTTTGT
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTT CTGCAGGAAG CTGCGGATGT
201 CTTCCGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGTT TTGGTTTTTG TCCAACCTCA TGCCTGCTTC
301 TTTTCTTCG CCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTCAAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TGCAGCGCGG CGTAAGTGT TCCGTGGCG AGGGTTTGA
501 CGATGTTTCG CTCCATCAGT TGATGGGCGA CGGTGCAAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTG GAAACCTGAT GGCAGCGCCG
601 GATTTCCGGG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTTCCAGGTT TTCAAGGGTG TATTCATAA TGCCGTGCGT CATGCCGATC

```


1020

```

701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCGAGGC ATTCGCGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTCCGGG CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCGTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```

a642.pep Length: 407
1 ACRRICPLSA ISAVQYVFAD VVQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRAQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVFSQV FKGVFHNAVR HADQLQAAAD KDVLERAQTG
251 SVALGEFHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVAFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFV RLHFSGNRRA
351 GGFGFGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

m642/a642 95.8% identity in 407 aa overlap

```

m642.pep      10      20      30      40      50      60
ACRRICPLSAISAVQYIFADVQEGCGVFVFRLYEDKESGDDFADKDFLQAGAGIGQGVF
|||||
a642          10      20      30      40      50      60
ACRRICPLSAISAVQYVFADVQEGCGVFVFRLYEDKESGDDFADKDFLQAGAGIGQGVF
|||||

m642.pep      70      80      90      100     110     120
LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLNVNFGIKHIV
|||||
a642          70      80      90      100     110     120
LQEAADVFGQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLNVNFGIKHIV
|||||

m642.pep     130     140     150     160     170     180
RAFKNREGADVDSDIAGGVSAFKTLRTQEFQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
|||||
a642         130     140     150     160     170     180
RAFKNREGADVDSDIAGGVSAFKTLRAQEFQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
|||||

m642.pep     190     200     210     220     230     240
RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVFSQIFKDVFNHNAVRHADQLQAAAD
|||||
a642         190     200     210     220     230     240
GRNGMADVAVKNLGNLMAAPDFAAFVIDESDVVADVFSQVFKGVFNHNAVRHADQLQAAAD
|||||

m642.pep     250     260     270     280     290     300
KDVLERAQTG SVALGEFHGGCRHFGIDAVDGVTDGAQAFGCEGFAADVCFGDEQQVDDF
|||||
a642         250     260     270     280     290     300
KDVLERAQTG SVALGEFHGGCRHFGIDAVDGVTDGAQAFGCEGFAADVCFGDEQQVDDF
|||||

m642.pep     310     320     330     340     350     360
GEFAVFALEFGGNEEEVALRV ALPVFRGVDV NGLSVDIFVVG LHFACNRRAGGFGFGNTQT
|||||
a642         310     320     330     340     350     360
GEFAVFALEFGGNEEEVALRV ALPVFRGVDV NGLSVGIFVVR LHFSGNRRAGGFGFGNAXT
|||||

m642.pep     370     380     390     400
AALAFENHLQTLRDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
|||||
a642         370     380     390     400
AALAFENHVQTLCDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
|||||

```

1021

370 380 390 400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2063>:

g643.seq

```

1 ATGGTGTTC CTTTGATGTT GTTGGCGACA ATCAGgTcgg CTACGCTGAc
51 gttgtancGt TTGGcaATGt tGaaCAgggt gtcgccTTCT ACAACGCGGT
101 GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTCCAAACG TGCCCGCGT TtgCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGagatGGTT TCTTCAGCCT GCCGGCGCag gTTGTTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGat
351 GACCTGCGCg aGTGtTCCGG TTTGGGTTTC agacgGCATG GCAGTCTGTT
401 TTTcggTTTg a

```

This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>:

g643.pep

```

1 MVLPLMLLAT IRSATLTLXR LAMLN RVSPS TTRWMLAWSG EVSASPSAAL
51 ATRVSKRARR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFGGMTCA SVAVWVSDGM AVCFSV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2065>:

m643.seq

```

1 ATGGTGTTC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51 GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTCCAAACG TACCCGCGT TTGCCGTCGG CGGCAGCGGT
201 ATGTTGCGGA GATGCGGAAA TTTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGAGATGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAT
351 GATCTGCGCG AGTGTTCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCGGTTTg A

```

This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>:

m643.pep

```

1 MVLPLMLLAT IRSATLTL*R LAMLN RVSPS TTRWMLAWSG EISASPSAAL
51 ATRVSKRTRR LPSAAVCCG DAEILCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGMICA SVAVWVSDGM AVCFSV*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB.

ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from *N. gonorrhoeae*:

m643/g643

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
g643	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEVSASPSAALATRVSKRARR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFWGMICA					
g643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFGGMTCA					
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMVAVCFVSX					
g643	SVAVWVSDGMVAVCFVSX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2067>:

1022

a643.seq
 1 ATGGTGTTC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
 51 GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
 101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTGCCCGTC GGCAGCTTTG
 151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAACGGT
 201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
 251 CGATGACGGC AGAGATGGTT TCTCAGCCT GTCGGCGCAG GTTGTTCGG
 301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
 351 GATCTGCGCG AGTGTTCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
 401 TTTCGGTTTG A

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

a643.pep
 1 MVLPLMLLAT IRSATLTL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL
 51 ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
 101 ATSCMSSSAA CMSFWGTICA SVAVWVSDGM AVCFSV*

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAAL	ATRVSKRTRR				
a643	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAAL	ATRVSKRTRR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAA	CMSFWGMICA				
a643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAA	CMSFWGTICA				
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMVAVCFVSX					
a643	SVAVWVSDGMVAVCFVSX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

g644.seq
 1 ATGCCGCTCG AAAGGccgGC GGATTGTGTC CCGGTGCACT TTGTGGTAAA
 51 GTTTAGAAAA TTAACCTAA ACTGTGGCAG CGGTTTGGAC CGGCCGCCGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAG CCATGGACAC GGCTGCTTTT TTAAGcaca tcgaatCCGC
 201 ATTcCCCCGC ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC
 301 GACAAAAAAG ACGGCGGGCG CAAGGCGAGT CAGTTTGAAA TCCAAGAAGT
 351 CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTG CAGCCTCTGC AAGagttcgg cggcgaagcG
 451 CAAGTCGCAC AAGGTTTGA CATGATTTTC AAagggcga ggcgcggttt
 501 gggcgTtacc gaaccgaAa cctccggcgc gGgaATTGCA CGCGAAAtgc
 551 agtcctgcta cgaatatacc gacgaacaAA CCATTACGT caaCGCCGCG
 601 AAATACTGGC AGGGCAATTC GCAAAGCGAC TTCTcctcg ttgcccga
 651 agagcgcaaa aacGGcaaac tcgccaaagt CATCGACCTG CTGCTCGTCC
 701 CCAAAACATA CATCCGCTGC GAAACCTCG CATCCGAAGG CCTGCGCGCC
 751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
 801 GATGAAATC TCCCGGGGCG ACGCTGCCGG TTGCGCGCG TCCAAAACA
 851 TCTTTATCCG CAGCCGCCGT CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGACAACCT GAACCGATAT GTCCGCAACG ATATCAGATT
 951 CGTCGATTAC GAACGCCGCG AAATCCAACG CCGCCATCAG GTTTCGAAA
 1001 TCCTTTACCG CTACGTCTGC CATTCCGTTT CGcccgtegc GCccgTCGCC
 1051 CATCAATTGA TGGAGGCGAA catcgTCAAA ACcctCGCCA CGGAATACAC
 1101 TTAacgCGCC GCGCAAATGT TGCAAAACT CTGGGGCGCG AAGGGTTTG
 1151 AACGCGGACA CCCAGCCGGC AATATCGCCA TCGATATCCG CCCCTTACG
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATT ACGACCAATT
 1251 CGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATTAAG TTGACAAAA
 1301 accaaaCCCT Gctcgacgcc gtgCAAaccg atGTCcgctt tgCCGCCGTT
 1351 GCCcgcGacT ACGCTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCTGACC GACGCTGCG CCCTGCAAAA AGTCTTCATC GGCAAAATCA

g644.pap

1	MPSPERPADCC	PVHFVVKFRK	LTLCNCRGRD	RPPINGNRQR	KPMIHTEPSA
51	QPSTMDTAAF	LKHIESAFPR	IFSDGIDLMR	YLPDGKWLAL	QAGLLHFFFL
101	DKKHGGRRKS	QEFIGEVLRI	AGHYGVPPVL	RTGIEGALVL	QPLQEGFGEA
151	VQAQGLDMIF	KGESRRLGVT	EPETSGVAIA	REMQSCYEYT	DEQTIYVNAA
201	KYWQGNQSOD	FLLVAAKERK	NGKLAKVIDL	LLVPKTYIRC	ETLASEGLRA
251	VRYAVNSRDA	EMPATAMVKL	SRGEAAGLRA	FQNFIIRSRL	QLIGMTHGIM
301	EYILDNLNRY	VNRDIRFVDY	ERREIQRHRQ	VESEILRYVC	HSVSPVAPVA
351	HQLMEANIVK	TLATEYTYAA	AQMLQKLLGA	KGFERGHYPAG	NIAIDIRPFT
401	IFEGPNMDLY	AEIYDQFVRA	TAEKEAGIKI	LDKNQTLTLD	VQTDVRFRAV
451	ARDYALPDRI	RSFLQHEFTL	DACALQKVF	GKIIARLFVF	VQEEHEDTTA
501	FLLDNRKDI	LDRCYCG*			

m644.seq

1	ATGCCGCTCTG	AAAGGTCGGC	GGATTGTTGC	CCGGCGCACT	TTGTGGTAA
51	GTTTAGAAAA	TCAACTCTAA	ACTGTGGCAG	CGCGTTTGC	CGCGCCGCCA
101	TTAATTGGAA	CCGACAGAGG	AAGCCGATGA	TACACATCGA	ACCGAGCGCG
151	CAGCGCTCAA	CTATGGACAC	GGCTGCTTTT	TTAAAGCACA	TCGAATCCGC
201	ATTCCGCGAG	ATTTTTCAG	ACGGTATCGA	CCTGATGCGA	TACCTGCCCG
251	AAGACAAATG	GCTTGCCTTG	AAGCAGCGCG	GTTTGCTGTT	GCCCTTCTCT
301	GACAAAAAAT	ACGGCGGGCG	CAGGGCAGC	CAGTTTGA	TCCAAGAA
351	CcTGGCGATT	CGCGGGCATT	ACGGCGTGCC	CGTTACGCTG	CGTACCGGCA
401	TCGAAGCGCG	GCTGGTGTG	CAGCCACTGC	AAGAGTTCGG	CGATGAAGCG
451	CAAGTCGGCG	AAGGTTTGA	GATGATTTT	AAGGCGAGG	CGCGCGGTTT
501	GGGTGTACC	GAACCCGAA	CCTCGGGCG	GGCGATTGCA	CGCGAAATGC
551	AGTCTCTACTA	CGAATATATC	GACGAGCAAA	CCATTTACGT	CACCGCCGCG
601	AAATACTAGG	AGGCAACTC	CAGGCGGAC	TTCTCTCTGT	TTGCGCGCAA
651	AGAGCGCAA	AACGGCAAAC	TCGCCAAAGT	CATCGACCTC	CTGCTCGTCC
701	CCAAAACATA	CATCCGCTGC	GAAACCCCTG	CATCCGAAGG	CTTGCGCGCC
751	GTCGGTTACG	CCGTCAACCG	CATCGATGCC	GAAATGCGTG	CAACCCCGGT
801	GATGAAACTC	TCCCAGAGCG	ACGCTGCCGG	TTTGCGCGCG	TTCCAAAACA
851	TCTTTATCCG	CAGCGCCCTG	CAGATGATCG	CGATGACGCA	CGGCATTATG
901	GAATACATCT	TGAAAAATCT	GGAACGATAC	GTCGCCAAGC	ACATCAAA
951	CGTCGATTAC	GAACGCCGCG	AAATCCGGCG	CCGCCATCAG	GTTTCCGAGA
1001	TTCTTTACCG	CTACGCTGCG	CATTCCGTTT	CGCCTGTTTG	CCCGGTCGCC
1051	CATCAGCTGA	TGGAGGCGAA	CATCGTCAAA	ACCCCTGCCCA	CGCAATACAC
1101	TTACGCGGCC	CGCAAAATGT	TGCAAAAAC	CTTGGGTGCG	AAGGGTTTTG
1151	AACGCGGACA	CACCGCCGCG	AATATCGCTA	TCGACATCCG	CCCCCTCACG
1201	ATTTTGTGA	GCCCGAACGA	TATGCTTTAT	GCGGAAATTT	ACGACCAGTT
1251	TGTCCGCGCC	ACGGCCGAAG	AAAAAGAAC	AGCCATGAAG	TTGGACAAAA
1301	ACCAAACCTT	GCTCGACCGC	CTGCAAACTC	ATGCCCGCTT	TGCCGCGGTC
1351	GCCCGCGACT	ACACTTTGCC	TGAAGACATC	CGCAGCTTTC	TGCAGAACCA
1401	CACCTGACC	GATGCTGGC	CCCTGCAAAA	AGCTTTTATC	TGC AAAATCA
1451	TCGCCCCACT	CTTTGTCTTC	GTACAGCGCA	AACACGAAGA	CACCGCAGCC
1501	TTCTGTCTGA	ACGACATCCG	CAAAGATATA	TTGGAAGTCC	GATATTGCGG
1551	GTAG				

m644.p0p

1	MPERSADCC	PAHFVVKFRK	STLNCGRFRD	RPPINGNRQR	KPMIHTEPSA
51	QPSTMDTAAF	LKHEISAFRR	IFSDGIDLMR	YLPEDKWLAL	KQAGLLHFPF
101	DKKYQGRGKS	QFIEQEVLR	AGHYGVPTVL	RTGIEGALVL	QPLQEFGEDE
151	QVAQGLEMIF	KGEGGGLGVT	EPETSGAIA	REMQSYEYI	DGQTYIVNAA
201	KYWQGNSQSD	FLVAAKERK	NGKLAKVIDL	LLVPRTYIRC	ETLASEGLRA
251	VRVYANRIDA	EMPATAVMKL	QSQDAAGLRA	FQNIIFRSRL	QLIGMTHGIM
301	EYILENLERY	VRNDKIFVDY	ERREIARRHQ	VSEILRYRYC	HSVSPVAPVA
351	HQLMEANIVK	TLATEYTYAA	AQMLQKLLGA	KGFERGH TAG	NIAIDIRPFT
401	IFEGPNMLPY	AEIYDQFVRA	TAEKEAGMK	LDKNQTLDDR	LQTDARFAAV
451	ARDYTLDPED	RSFLQCHTTL	DACALQKVFI	GKIIARLFVF	VQAKHEDTAA
501	FLLDNRDKDI	LDRCRYG*			

10 20 30 40 50 60
 m644.pep MPSERSADCCPAHFVVKFRKSTLNCGRREFDRPPINGNRQRKPMIHTEPSAQPSTMDTAA
 |||||
 α644 MPSERPADCCPVHFVVKFRKLTLCGRREFDRPPINGNRQRKPMIHTEPSAQPSTMDTAA

1024

	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLPFLDKKYGGRKGSQFEIQEVLRI					
g644	70	80	90	100	110	120
	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLPFLDKKHGGRKGSQFEIQEVLRI					
m644.pep	130	140	150	160	170	180
	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQVAQGLEMIKFGEGGGLGVTEPETSGAAIA					
g644	130	140	150	160	170	180
	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQVAQGLDMIKFGESRRGLGVTEPETSGAAIA					
m644.pep	190	200	210	220	230	240
	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLLVPKTYIRC					
g644	190	200	210	220	230	240
	REMQSCYEYTDQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLLVPKTYIRC					
m644.pep	250	260	270	280	290	300
	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
g644	250	260	270	280	290	300
	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSRGDAAGLRAFQNI FIRSRLQLIGMTHGIM					
m644.pep	310	320	330	340	350	360
	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLM EANIVK					
g644	310	320	330	340	350	360
	EYILDNLNRYVRNDIRFVDYERREIQRRHQVSEILYRYVCHSVSPVAPVAHQLM EANIVK					
m644.pep	370	380	390	400	410	420
	TLATEYTYAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
g644	370	380	390	400	410	420
	TLATEYTYAAQMLQKLLGAKGFERGHPAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
m644.pep	430	440	450	460	470	480
	TAEKEAGMKLDKNQTL LDR LQTDARFAAVARDYTL PEDIRSFLQEH L TDACALQKVFI					
g644	430	440	450	460	470	480
	TAEKEAGIKLDKNQTL L DAVQT D VRF AAVARDYAL PEDIRSFLQEH L TDACALQKVFI					
m644.pep	490	500	510			
	GKIIARLFVVFQAKHEDTAAFL LNDIRKDILD CRYCGX					
g644	490	500	510			
	GKIIARLFVVFQEEHEDTAAFL LNDIRKDILD CRYCGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

a644.seq

```

1  ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCTTG AAGCAGGCGG GTTGCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNN
401 NNGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCCG CGATGAAGCG
451 CAAATCGCAC AGGGTTTGGA CATGGTTTTC AAAGGCGAGG GCGGCGGTTT
501 AGGCGTTACC GAACCCGAAA CCTCCGGCGC GCGGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTACGT CAACGCCGCG
601 AAATACTGCG AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCGCCAA
651 AGAGCGCAAA AACGGCAAAC TCGCCAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAACTC TCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA

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1025

```

851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTTG
1151 AACCGGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
1251 TGTCGCGGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCGACT CTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```

a644.pep
1 MPERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51 QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAIA REMQSYEYET DGQTIYVNA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI FISR LQLIGMTHGIM
301 EYTLENLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAV
451 ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFV VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

```

m644/a644 97.3% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
a644	MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGRKGSQFEIQEVLRI					
a644	LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	130	140	150	160	170	180
	AGHYGVPVTLRTGIEGALVLQPLQEFGDEAQVAQGLEMIFKGGGGGLGVTEPETSGAIA					
a644	AGHYGVPVXXXXXEGALVLQPLQEFGDEAQIAQGLDMVFKGGGGGLGVTEPETSGAIA					
	130	140	150	160	170	180
m644.pep	190	200	210	220	230	240
	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
a644	REMQSYEYTDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	250	260	270	280	290	300
	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FISR LQLIGMTHGIM					
a644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FISR LQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	310	320	330	340	350	360
	EYILENLERIVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					
a644	EYILENLERIVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					

1026

	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a644						
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 . pep	TAEKEAGMKLDKNQTLDRLOTDAFPAVARDYTLPEDIRSFLQEHTLTDACALQKVFI					
a644						
	430	440	450	460	470	480
	490	500	510			
m644 . pep	GKIIARLFVVFQAKHEDTAAFLNDIRKDILDCRYCGX					
a644						
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645 . seq

```

1  ATGATGATGG TGTGGCGTT GGGGATGTCG ATGCCGGTT CGATGATGGT
51  GGAACAGAGC AACACATTGA ATCTTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCAGCG AGTTGTCCGT GCGCCACGCC GATACGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAata CCTGTCTCC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTCACG
301 GCGAGGCGGC GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CGCGCAGACC
351 TTCGAGCGCC ATGCTGAGGG TCGCGGAAT CGGCGTGGCG GTCATGGTTA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTGA GCTGCTCTT CTGTCGCACG
451 CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
551 CGTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGC GCG TGTGCTCGA CCAGAAGCGT GGTGCGGCGC AGTACGCGCA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGAAG GCGGACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGcgcgcat ggcggcggc TGGTCTTCGG
851 TTTCTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

m645 . pep

```

1  MMMVLALGMS MPVSMMEQS NTLNLCKKS RMTSSSSRSR SCPCATPIRA
51  SGRSVSSRSR IFSIVSTSLC RNKTCPPRLS SRNTASRTLP SLNGLTKVFT
101 ARRLGAVVI SEKSRPPSSA MLVRGIGVA VMVRMSTLAR RRLSCSFCRT
151 PKRCSIIIN KPKFLNFMSS CTNLCVPITI STVPSAMPSS VALVALLLLK
201 RERLATFTGK SAKRSKAFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT SRSIGFACVK SLITAAMAAA WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645 . seq

```

1  ATGATGATGG TGTGGCGTT GGGGATATCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAATA CCTGTCTCC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTAAAGG GTTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC GGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAACGCC ATACTTAAAG TACGCGGAAT CGGCGTGGCG GTCATGGTAA
401 GGATATCAAC ATTGGCGCGC AGGCGTTGA GCTGCTCTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTTGAATTT
501 GATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGC GCG TGTGCTCGA CCAAAAGCGT GGTGCGAGCA AGTACGCGCA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGGCGATCCA TCGGCTTCGC
801 TTGCGTCAAA TCTTTAATCA CGGCGCGCAT GCGGCGGCC TGGTCTTCGG

```

1027

851 TTTCTTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:

m645.pep
 1 MMVLALGIS IPVSMVEQS NTLNRCKKS RMTCSSRSR SCPCATPMRA
 51 SGSRVSSSR IFSIVSTSLC RKNTCPPLRS SRNTASRTLP SLKGLTKVLT
 101 ARRRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
 151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
 201 RERLATFTGK SAKRSKAFCA CCSTKSUVGA STATCLPPIT ATNAARRATS
 251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMVLALGISIPVSMVEQSNLNRCKKSRMTCSSRSRSCPCATPMRASGSRVSSSR					
g645	MMVLALGMSMPVSMVEQSNLNLCKKSRMTCSSRSRSCPCATPIRASGSRVSSSR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCPPLSSRNTASRTLPSLTKGLTKVLTARRRLGAVVISEKSRSPSNA					
g645	IFSIVSTSLCRKNTCPPLSSRNTASRTLPSLNLGLTKVLTARRRLGAVVISEKSRSPSSA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRISTLARRLSCSFRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI					
g645	MLRVRGIGVAVMVRISTLARRLSCSFRTPKRCSSSIINKPKFLNLMSSCTNLCPITI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALLLKRRERLATFTGKSAKRSKAFCAACCSTKSUVGASTATCLPPIT					
g645	STVPSAMPSSVALVALLLKRRERLATFTGKSAKRSKAFCAACCSTRSVVGASTATCLPPIT					
	190	200	210	220	230	240
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPTSPHTRRSIGFACVKSLLITAAMAAWSSVSSX					
g645	ATNAARRATSVLPKPTSPHTRRSIGFACVKSLLITAAMAAWSSVSSX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq
 1 ATGATGATGG TGTGGCGTT GGGAAATGTCG ATACCGGTTT CGATGATGGT
 51 GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAGTTCG CGCATGACTT
 101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
 151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
 201 TTCATTGTGC AGGAAAAATA CTGCCC GCCGCTTTGAGT TCGCGCAATA
 251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTGACAAA GGTTTTGACG
 301 GCGAGGCGGC GGCTGGGCGC AGTGGAATC AGCGAGAAGT CGCGCAGTCC
 351 TTCCAGCGCC ATAATTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
 401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
 451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
 501 TATGTCGTCC TGCACCAAGT TGTGCGTACC GATAACAATA TCGACCGTGC
 551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
 601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAGC GGTGCGCAAA
 651 ATTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTGCGTGGC AGTACGGCAA
 701 CTTGTTTGCC ACCCATTACC GCCACAAACG CGGCGCGCAG GCGCACTTCG
 751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
 801 CTGCGTCAA TCTTAATCA CGGCGCGCAT GCGGCTGCC TGGTCTTCGC
 851 TTTCTTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

a645.pep
 1 MMVLALGMS IPVSMVEQS NTLNRCKKS RMTCSSRSR SCPCATPMRA

1028

```

51  SGRVSSRSR MFSMVSTSLC RKNTCPPLRS SRNTASRTL P SLNGLTKVLT
101 ARRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSAKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/a645 96.9% identity in 286 aa overlap

```

              10      20      30      40      50      60
m645.pep      MMMVLALGISIPVSMVSEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGRVSSRSR
a645          MMMVLALGMSIPVSMVSEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGRVSSRSR
              10      20      30      40      50      60

              70      80      90      100     110     120
m645.pep      IFSIVSTSLCRKNTCPPLRSSRNTASRTLPSLKGLTKVLTARRRLGAVVISEKSRSPSNA
a645          MFSMVSTSLCRKNTCPPLRSSRNTASRTLPSLNGLTKVLTARRRLGAVVISEKSRSPSSA
              70      80      90      100     110     120

              130     140     150     160     170     180
m645.pep      ILKVRGIGVAVMVRISTLARRRLSCSFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
a645          ILKVRGIGVAVMVRMSTLARRRLSCSFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI
              130     140     150     160     170     180

              190     200     210     220     230     240
m645.pep      STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTKSVVGASTATCLPPIT
a645          STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTRSVVGASTATCLPPIT
              190     200     210     220     230     240

              250     260     270     280
m645.pep      ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
a645          ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
              250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

```

g647.seq
1  ATGCAAAGGC TCGCCGCGAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGACGCT
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAGTAGCGT AGTTGATGAC ACCGATGCCG
251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

```

g647.pep
1  MQRLAADGIQ IFFVGVDGQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
51 GFKGTVGQTE RGTVAVADTV FRQIVGVVDD TDAERTAVHS RGTRGFYRIS
101 LII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

```

m647.seq
1  ATGCAAAGGC TCGCCGCGAGA CGGCATCCAA ATCTTTTTTG TAAGTGTGCA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

```

m647.pep
1  MQRLAADGIQ IFFVSVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

```

	10	20	30	40	50	60		
m647 . pep	MQR	LAADGIQ	IFFVSVDGQ	FALRINGLV	KERARTVF	FGKVCRCFEQ	VILYGFKGT	VGQT
g647	MQR	LAADGIQ	IFFVSVDGQ	FALRINGLV	KERARSVF	FGKVCRCFEQ	VILYGFKGT	VGQT
	10	20	30	40	50	60		
	70	80	90	100				
m647 . pep	RGT	VAVADTV	FRQII	SVNHADA	ERTA	AHSRGR	TGFRYIS	RLIIX
g647	RGT	VAVADTV	FRQIV	GVVDDT	DAERT	AVHSRGR	TGFRYIS	RLIIX
	70	80	90	100				

```
a647.seq
1 GTGCAAAGGC TCGTTACACA CAGCGTCCAA GTCTTTTTTG TAGGTGTCTGA
51 TGGGCAGTTT GCCTTGCAGG TAAACGGTCT GGTTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAAGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCGCTGTAGC
201 GGACACCGTT TTTCCGCAAA TAATACGCAT AGTTGATCAC GCCGATACCG
251 AGCGAACGGG GGCCCATAGT GGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA
```

a647.pep
1 VQRLVTHSVQ VFFVGVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
51 GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAAS GGTRGFYRIS
101 LII*

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
a647	VQRLVTHSVQVFFVGVDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTVAVADTVFRQIISIVNHADAERTAHSRGTRGFYRISLIIX					
a647	RGAVAVADTVFRQIIRIVDHADTERTAHSGGTRGFYRISLIIX					
	70	80	90	100		

g648.sog

1	ATGAACAGGC	GCAACGCGCG	GATCGAACGG	GCTGTGCGTA	TTGCAGTGAT
51	CGAGCTTTTG	AATGTAGATG	CGCCCGGTCC	CGGCACGCTC	CTGCATCAGC
101	GTGGAAACA	GATCGGCAGC	CGGAATGATA	CGCTTGCGTA	TGTTCCGGTC
151	TTGCTCGTAT	TTCGTATAGA	GCCGCTCAAA	TTCTGCTTTG	TCGGCAAAAA
201	ACGCTTTCGT	CAACCCCGAA	ACCTCGTTGG	CGGAAAAACG	CGTAATGTTG
251	CGGCCCTTAA	TCAGCGGGGT	GTACAGCAGG	CGGTGTGATT	GACAGCCATA
301	ATCAAGCTGG	CGGATACGGT	TGCTCTCCAC	GCCCCGGTTG	TTTTTCAACA
351	CCAGCAGGCT	TTCCGGCTTCA	ATATGCCACA	AGGGGTAGAA	CAGGGTTGCC
401	GCGCCGCGCG	GCACGCCACC	TTGGCAACA	GATTTGACCG	CCGGCTGAAA
451	CATCTTAAAG	AAGGGAATGC	AGCCGGTATG	CCGGGCTTCA	CCGCCCCGGA
501	TTTCGCTGTC	CAGCCCGCGG	ATACGTCGCG	CATTGATGCC	GATGCCCGCG
551	CGTTGGGAAA	CGTATTTTCA	CAATCGCGCT	GTAGTGGCAT	TGATGGAATC
601	CAAACTATCG	TCGCATTCAA	TCAGCACACA	GCTTTGA	

g648 . pep

1030

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1  MNRNRNARIEK AVRIAVIDVL NVDPAPGGTL LHQRGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAALNQAG VQQAVDLHAI
101 IKLADTVVFH APVVFQHQQA FGFNMPQGV E QGCRAAAHAT LRTFRDRRLK
151 HLKEGNAAG FGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

m648.seq

1	ATGAACAGGC	CGCAGCGCG	GATCGAACGG	GCTGTGCGTA	TTGCAGTGAT
51	CGACGCTTTTG	AATGTAGATG	CGCCGGTTG	CGGCACGCTG	CTGCATCAGG
101	TGGGAAAAAC	GGTCCGCGAG	CGGATCGATC	CGTTGCGCGA	TATCAGGCTG
151	TTGCTCGTAT	TTCGTATAGA	GCCGCTCAAA	TTCGTCTTGG	TCGGCAAAAA
201	ACGCTTCGTA	CAATCCCGGA	ACCTCGTTGG	CGCAAAACATG	CGTAATTTGT
251	CCGCCCTTAA	TCAGGCGGGT	GCACAGCAGG	CGGTTGATTG	GCACGCCGTA
301	ATCAAGCTGA	CGGATACGGT	TGCTTCCAC	ACCGCGTTG	TTTTTCAACA
351	CCAGCGCGCT	TTCGGCTTCG	ATATGCCACA	AGGGGTAGAA	CAAGGTTGCC
401	CGCGCCGGCT	GCACGCCCGC	TTGCGAACAG	GATTTGACCG	CCGCTTGAAA
451	CATTTTAAAG	AAGGGAATGC	AGCCGGATG	CGCGCCTTCG	CGCGCCCGAA
501	TTTCGCTGTC	CAAACCTCCG	ATACGTCGG	CATTGATGCC	GATGCCCGCA
551	CGCTGGGAAA	CGTATTTGCA	AATCGCGCTG	GTAGTGGCAT	TGATGGAATC
601	CAAACTATCG	TCCGATTTCA	TCAGCACACA	GCTTGA	

This corresponds to the amino acid sequence <SEO ID 2090; ORF 648>:

m648.pgp

```

1  MNRRDARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
51  LLVERIEPLK FVLVGKRFV QSRNLVGRKQ RNVAAALNQG VQQAVDLHVA
101 IKLTDTVVFH TAVFVQHQQA FGFDMPOGVE QGCRAAAHAA LRTGFDRRLK
151 HFKEGNAQMT PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201 QIVAFNAQHT A*

```

m648/g648 91.5% identity in 211 aa overlap

	10	20	30	40	50	60
m648 . pep	MNRRDARIERAVRIAVIDVLNVDPAGSGTLLHQRGKQVGS	RNDALADIRVLLVFRIEPLK				
g648	MNRRNARIERAVRIAVIDVLNVDPAGPGTLLHQRGKQVGS	RNDTLAYVRVLLVFRIEPLK				
	10	20	30	40	50	60
m648 . pep	70	80	90	100	110	120
	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQA	VDLHAVIKLTDTVVFHTAVVFQHQQA				
g648	FVLVGKKRFVQPRNLVGRKQRNVAALNQAGVQQA	VDLHAIKLDATVVFHAPVVFQHQQA				
	70	80	90	100	110	120
m648 . pep	130	140	150	160	170	180
	FGFDMPPQGVQGCRAAAHAALRTGFDRRLKHFKEGNAAGMP	RFAAPDFAVQTADTSGIDA				
g648	FGFNPPQGVQGCRAAAHAALRTGFDRRLKHLKEGNAAGMP	GFAPDFAVQPADTSGIDA				
	130	140	150	160	170	180
m648 . pep	190	200	210			
	DARTLGNVFHNRRAGSGIDGIQTIVAFNQHTAX					
g648	DARALGNVFHNRRAGSGIDGIQTIVAFNQHTAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

a648.seq

1	ATGAACAGGC	GCAACGCGCG	GATCGAACGG	GCTGTGCGTA	TTGCAGTGAT
51	CGACGTTTGT	AATGTAGATG	CGCCCGGTTT	CGGCACGCTC	CTGCATCAGC
101	GTGGAAAAACA	GGTCGGCAGC	CGGAATGATG	CGCTTGCCTA	TATCAGGGTC
151	TTGCTCGTAT	TTCTATAGA	CGCGCTCAAA	TTCTGCTTTG	TCGGCAAAAA
201	ACGCTTCGTA	CAATCCCGGA	ACCTCGTTGG	CGGAAAAACG	CCTAATGTTG
251	CCGCCCTTAA	TCAGGCGGGT	GTACAGCAGG	CGGTTGATTT	GCACGCCGTA
301	ATCAAGCTGA	CGGATACGGT	TGTTTCCAC	GCCCGGTTG	TTTTTCAACA
351	CCAGCAGGCT	TTCCGGTTCG	ATATGCCACA	AGGGGTAGAA	CAAGGTTGCC
401	GCGCGCCCGC	GTCAGCCACC	TTGCCAACAG	GATTTGACTG	CCGCCTGAAA
451	CATTTTAAAG	AAGGGAATGC	AGCCGGTATG	CCGTGCTTCG	CGCCCCCGGA

1031

501 TTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCA
 551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
 601 CAGGCTGTCTG TCGCATTCTGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648.pep
 1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
 101 IKLTDTVVFH APVVFQHQQA FGFDMPOGVE QGCRAAAHAT LRTGDCRLK
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
 201 QAVVAFDQYA A*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
a648	:					
	10	20	30	40	50	60
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
a648						
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
a648						
	70	80	90	100	110	120
m648.pep	FGFDMPOGVEQGCRAAAHAALRTGFDRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
a648						
	130	140	150	160	170	180
m648.pep	FGFDMPOGVEQGCRAAAHAALRTGFDRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
a648						
	130	140	150	160	170	180
m648.pep	DARTLGNVFHNRAAGSGIDGIQTIVAFNQHTAX					
a648						
	190	200	210			
m648.pep	DARTLGNVFHNRAAGSGIDGIQTIVAFNQHTAX					
a648						
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGACTGGTAT CAACAACCTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAA CATATCAGCA
 101 AGGCAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCAGGAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGCACCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGCGCTTAT GAGGCTTCG ATGATTTCGA CCGCGGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

g649.pep
 1 M~~LA~~ILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECRKYLER
 51 RAAWYRSQGN VQELRENKKA RKAFTLPEYA EQKIQCRAAY EAFDDFDGGR
 101 FRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACCTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAA CATATCCGCA
 101 AGGCAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCAGGAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGCGCTTAT GAGGCTTCG ATGATTTCGA CCGCGGCAGT
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

1 MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
 51 RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCAAAY EAFDDFDGGS
 101 FRR*

m649/g649 96.1% identity in 103 aa overlap

	10	20	30	40	50	60
m649.pep	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN					
g649	MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERRAAWYRSQGN					
	10	20	30	40	50	60
	70	80	90	100		
m649.pep	VQELRENKKARKAFRSLPYAEQKIQCAAAYEAFDDFDGGSFRRX					
g649	VQELRENKKARKAFRTLPHYAEQKIQCAAAYEAFDDFDGGRFRRX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

a649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATATG GGA CTGGTAT CGACAAC TGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAA CATATCCGCA
 101 AGGCAAACAA GCAGATGCTG CACCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
 251 CCAATGCCG GCGGCTTAT GAGGCTTCG ATGATTTCA CGGCAGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:

a649.pep
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
 51 RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQKTQCAAAY EAFDDFDGSR
 101 FRR*

m649/a649 96.1% identity in 103 aa overlap

	10	20	30	40	50	60
m649.pep	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN					
a649	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN					
	10	20	30	40	50	60
	70	80	90	100		
m649.pep	VQELRENKKARKAFRSLPYAEQKIQCAAAYEAFDDFDGGSFRRX					
a649	VQELRENKKARKAFRSLPYKEQKTQCAAAYEAFDDFDGSRFRRX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

g650.seq
 1 ATGTCCAAAC TCAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
 51 TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
 101 CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
 151 TATTTCCAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
 201 GGGCGAAGTC AATCCGAAC TGGTACGCC CCACGAAAGC AAATTCATCG
 251 CAAGCCGAG CTATTTCGAC AGGGTCGTCA ACCGGAGCCG ACCCTATATG
 301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCCG
 351 CCGTCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
 401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
 451 GGCTTGAAA AAACaccgGT TTACGacggc aggcacGacg TTtacgcaGc
 501 taccgatgcc gcactCAACT AtctGcaATA TCTCTatggA CTGTTGCGCG
 551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
 601 CCGGCCGTC ACGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
 651 CCTGCGTATG CCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
 701 TCGCAACAT TATTGCCACC CCCCAATCTT TCGGCATGAA TATCAGCGAC

1033

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751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTGAATCC TGCATTCAAC GTCCCGCGct tcatCCCCAA AAaacaacgc
901 aaactGCTGC TTCCTGTGCG GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCTGTTT CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGCcggcag gcaCGGTGAA CGTCAGCATT gccGaatcc aacCCgccgc
1251 cgcaCAGACA gcggaacatta ccgtcgacc ttgcccga gaaaccgtcc
1301 gtacgggaac ccgatccctt tgtccgcaTt accgaacccg ccctTGCAGC
1351 AGCCGCAGCG CaacctCAA cgcAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

```

g650.pep
1 MSKLKTIALT ASGLSVC PGF LYAQTSSHQ VGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWDE LRQGFMRGEV NPFLVRRHES KFIASRSYFD RVVNRSRPYM
101 YHIANEVKKR NMPAEAAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNLLNG NLVNAGRSIL VAKNGKTLHT ASESUVSIDI DNTPD TYRSN
401 MPAGTVNVSI ARIQPAQAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

```

m650.seq
1 ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGGCGAG CTGGGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
451 GGCCTGGAAA AAACACCGGT TTACGACGGC AGGCACGACG TTTACGCCCG
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGCG
551 ACTGGCCGCT TGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCCAAG CTGCTCGCGG
701 TGCGCAACAT TATTGCCACT CCCCATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCTAAACCC CGCATTC AAC GTCCCCGCT TTATCCCCAA AAGCAAACGC
901 AAATGCTGCT TTCCTGTGCG GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTT CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTGCGCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCTT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

```

m650.pep
1 MSKLKTIALT ASGLSVC PGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWGE LRQGFMRGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNLLNG NLVNAGRSIL VAKNGKTLQT ASESUVSIDI DNTPD TYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTPCPD
451 SRSATSNRKT DRHAV*

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m650/g650 96.1% identity in 465 aa overlap

1034

m650.pep	10	20	30	40	50	60
	MSKLTIALTASGLSVC PGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	MSKLTIALTASGLSVC PGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWDE					
	10	20	30	40	50	60
m650.pep	70	80	90	100	110	120
	LRQGRFMGEVNP ELVRRHESKF IASHSYFN RVINRSR PYMYH IAN EVKKRNMPAE AALLP					
g650	LRQGRFMGEVNP ELVRRHESKF IASRSYFDRV VNRSR PYMYH IAN EVKKRNMPAE AALLP					
	70	80	90	100	110	120
m650.pep	130	140	150	160	170	180
	FIESAFVTKAKSHV GASGLWQF MPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTKAKSHV GASGLWQF MPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	190	200	210	220	230	240
	LFGDWPLAFAAYNW GEGNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
g650	LFGDWPLAFAAYNW GEGNVGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
	190	200	210	220	230	240
m650.pep	250	260	270	280	290	300
	PQSFGMNISDIDNKP YFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	PQSFGMNISDIDNKP YFQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
	250	260	270	280	290	300
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLN AAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLN AAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPD TYRSNMPAGTVNVGIARIRPAAQQT					
g650	NLVNAGRSILVAKNGKTLHTASESVVSIDIDNTPD TYRSNMPAGTVNVSIARIQPAQAQT					
	370	380	390	400	410	420
m650.pep	430	440	450	460		
	ADITVAPLPQKTVRTXTRSPCPYCR TCPCDSRSATS NRKTD RHA V X					
g650	ADITVAPLPQETVRTGTRSPCPHYRTRPCDSRSATS NRKTD CHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

```

a650.seq
1  ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCGTCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATACGCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGAGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGTACCGG CAGGCATTAC
451 GGCCTGGA AAACACCGGT TTACGACGGC AGGCACGACA TTTACGCCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTTCCCAAG CTGCTCGCCG
701 TGCGCAACAT CATTGCCGCC CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCGTATTT TCAGGCAGTC GAACCGGACC GTCCGTCGGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCGCGT TCATCCCCAA AAGCAAACGC

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1035

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901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CTTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAA CCGAAAAACA GACCGCCATG CCGTCTGA

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This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

```

a650.pep
1  MSKLKTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWSE LRQGRMGEV NPVLRRHES KFIASHSYFN RVINRSRPMY
101 YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDIIAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGNVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAA PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTNYSRN
401 MPAGTVNVGI ARIRPAAQQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

m650/a650 99.1% identity in 465 aa overlap

m650.pep      10      20      30      40      50      60
MSKLKTIALTASGLSVCPGFLYAQTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE
|||||
a650          10      20      30      40      50      60
MSKLKTIALTASGLSVCPGFLYAQTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWSE

m650.pep      70      80      90      100     110     120
LRQGRMGEVNPVLRRHESKFIASHSYFN RVINRSRPMYHIANEVKKRNMPAEALLP
|||||
a650          70      80      90      100     110     120
LRQGRMGEVNPVLRRHESKFIASHSYFN RVINRSRPMYHIANEVKKRNMPAEALLP

m650.pep      130     140     150     160     170     180
FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG
|||||
a650          130     140     150     160     170     180
FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDIIAATDAALNYLQYLYG

m650.pep      190     200     210     220     230     240
LFGDWPLAFAAYNWEGNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT
|||||
a650          190     200     210     220     230     240
LFGDWPLAFAAYNWEGNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAA

m650.pep      250     260     270     280     290     300
PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
|||||
a650          250     260     270     280     290     300
PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR

m650.pep      310     320     330     340     350     360
KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
|||||
a650          310     320     330     340     350     360
KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG

m650.pep      370     380     390     400     410     420
NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTNYSRNMPAGTVNVGIARIRPAAQQT
|||||
a650          370     380     390     400     410     420
NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTNYSRNMPAGTVNVGIARIRPAAQQT

```


1036

	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDHRAVX					
a650	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDHRAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

g652.seq

```

1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCGCG CTACAAGGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATACTTGGA GGTGTTGGTTA
551 ACGAATTCCC GATTATTTC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATTG GGCAAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTCTGTA CCAATCCGAA AATCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCTGAAAGC cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCACcgc cggCGAAAC CGAAGACAGT Accattgccg
851 ATTGGGAGT CGCCACCAAC TGTATGCAGA TTAACcgg TTCTTTGAGc
901 cgtTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCgcctACT ACCCGGCGAA AGCCGCATTC TACCAACTGG
1001 GCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

g652.pep

```

1  MIELDGTENK GNIGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNLSNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKD GK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
201 EGWKKLLTEKL GKVKQLVGDD LFTVNPRIKA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAKYNQ LLRIEELAE AAYYPGKAAF YQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

m652.seq

```

1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GACTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCGCG CTACAAGGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAACTG GGCGGTAGAG TTCAATTGGT
651 TGCGGACGAC TTGTTCTGTA CCAATCCAAA AATCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCTGAAAGC CGTCTGACTT GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAa CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCGGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

m652.pep

```

1  MIELDGTENK GNIGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNLSNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC

```

1037

```

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFPIIS IEDGMDENDW
201 EGWKLLETKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAIDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGK*

```

m652/g652 98.2% identity in 335 aa overlap

```

          10      20      30      40      50      60
m652.pep  MIELDGTENKGNLGANATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
          |||||
g652      MIELDGTENKGNLGANATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
          10      20      30      40      50      60

          70      80      90     100     110     120
m652.pep  EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
          |||||
g652      EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
          70      80      90     100     110     120

          130     140     150     160     170     180
m652.pep  SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
          |||||
g652      SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
          130     140     150     160     170     180

          190     200     210     220     230     240
m652.pep  GLVNEFFPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
          |||||
g652      GLVNEFFPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
          190     200     210     220     230     240

          250     260     270     280     290     300
m652.pep  LLVKVNQIGTLSETLKAIDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
          |||||
g652      LLVKVNQIGTLSETLKAIDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
          250     260     270     280     290     300

          310     320     330
m652.pep  RSDRMAYNQLLRIEELAEAAADYPSKAAFYQLGKX
          |||||
g652      RSDRMAYNQLLRIEELAEAAAYYPGKAAFYQLGKX
          310     320     330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

```

a652.seq
1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGCGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCGCG CTACAAAGCG GCGGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GGATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGGCAAG TCCAACCTGT
651 TGCGCAGCAG CTCTTCGTTA CCAACCCGAA AATCCTTGCC GAAGGCATTG
701 AAAAAGGCGT GGCAACGCA CTATTGGTCA AAGTCAACCA AATCGGTACT
751 TTGAGTGAAA CCTGAAAGC CGTCGACTTA GCCAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCGGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

```

a652.pep
1  MIELDGTENK GNLGANATLA VSMVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC

```

1038

151 ASSEFYKD GK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
 201 EGWKLLETKL GSKVQLVGDD LFTNPKILA EGIEKGVANA LLVKVNQIGT
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
 301 RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGK*

m652/a652 99.7% identity in 335 aa overlap

m652.pep	10	20	30	40	50	60
	MIELDGTENKGNLGANATLAVSMVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
a652	MIELDGTENKGNLGANATLAVSMVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
m652.pep	70	80	90	100	110	120
	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDSKGFPPTVGDEGGFAPNLN					
a652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDSKGFPPTVGDEGGFAPNLN					
	70	80	90	100	110	120
m652.pep	130	140	150	160	170	180
	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGYHLEAEGRSYTNAEFAEYLE					
a652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
m652.pep	190	200	210	220	230	240
	GLVNEFFIISIEDGMDENDWEGWKLLETKLGGVQLVGDDLFVTNPKILAEGIEKGVANA					
a652	GLVNEFFIISIEDGMDENDWEGWKLLETKLGGVQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
m652.pep	250	260	270	280	290	300
	LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
a652	LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
	250	260	270	280	290	300
m652.pep	310	320	330			
	RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGKX					
a652	RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACCA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GTGCGGCCGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
151 CTTCCGCGAC GCGACAAATC CCGCTATTCC GGCAAAGGCG TATTGAAGGC
201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAACAAAG GCAATTTGGG TCGCAATGCG ACTTTGGCGG TCTCTATGGC
351 GGTTCACGCG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGGCGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCGAAAAT CTTTCGCGA AGCGTTGCGC TGCGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGTAAAGG CTTCCCGACC
601 ACAGTCGCGC ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AAGCGGCCGA AGCCGCCGGC TACAAGGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGCTCTACA CCAACGCGGA
801 ATTTGCCGAA TACTTGGAAG GCTTGGTTAA CGAATTCCTG ATTATTTCCT
851 TTGAAGACGG GATGGACGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAATTGG GCAAAAAAGT TCAATTGGTC GCGGACGACT TGTTCTGTAAC
951 CAATCCGAAA ATTCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1051 GTCGATCTGG CAAAATGCAA CCGCTACGCC AGCGTGATGA GCCACCGCTC
1101 CGCGGAAACC GAAGACAGTA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT TAAACCCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCTACTA
1251 CCCCAGCAA GCCGCATTCT ACCAAGTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

1039

g652-1.pap

```

1  MSAIVDIFAR EILDSRGNPT VECVLLLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNAN TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPF
201 TVGDEGGFAP NLNSHKEALQ LMVEAAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKVLQV GDDLFTVTPK ILAEGIEKGV ANALLVKVNQ IGTLSSETLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAYYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCCG GAAATTTTGG ACTCAGCGCG
51  CAACCCACCA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCCGCGACG GCGACAAATC CCGTTATTCG GGCAAGGGCG TATTGAAGGC
201 GGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTGGG TCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTGCACGC GCCCGTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGCGCGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGCGC AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCGAAAAT CTTTCGCGCA AGCGTTGCGC TCGCGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCGCCGAC
601 ACAGTCGCGC ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGCGCAGCGA AGCCGCGCGC TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAAAT ACCACTTGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAAAGTGG GCGGTAGAGT TCAATTGTT GCGCAGGACT TGTTCGTAAC
951 CAATCCAAAA ATCTTGGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CCGCGAAACC GAAGACAGCA CCATTGCGGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAACCCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCAGCAAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pap

```

1  MSAIVDIFAR EILDSRGNPT VECVLLLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNAN TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPF
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKVLQV GDDLFTVTPK ILAEGIEKGV ANALLVKVNQ IGTLSSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAADYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLLLESGVMGRAAVPSGASTGQKEALELRDGDKSRY					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLLLESGVMGRAAVPSGASTGQKEALELRDGDKSRY					
	10	20	30	40	50	60
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVIINGGEHANNSLNIQEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVIINGGEHANNSLNIQEFMIMPVGAKSFREALR					
	130	140	150	160	170	180
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVIINGGEHANNSLNIQEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVIINGGEHANNSLNIQEFMIMPVGAKSFREALR					
	130	140	150	160	170	180

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKL	CDKSGFP	TTVGDEGGF	APNLNSHKEAL	QLMVEATEA	AAGYKAGEDVLFA
g652-1	CGAEIFHALKKL	CDKSGFP	TTVGDEGGF	APNLNSHKEAL	QLMVEATEA	AAGYKAGEDVLFA
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYK	DGKYHLEA	EGRSYTNAE	FAEYLEGLV	NEFPIISIE	DGMDENDWEGWKLLT
g652-1	LDCASSEFYK	DGKYHLEA	EGRSYTNAE	FAEYLEGLV	NEFPIISIE	DGMDENDWEGWKLLT
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGRVQL	VGGDDL	FVTNPKIL	AEGIEKGV	ANALLVKV	NQIGTLSETLKA
g652-1	EKLGGRVQL	VGGDDL	FVTNPKIL	AEGIEKGV	ANALLVKV	NQIGTLSETLKA
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVMSHRSGET	EDSTIADL	AVATNCMQ	IKTGSLSR	SDRMAKYN	QLLRIEELAE
g652-1	SVMSHRSGET	EDSTIADL	AVATNCMQ	IKTGSLSR	SDRMAKYN	QLLRIEELAE
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACCA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCCGCGAG GCGACAAATC CCGTTATTTC GGCAAGGGCG TATTGAAGGC
201 GGTGCAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TGGCAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTGTCACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTCCGCGA AGCGTTGCGC TCGCGTGCGG
551 AAATTTTCCA CGCCTTGAAA AACTGTGCGC ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGGCG TACAAAGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGTCTCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAACTGG GCGGCAAGT CCAACTCGTT GCGGACGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGGCGTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECVLLLESG VMGRAAVPSG ASTGQKEALE
51  LRDKGKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANN S NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDKSGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEA EG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKVQLV GDDL FVTNPK ILAEGIEKGV ANALLVKVNQ IGTLSLTKA
351 VDLAKRNR YA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEE E LAEADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLLSGVMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNPTVECDVLLSGVMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

m652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

m652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
a652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
              130     140     150     160     170     180

m652-1      CGAEIFHALKKLSDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1      CGAEIFHALKKLSDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
              190     200     210     220     230     240

m652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDWEGWKLLT
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDWEGWKLLT
              250     260     270     280     290     300

m652-1      EKLGGRVQLVGDDLFVTNPKILAEGLIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
a652-1      EKLGGRVQLVGDDLFVTNPKILAEGLIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
              310     320     330     340     350     360

m652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEAAADYPSK
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEAAADYPSK
              370     380     390     400     410     420

m652-1      AAFYQLGKX
a652-1      AAFYQLGKX
              429

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1  ATGGCGGcgg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTTCCGG
51  ATCGTTCGGG ATGGCGTTTT TGtTgacggT GATGTGCGct ttgcccaAAG
101 CGGCTtcggc ggctttgcCg gtgatTTTCA TCGGTTGCAG GtcgacgaGG
151 AAAacgTGGC TTTCGGTGCG GCCGGAaacy atgcyCaaac cgCGTttaac
201 caactcttcc gccATGACGG CAGCATTGAT TTCACTTGT TTGCGTATT
251 GTTTGAactC GGGTTGcaac gttctTTAA acgctACGGC TttgCGGCG
301 ATAACGTgca tcaACGGAcc gCCTTGcAGG CTGGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTGTGG GTGGTAGTgG ttACgaaGtc GCAGaatggc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1  MAAEPMRMPE VTYGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMTAAALFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRRVLV VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTTCCGG
51  ATCGTTCGGA ATGGCGTTTT TGTTGACGGT GATGTGCGCT TTGCCCAAAG
101 CGGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCACGAGG

```

1042

```

151 AAAACGTGGC TTCGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTCACTTGT TTTGCGTATT
251 GTTTGAAGTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAGG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTTGG GATATTCGCC GCCGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```

m653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRLVW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/g653 96.9% identity in 163 aa overlap

```

m653.pep      10      20      30      40      50      60
MAAEPMRMPEVT KGFSGSFGMAFLLTMCA LPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||
g653          10      20      30      40      50      60
MAAEPMRMPEVT YGFSGSFGMAFLLTMCA LPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||

m653.pep      70      80      90     100     110     120
MRKPRLTNSSAMAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
|||||
g653          70      80      90     100     110     120
MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF
|||||

m653.pep      130     140     150     160
SWVLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATRPAX
|||||
g653          130     140     150     160
SWVLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATSPAX
|||||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```

a653.seq
1  ATGGCGGCGG AACCGATGCG GATGCCGAG GTAACGAAG GTTTTCCGG
51  ATCATTCCGG ATGGCGTTT TGTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGG GGCTTTGCCG GTAATTTCA TCGTTGCGG GTCAACGAGG
151 AAAACGTGGC TTCGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTCACTTGT TTTGCGTATT
251 GTTTGAAGTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGGCC ACCTTGCAGG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGGATTGG GATATTCGCC GCCGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```

a653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRLVW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/a653 100.0% identity in 163 aa overlap

```

m653.pep      10      20      30      40      50      60
MAAEPMRMPEVT KGFSGSFGMAFLLTMCA LPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||
a653          10      20      30      40      50      60
MAAEPMRMPEVT KGFSGSFGMAFLLTMCA LPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||

m653.pep      70      80      90     100     110     120
MRKPRLTNSSAMAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
|||||
a653          70      80      90     100     110     120
MRKPRLTNSSAMAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
|||||

m653.pep      130     140     150     160
SWVLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATRPAX
|||||
a653          130     140     150     160
SWVLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATRPAX
|||||

```

g656.seq

```
1 ATGCCGCGTT TCTCCGGTTC GATTCTCTCG ATGATTTCGA TCGCCGCGGAC
51 TTTtggcGCG CCGGAGAGTG TGCcggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TTCAAACAGC ctTCGACGTT GGAACACGATG
151 TGCATCACAT GGGAGTATTT TTAATCACC ATTTTGTCCG TGACTTTGAC
201 TTCGCTGTT TTGCTGATGC GTCCGACATC GTTGCGCCCC AAATCGATAA
251 GCATAACGTG TTCGGCgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCGGCGGG GGTTTTGGCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGAGC ATGAGTcat CGCGTTCGCG GCGGACGAGG ATTTCCGGCG
401 AGGAACCGAC GATGTGAAA TCGCCGAAT CGTAG
```

g656.pap
1 MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM
51 CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSIITCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRTT ISGEEPTMWK SPKS*

m656.seq

1	ATGCCGCGTT	TGCTCGGTTT	GACTTCTTCG	ATGATTTCCT	TGGCGCGGAC
51	TTTGGGTGCG	CCGGAGAGTG	TGCCGGGCAGG	GAAGGTAGCG	GCGAGGATGT
101	CCATGTTGGT	CATGCCGCTCT	TTCCAGACGC	CTTCGACGTT	GCGAAACGATG
151	TGCATTACAT	GGGAGTATTT	TTCAATCACC	ATTTTGTCGG	TAACTTTGAC
201	TTCGCCGGTT	TTACTGATGC	GGCCGACGTC	GTTGCGTCCT	AAGTCAATCA
251	ACATGACGTG	TTCGGCGATT	TCCTTGGCAT	CGCTTAACAA	ATCTTGTTTCG
301	TGGCAAGGT	CTTCGGCGGG	GGTTTGGCG	CGCAGGCGCG	TGCCGGCGAT
351	GGGGCGGACG	ATAACGTCGT	TGCGTTTCGG	TCGGACGAGG	ATTTGCGGCG
401	AGGAGCCGAC	GATGTGAAA	TCGCCGAAT	CGTAG	

m656.pep
1 MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51 CITWEYFSIT ILSVTLTSPV LLMRPTSLRP K SINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT ITSLSRRTR ISGEPTMWK SPKS*

Homology with a predicted ORF from *N. gonorrhoeae*

		10	20	30	40	50	60
m656.pep		MPRL	GSTSSMIS	MARTIL	GAPESV	PAGKVA	ARMSMLVMP
		:		:	:	:	:
g656		MPRF	SGSISSMIS	IAIT	FGAPESV	PAGKVA	ARMSILVTP
		:		:	:	:	:
		10	20	30	40	50	60
		70	80	90	100	110	120
m656.pep		ILSV	TLTSPV	LLMRPT	SLRPKS	INMTCS	AISLASLNK
		:	:	:	:	:	:
g656		ILSV	TLTSPV	LLMRPT	SLRPKS	ISITCS	AISLASLNK
		:	:	:	:	:	:
		70	80	90	100	110	120
		130	140				
m656.pep		ITSL	RSRRTR	ISGEEPT	MWKSPK	SX	
		:		:	:	:	
g656		MTSS	RSRRTR	ISGEEPT	MWKSPK	SX	
		130	140				

1044

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTG GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTCGACGTT GGAAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCCG TAACTTTGAC
201 TTCGCCGGTT TTAATGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCG
301 TTGGCAAGGT CTTCCGCGGG GGTTTTGGCC CGCAGGCGCG TGCCGCGGAT
351 GGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTCGCGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRTR ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT					
a656.	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
	130	140				
m656.pep	ITSLRSRRTRISGEEPTMWKSPKSX					
a656	MTSSRSRRTRISGEEPTMWKSPKSX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCGCGT TGGACGAATT
201 GGCAAAATGC GCGGCGGTta cgACCGAATT TGAaaacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATACCAACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTCAAGAA AAAGCGTGGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCGGTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattec ATCGTCcccg CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GGCGCAACgc tTGGCGGACG AATTGGATTA TGTCGGCgta
751 TTGGCGGTAG AAATGTTTGT TGTCGGCGAC ACACATGAAT TGCTCGTCAA
801 TGAAACCGCC CCGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
851 GCGCCCGAGA CCAGTTCCAA CAGCAGGTAC GCATTATGTG CAAcctGCCG
901 cccGccgACA CCAAATTATT aTCCCtttgC TGTATGGCGA ATATTTGGGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGGCCGAA TGCACACCTG CACCTATACG GAAAAAAAC CGCACAGAAA
1051 GGTCGGAAAA TGGGACACTT TaccgTTTTG ACCACCGATT CGGACaccgc
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657.pap

1	<u>MNTPPILPPA</u>	<u>MLGILGGGQL</u>	<u>GRMFAVAAKT</u>	<u>MGYKVTVLDP</u>	<u>DPNAPAAEFA</u>
51	DRHLCAPFDD	RAALDELAKE	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	KTLDELKAAF	AHGGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQARQTAQR	LADEL DYVG

m657.seq

1	ATGAAAAACA	TATCTCTTTC	TCCGCCCGCC	ATGCTTGCCA	TCCTCGCGCG
51	CGGACAATTA	GGCAGAAATGT	TTACCGTTGC	CGCCAAAACC	ATGGGCTACA
101	AAGTAACCGT	TCTCGACCCC	GATCCGGACG	CGCCGGCAGC	AGAATTGCAAT
151	GACCGCCATT	TGTGCGCGCC	GTTTAACGAC	CAAGCTGCTT	TGGACAGGATT
201	GGCAAAATGC	CGCGCGGTGA	CCACTGAATT	TGAAAACGTC	AATGCCGATG
251	CGATGCGCTT	TTTGGCAAAA	CATACCAATG	TTTCCCCTAG	CGGCGATTGT
301	GTGGCGATTG	CACAAAAACG	CATTTCAGGA	AAGGCATGGA	TACGCAAAAG
351	GGGATTGCAA	ACCGCGCCGT	ATCAAGTGGT	TTGTAAGCTT	GAAGACATCA
401	CTGAAGCAAG	CGCGCAATTT	TTGCGCGGTA	TCTGAAAAC	TGCTACGTTG
451	GGCTACGACG	GCAAAGGTCA	AATCCGCGTA	AAAAATTGG	ATGAACTCAA
501	AGCCGCGTTT	GCCGAACAG	GCGGCGTGGA	TTGCGTTTTG	GAAAAAATGG
551	TGATTTCGCG	CAGTGAATTT	TCCGTAAATG	TATGCGCGTT	GAACAATGAC
601	AACGTGCAAA	CTTCGACACC	TGCCGAAAAC	ATCCACGAAA	ACGGCATCTT
651	GGCTATTTC	ATTCGTCCCC	CGCGACTGAG	TGCCACGTG	CAGCAACAGG
701	CGCGGCAGAT	GGCGCAACGC	TTGGCGGACG	AATTGGATTA	TGTCGGCGTA
751	TTGGCGGTAG	AAATGTTTGT	TGTCGGTGAC	ACCGATGAAT	TGGTCGTCAA
801	CGAAATCGCC	CCGCGCCCCG	ACAATTCGGG	ACACCATACG	ATAGATGCTT
851	GCGCAGCAGA	CAGTTCTCAG	GAGCAGGTAC	GCATTATGTG	CAACTGCGCG
901	CCTGCGGATA	CCAAATTACT	GAGTCTTTCG	TGTATGGCAA	ATATTTTGGG
951	CGACGTTTGG	CAGGAAGACG	GCGGCGAACC	GGATTGGCTG	CCCTTGCAAA
1001	GCCATCCGAA	TGCACACCTG	CACCTTTACG	GCAAAAAAAC	CGCGCACAAA
1051	GGGCGGAAAA	TGGGCAACTT	TACCGTTTTA	ACCAACCGATT	CGGACACCGC
1101	ATTTCAAGAA	GCAAAAAAAC	TGCATCAGTC	CCTATAA	

m657.ppt

1	MKNISLSPPA	MLGILGGGQL	GRMETVAAKT	MGYKVTVLDP	DPDAPAAEFA
51	DRHLCAFFND	QAALDELAKC	AAVTETEFNV	NADAMRFLAQ	HTNVSPSGDC
101	VAIAQNRIOE	KAWIRKAGLO	TAPYQVVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	KTLDLKAFAF	AEHGGVDCVL	EKMVDLRSEI	SIVVCLRLND
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQMAQR	LADELVDYGV
251	LAVEMFVVGD	THELVVNEIA	PRPHNSGHHT	IDACAADQFQ	QQVRIMCNLP
301	PADTKLLSSC	CAMNVLGDVW	QEDGGEPDWL	PLQSHPNNAH	FLYGKKTAAH
351	GRKMGHETVL	TTDSDTAFOE	AKKLHOSI.*		

Homology with a predicted ORF from *N. gonorrhoeae*

m657/q657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPDPDAPAAEFADRHLCAPFND					
	:: :					
g657	MNTPPILPAMLGILGGGQLGRMFVAFAAKTMGYKVTVLDPDPNAPAAEFADRHLCAPFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m657.pep	QAALDELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ					
	:					
g657	RAALDELAKCAAVTTEFENVNADAMRSLAKHTNVSPSGDCVSIQNRIQEKAWIRKAGLQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m657.pep	TAPYQVCKAEDITEASAQFLPGILKTATLGYDGKGQIRVKTLDELKAAFAEHGGVDCVL					
g657	TAPYQAVCKAEDITEASAQFLPGILKTATLGYDGKGQIRVKTLDELKAAFAEHGGVDCVL					
	130	140	150	160	170	180

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNNDENVQTFDPAENIHENGILAYSIVPARLSADVQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
g657	LADEL DYVGV LAVEMFVVGDTHELVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHRNAHLHLYGKKTAKHGRKMGHFTVL					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAKHGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTSDTA FQEAKKLHQS LX					
g657	TTSDTA FQEAKKLHQS LX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1  ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTCGGCA TTCTTGCGCG
51  CGGACAATTA GGCAGAATGT TTA CTGTGTC TGCCAAAACC ATGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGAAGAATT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCCAG CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATTCAGGAA AAGGCATGGA TACGCAAAGC
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCGGCA TCCTGAAAAC CGCTACATTG
451 GGCTATGACG GCAAAGGCCA AATCCGCGTC AAAACGGTGG ATGAAC TCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
551 TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGTCT GAACAATGAC
601 AACGTGCAAA CTTTCGATCC TGCCGAAAAC ATTCACGAAA ACGGTATCCT
651 CGCCTACTCC ATCGTCCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAAT GCGCGAGCGT TTGGCCGATG AATTGAACTA CGTCGGCGTA
751 TTGGCGGTAG AAATGTTTGT TGTCGGCGAC ACGCATGAAT TGGTCGTCAA
801 CGAAATCGCG CCGCGTCCGC ACAATTCGCG CCACCATACC GTCGACGCCT
851 GCGCGGCAGA CCAATTCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGCTGACA CCAAATTGCT GAGTTCTTGC TGTATGGCGA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCCGGCCGGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATT TTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1  MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTALEELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
101 VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESIQF LPGILKTATL
151 GYDGKGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQARQMAQR LADELNYVGV
251 LAVEMFVVGDTHELVVNEIA PRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGEPDWF PLQSRPDAHL HLYGKKTAKH
351 GRKMGHFTIL STSDTA FQE AKKLHQS L*

```

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDA PAAEFADRHL CAPFDN					

a657	MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAPAAEFADRHLCAFPDN	10	20	30	40	50	60
m657.pep	QAALDELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ	70	80	90	100	110	120
a657	QTALEELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ	70	80	90	100	110	120
m657.pep	TAPYQVVKCAEDITEASAQFLPGILKTATLGYDGKGQIRVKTLDDELKAAFAEHGGVDCVL	130	140	150	160	170	180
a657	TAPYQAICKAEDITEESIQLPGILKTATLGYDGKGQIRVKTVDDELKAAFAEHRGVDCVL	130	140	150	160	170	180
m657.pep	EKMVDLRLSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR	190	200	210	220	230	240
a657	EKMVDLRLGEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADIQQQARQMAQR	190	200	210	220	230	240
m657.pep	LADELNVYGVVLAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP	250	260	270	280	290	300
a657	LADELNVYGVVLAVEMFVVGDTHELVVNEIAPRPHNSGHHTVDACAADQFQQQVRLMCNLP	250	260	270	280	290	300
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHPNAHLHLYGKKTAAHKGRKMGHFTVL	310	320	330	340	350	360
a657	PADTKLLSSCCMANILGDVWQEDGGEPDWFPQSRPDAHLHLYGKKTAAHKGRKMGHFTIL	310	320	330	340	350	360
m657.pep	TTSDSDFQAEAKKLHQSXLX	370	379				
a657	STDSDTAFQAEAKKLHQSXLX	370					

g658.seq

1	ATGGTGGCCG	GAATGTGCG	TGCGCGGGGC	GGTTTCATTG	ACGAGCAATT
51	CATGTGTGTC	CCGACAACA	AACATTTCTA	CCGCCAATac	GCCGACATAA
101	TCCAATTTCG	GCGCCA ^g cgg	TTGGCGCGTC	TGCGCGCCTT	GCTGTGCAC
151	GTCGGCACTC	AGCCGCG ^c gg	gGACGATGga	atAAGCCAAG	ATGCCGTTTT
201	CGTGGATGTT	TTGCGCGGGG	TCGAAGSTTT	GCAGTTTTTC	ATCGTTCAGA
251	CGGCATACGA	TCACGGAAAT	CTCGCCGCGC	AAGTCCACCA	TTTTTTCCAA
301	AACGCAATCC	ACGCGCCGCT	GTCGGCAAA	CGCGGCTTTG	AGTTCGTCCA
351	ACGTTTTGAC	CGGGATTTGA	CCTTTGCCGT	CGTAGCCCAA	CGTAGCCGTT
401	TTCAGGATGC	CGGGCAAAAA	TTGCGCGCTT	GCTTCAGTAA	TGCTTCGGC
451	CTTGCAAAAC	GCCTGATACG	GCGCGGTTTG	CAAGCCTGCT	TTGCGTATCC
501	AGCCTTTTT	CTGAATGCGG	TTTTGTGCAA	TGGACACGCA	GTCGCCGCTG
551	GGGGAACAGT	TGTTATGCTT	TGCCAGAGAG	CGCATCGCGT	CGGCAttgac
601	gtTTTCAAAT	TCGGTcgtaA	CCGCCGCGCA	TTTTGCCAAT	TCGTCCAACG
651	CGGCCCGGTC	GTCAAACGGC	GCGCACAAT	GGCGGTCGGC	AAATTCGCCC
701	CCCGGCGCAT	TCGGGTCCGG	ATCGACAACG	GTTACTTTGT	AGCCCATGGT
751	TTTAGCGGCA	ACGGCAAAACA	TTctgcctAA		

g658.pep
1 MVAGIVRARG GFIDEQFMCV ADNKHFYRQY ADIIQFVRQA LRLRLPRLLH
51 VGTQPRGDDG ISQDAVFVDV FGGVEGLHVF IVQTAYDHGN LAAOVHHEFO

1049

```

101 NAIHAAVFGK RGFEFVQRF ADLTFVAVQA RSRFQDAGQK LRACFSNVFG
151 LANRLIRRLG QACFAYPRFF LNAVLCNGHA VAAGGNVGM LQRAHRVIGID
201 VFKFGRNRRA FCQFVQRGPV VKRRAQMAVG KFRRRRIRVG IENGYFVAHG
251 FSGNGKHSAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

```

m658.seq
1 ATGGTGTCCG GAATTGTGCG GCGCGGGGCG GATTCGTTG ACGACCAATT
51 CATGCGTGTC ACCGACAACA AACATTTCTA CCGCCAATAC GCCGACATAA
101 TCCAATTCGT CCGCCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTTGTC ATTGTTCAAA
251 CCGCATACGA TTACGGAAAT TTCCTGCGC AAATCCACCA TTTTTCCTAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAA CGCGGCTTTG AGTTCATCCA
351 ATGTTTTTAC GCGGATTGTA CCTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CCGGCAAAAA TTGCGCGCTT GCTTCAGTGA TGTCTTCAGC
451 CTTACAAACC ACTTGATACG GCGCGGTTT CAATCCCGCT TTGCGTATCC
501 ATGCCTTTTC CTGAATGCGG TTTGTGCAA TCGCCACACA ATCGCCGCTA
551 GGGGAAACAT TGGTATGTTT TGCCAAAAG CGCATCGCAT CGGCATTGAC
601 GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAT TCGTCCAAAG
651 CAGCTTGGTC GTTAAACGCG GCGCACAAAT GCGGTCGCGC AAATCTGTCT
701 GCCGCGCGCT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGTT
751 TTTGGCGGCA ACGGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

```

m658.pep
1 MVSGIVRARG DFVDDQFMRV TDNKHFYRQY ADIIQFVRQA LRHLPRLLH
51 VGTQSRGDDG ISQDAVEVDV FGRVESLHV IVQTAYDYG NFTAQIHFFQ
101 NAIHAAVFGK RGFEFIQCFY ADLTFVAVQA RSRFQDAGQK LRACFSDVFS
151 LTNHLIRRLG QSRFAYPCLF LNAVLCNRHT IAARGNIGMF CQKAHRIGID
201 VFKFSGHRRR FCQFVQSSLV VKRRAQMAVG KFCRRVRIG VENG YFVAHG
251 FGGNGKHSAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

```

m658.pep      10      20      30      40      50      60
MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLHVGTSRGDDG
||:||||| :||:| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
g658          10      20      30      40      50      60
MVAGIVRARGGFIDEQFMCVADNKHFYRQYADIIQFVRQALRRLPRLLHVGTPRGDDG

m658.pep      70      80      90      100     110     120
ISQDAVEVDVFGRVESLHVIVQTAYDYG NFTAQIHFFQNAIHAAVFGKRGFEFIQCFY
||||| :||:| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
g658          70      80      90      100     110     120
ISQDAVEVDVFGGVEGLHVFIVQTAYDHGNLAAQVHHFFQNAIHAAVFGKRGFEFVQRF

m658.pep      130     140     150     160     170     180
ADLTFVAVQRSRFQDAGQKLRACFSDVFSLTNHLIRRLGQSRFAYPCLFLNAVLCNRHT
||||| :||:| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
g658          130     140     150     160     170     180
ADLTFVAVQRSRFQDAGQKLRACFSNVFGLANRLIRRLGQACFAYPRFFLNAVLCNGHA

m658.pep      190     200     210     220     230     240
IAARGNIGMFQKAHRIGIDVFKFSGHRRR AFCQFVQSSLVVKRRAQMAVGKFCRRVRIG
:|| :||:||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
g658          190     200     210     220     230     240
VAAGGNVGM LQRAHRVIGIDVFKFGRNRRAFCQFVQRGPPVVKRRAQMAVGKFRRRRIRVG

m658.pep      250     260
VENGYFVAHGFGGNGKHSAX

```

1050

g658
 :|||||:|||||
 IENGYFVAHGFGNGKHSAX
 250 260

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

a658.seq
 1 ATGGTGGCCG GAATTGTGCG GACGCGGCGC GATTTCGTTG ACGACCAATT
 51 CATGCGTGTC GCCGACAACA AACATTCTA CCGCCAATAC GCCGACGTAG
 101 TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT
 151 GTCGGCACTC AGTCGGGCTG GGACGATGGA GTAGGCGAGG ATACCGTTTT
 201 CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTGTGC ATTGTTTCAGA
 251 CGGCATACGA TAACGGAAAT TTCGCGCGC AAGTCCACCA TTTTTCCTCA
 301 AACGCAATCC ACGCCGCGGT GTTCGGCAA CGCGGCTTTG AGTTCATCCA
 351 CCGTTTGAC GCGGATTTGG CCTTTGCCGT CATAGCCCAA TGTCGCGTT
 401 TTCAGGATGC CGGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC
 451 TTTGCAAATT GCTTGATACG GCGCGGTTTG CAGGCTGCTT TTGCGTATCC
 501 ATGCCTTTTC CTGAATGCGG TTTTGCAGCA TGGCAACGCA GTCGCGCTG
 551 GGGGAAACAT TGGTATGTTT GCGGAGAAA CGCATCGCAT CGGCATTGAC
 601 GTTTTCGAAC TCGGTGCTAA CAGCCGCACA TTTTGCCAAT TCTTCCAAAG
 651 CGGTTTGTTT GTCAAACGGC GCACACAAAT GGCGGTCGGC AAATTCGCT
 701 GCCGCGCAT TCGGTTGGG ATCGAGTACG GTTACTTTGT AGCCCATGGT
 751 TTTGGCAGCA ACAGTAAACA TTCTGCCTAA

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

a658.pep
 1 MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGOT LRHLSRLLLN
 51 VGTQSGWDDG VGEDTVFVNV FGRIESLHV IVQYAYDNGN FAAQVHHFFQ
 101 NAIHAAVFGK RGFEFIHRFD ADLAFVIAQ CSGFQDAGQK LYAFFSDVFG
 151 FANCLIRRLG QACFAYPCLF LNAVLRDNGA VAAGNIGMF GEKTHRIGID
 201 VFELGRNSRT FCQFFQSGLV VKRRTQMAVG KFRCRIRRVG IEYGYFVAHG
 251 FGSNSKHS*

m658/a658 75.3% identity in 259 aa overlap

m658.pep	10	20	30	40	50	60
	MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLHVGTSRGDDG					
a658	10	20	30	40	50	60
	MVAGIVRTRRDFVDDQFMRVADNKHFYRQYADVQFIGQTLRHLRLLNVGTQSGWDDG					
m658.pep	70	80	90	100	110	120
	ISQDAVFVDVFGRVESLHVIVQYAYDNGNFTAQIHFFQNAIHAAVFGKRGFEFIQCFY					
a658	70	80	90	100	110	120
	VGEDTVFVNVFGRIESLHVIVQYAYDNGNFAAQVHHFFQNAIHAAVFGKRGFEFIHRFD					
m658.pep	130	140	150	160	170	180
	ADLTFVAVQSRFQDAGQKLRAFSDVFSLTNHLIRRLQSRFAYPCLFLNAVLCNRHT					
a658	130	140	150	160	170	180
	ADLAFVIAQCSGFQDAGQKLYAFFSDVFGFANCLIRRLQACFAYPCLFLNAVLRDNGA					
m658.pep	190	200	210	220	230	240
	IAARGNIGMFCQKAHRIGIDVFKFSGHRRAFQCFVQSSLVVKRRAQMAVGKFCRRVRIG					
a658	190	200	210	220	230	240
	VAAGNIGMFGEKTHRIGIDVFELGRNSRTFCQFFQSGLVVKRRTQMAVGKFCRRIRVG					
m658.pep	250	260				
	VENGYFVAHGFGNGKHSAX					
a658	250	260				
	IEYGYFVAHGFGSNGKHSAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

```

g661.seq
1  ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT GCCGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
151 ACCGGAAAAA CCTtgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
201 TGCCGTGCAG ATTGCCGGCA GCGACCccga acaGATGGCG Gatgcgccgc
251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
301 cccgccaaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
351 CGAGccgctg gttgcCgcca tTTtgaggc ggtggtcAAG GCGGCGGgcy
401 TACCGGTTAC cctCAAAACc cgtTtgggtt ggcacgcaga cgatcaaaac
451 ctgcCcgcg tgcgcaaat cgccgaagat tgcggcattg ccgccCttgc
501 cggtccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GCGcGTTAC
551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
601 CGGCGACATC actTCgcgcg AAAAAGCCGC CGccgTCTC AAACAAACCG
651 CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
701 TTCCGCGATT TGAAGCATT TCCGAACAC GCGTTTTTAC CGCCTGCCTT
751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACCACATC CGCGCCATGC
801 ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGCGAAAT GCCCGACGGC GAACAGGCGC GGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

```

g661.pep
1  MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
51  TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDDQDN
151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
201 RRHHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFPRFEAL CRTRRFTACL
251 EFGRMQSRHF EPHPRHARVL WXDRCARHRT QTHRLVHRRN ARRTTGA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

```

m661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGACCCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGAAGC CGTCGTCGT GCGGCAGGCG
401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TCGGGCATCG CCGCCCTTGC
501 CGTCC.ACGG ACGCACGCGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
551 GAACTCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGGCGACATT ACTTCGCCGC AAAAAGCCCA AGCCGTCTCT AAACAAACCG
651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
701 TTCCGCGATT TGAAACATTA TGCCGAACAC GGTGTTTTGC CGCCTGCCTT
751 GAGTTTGGCA GAATGCGCCG CCGCTATTTT GAACCACATC CGCGCCATAC
801 ACGCGTTTTA CCGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

```

m661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDDHQN
151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPRFETL CRTRCFAACL
251 EFGRMRRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRTTDS*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCDRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
g661	MHIGGYFIDNPIALAPMAGIADKPFRRLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
g661	ADEGGIVAVQIAGSDPEQMADAARYNVGLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
g661	VAAILEAVVKAAGVPVTLKTRLGWHDDQNLPVAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRNRRRHYDRARRARQAVVLPFRFETL					
g661	GALRTHRRDQKPSHPGLGQRRHHFAAKSRRRPQTNRNRRRHDRARRARQAVVFPFRFEAL					
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
g661	CRTRRFACLEFGRMQSRHFEPHPRHARVLWXDRRCAHRTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GCGGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGGAGGC GGTGGTCAAA GCGGCGGGCG
401 TACCCGTAC CCTCAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCCTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCACGCGC ACGCAAATGT ACAAAGGCGA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCG TCTGGGTCAA
601 CGGCGACATT ACCTCGCCGC AAAAAGCCCA AGCCGTCCTC AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG ACCGTGGTTC
701 TTCCGCGATT TGAAACATTA CGCCGAACAC GGTGTTTAC CGCCTGCCTT
751 GAGTTTGCA GAATGTACCG CCACTATTTT GAACCACATC CGAGCCATGC
801 ACGCGTTTCA CGGCGACACC GCCGTGTGCG GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQQMA DAARYNVSLG AQLIDINMG
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWHDDHQN
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRHYLAAKSP SRPQTNRRRR HYDRARRARQ TVVLPFRFETL RRTRCFACLE
251 EFGRMYRHYF EPHPSHARVL RRRRRCARHT QTHRLVHRRN ARRRTDTS*

```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCDRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					

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```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60
           70      80      90      100     110     120
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           |||||
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70      80      90      100     110     120
           130     140     150     160     170     180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||:|||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180
           190     200     210     220     230     240
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNNRRRRHYDRARRARQAVVLPREFTL
           ||:|
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNNRRRRHYDRARRARQTVVLPREFTL
           190     200     210     220     230     240
           250     260     270     280     290     299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           |||||:|||||
a661      RRTRCFTACLEFGRMYRHYFEPHPSHARVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAACCG TGTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGTctGC CAAATGCCTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggtcg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTTCGGAC GCAACAATTC GGTTTTGTG
601 GATTTTTCG GCAATcagaC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTGGAAATC CTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCGCTTGA TCGAAGAACG
801 CGTGCCGCAA CACCCGGAAC AATATTTCTG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLQFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VELIGRTEGL RALVKQFRKS SAPFLYLPDQ DFRNNSVFPV
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPV READNTVTIQ FYPAWKSEFS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAACCG TGTGAAACA

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1054

```

201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCTGC CGGACGTTTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CCGGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTGTG
601 GATTTTTTCG GTATTTCAGAC GGCAACGATT ACCGGATTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGAAATC CTTTCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACCGTTTTA TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTGG GCTGCACAAG CGTTTAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
51  KCFSEWSEEK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNRDSVFP
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PV READNTVT LH FYPAWKSFPF
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DEFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKP RRRIGEINLAKCFSEWSEEK					
g663	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKP RRRIGEINLAKCFPEWDEEK					
	10	20	30	40	50	60
m663.pep	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH YLDDALAAGEKVIILYPHFT					
g663	RKTVLKQHFHMAKLMLEYGLYASAKCLKSLVRYRNKH YLDDALAAGEKVIILYPHFT					
	70	80	90	100	110	120
m663.pep	130	140	150	160	170	180
	AFEMAVYALNQDIPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
g663	AFEMAVYALNQDVPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
	130	140	150	160	170	180
m663.pep	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVT LH					
g663	SAPFLYLPDQDFGRNNSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVT LQ					
	190	200	210	220	230	240
m663.pep	250	260	270	280	290	
	FYPAWKSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX					
g663	FYPAWKSFPSEDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAACTGCT TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGGCGAAAT CAATTTGGCA

```

1055

```

151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAACCG TGTGAAACA
201 GCATTTCAAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCCGC CGGGCGTTTG AAATCACTGG TCGCTACCG CAACAAACAT
301 TATTTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTT
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTTTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTGTG
601 GATTTCCTCG GTATTTCGGAC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGGAATC CTTTCCGAGT
751 GAAGATGCGC AGGCCGACGC GCAGCGCATG AACCGTTTGA TCGAGGAACG
801 CGTGC CGGAA CATCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

```

a663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51  KCFPEWDGKK RKTVLKQHEK HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDVSVF
201 DFFGIRTATI TGLSRIAALA NAKVIPAIPV READNTVTLH FYPAWESFPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

m663/a663 96.2% identity in 293 aa overlap

10 20 30 40 50 60
m663.pep MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKPRRRIGEINLAKCFSEWSEEK
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a663 MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKPRRRIGEINLAKCFPEWDGKK
10 20 30 40 50 60

70 80 90 100 110 120
m663.pep RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHYLDDALAAGEKVIILYPHFT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a663 RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHYLDDALAAGEKVIILYPHFT
70 80 90 100 110 120

130 140 150 160 170 180
m663.pep AFEMAVYALNQDIPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a663 AFEMAVYALNQDVPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS
130 140 150 160 170 180

190 200 210 220 230 240
m663.pep SAPFLYLPDQDFGRNDVSVFDFFGIQTATITGLSRIAALANAKVIPAIPVREADNTVTLH
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a663 SAPFLYLPDQDFGRNDVSVFDFFGIRTATITGLSRIAALANAKVIPAIPVREADNTVTLH
190 200 210 220 230 240

250 260 270 280 290
m663.pep FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a663 FYPAWESFPSEDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX
250 260 270 280 290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

```

g664.seq
1  ATGATACATC CGCACCCTT CCGCGCCTTT TTCATAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TAGCTGAcgg gCGGCACCGG ATGGGCGGTC
101 GGGCCTGCGT CTTGGGGGAA CTGGTTCTGG CGCAGCAGGC GGATGTTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGAAAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAT TATTCGTGTC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCCT TGTTCCTCAT CGCGCCCAT
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCaa
451 cCggaagcgc gtttcgtcCc acttcacgcC gtTTTTTCAA cgaTTCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTC

```

551 GA

This corresponds to the amino acid sequence <SEQ ID 2154; ORF 664.ng>:

g664.pep

```

1  MIHPHHFRAF  FINGHGVEIV  HLLIADGAHR  MGRACVFGE  LVLAQQADV
51  DAAHGAAGAV  AGKLLVAEHG  QPFLQRKLEP  VAAGYAVARP  VVEIFVSDHG
101 FNAFEIGIGG  GAAVGEDELG  VKNVQTLVFH  RAHIEIAYGD  DHENIQVIFQ
151 PEARFVPLHR  VFSTIPRQSR  PWVCPLRWCK  TRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

m664.seq

```

1  GTGATACATC  CGCACTACTT  CCGCGCCTTT  TTCATAAAGC  GTCATGGTGT
51  AGAAATTGTT  CATCTCCTCA  TAGCTGGCGG  GCGGCACCGG  ATGGGCGGTC
101 GGGCCTGCGT  CTTGCGGGAA  CTGGTGCTGG  CGCAGCAGGC  GGATGTTTTC
151 GATGCGGCGC  ACGGCGCGGC  TGGCGCGGTC  GCCGGAAAAT  TCTTGGTCGC
201 GGAACACGGT  CAGCCCTTCC  TTCAGCGAAA  GCTGGAACCA  GTCGCGGCAG
251 GTTACGCGGT  TGCCCGTCCA  GTTGTGGAAA  TACTCGTGTC  CGACCACGGA
301 TTCGATGCCT  TCGAAATCGG  TATCGGTGGC  GGTGCGGCTG  TCGGCAAGGA
351 CGAACTTGGT  GTTAAAGATG  TTCAAACCTT  TGTGTTCCAT  CGCGCCCAT
401 TTGAAATCGC  CCACGGCGAC  GACCATGAAA  ATATCCAAGT  CGTATTCCAA
451 ACCGAAGCGC  GTTTCGTCCC  ATTTTCATCG  GTTTT.CAA  CGATTCCACG
501 GCAAAGCCGA  CCTTGGGCTT  GTCCGCTTCG  GTGGTGTAAG  ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:

m664.pep

```

1  VIHPHYFRAF  FINGHGVEIV  HLLIAGGAHR  MGRACVFGE  LVLAQQADV
51  DAAHGAAGAV  AGKFLVAEHG  QPFLQRKLEP  VAAGYAVARP  VVEILVSDHG
101 FDAFEIGIGG  GAAVGKDELG  VKDVQTLVFH  RAHIEIAHGD  DHENIQVVFQ
151 TEARFVPFHR  VFXTIPRQSR  PWACPLRWCK  TRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m664/g664 91.8% identity in 183 aa overlap

	10	20	30	40	50	60
m664.pep	VIHPHYFRAFF	FINGHGVEIV	HLLIAGGAHR	MGRACVFGE	LVLAQQADV	FDAHGAAGAV
g664	MIHPHHFRAFF	FINGHGVEIV	HLLIADGAHR	MGRACVFGE	LVLAQQADV	DAAHGAAGAV
	10	20	30	40	50	60
m664.pep	AGKFLVAEHG	QPFLQRKLEP	VAAAGYAVARP	VVEILVSDHG	FDAFEIGIGG	AAVGKDELG
g664	AGKLLVAEHG	QPFLQRKLEP	VAAAGYAVARP	VVEIFVSDHG	FNAFEIGIGG	AAVGEDELG
	70	80	90	100	110	120
m664.pep	VKDQVTLVFH	RAHIEIAHGD	DHENIQVVFQ	TEARFVPFHR	VFXTIPRQSR	PWACPLRWCK
g664	VKNVQTLVFH	RAHIEIAYGD	DHENIQVIFQ	PEARFVPLHR	VFSTIPRQSR	PWVCPLRWCK
	130	140	150	160	170	180
m664.pep	TRFX					
g664	TRFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

a664.seq

```

1  GTGATACATC  CGCACCCTT  CCGCGCCTTT  TTCATAAAGC  GTCATGGTGT
51  AGAAATTGTT  CATCTCCTCA  TATCGGGCGG  GCGGCACCGG  ATGTGCGGTC
101 GGACCTGCGT  CTTGCGGGAA  CTGGTGCTGG  CGCAGCAGGC  GGATGTTTTC
151 GATACGGCGC  ACGGCGCGGC  TGGCGCGGTC  GCCGGAAAAT  TCTTGGTCGC

```

1057

```

201 GGAACACGGT CAACCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCTT TGTTTCCAT CGCACCCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
  1  VIHPPHFRAF FINGHGVEIV HLLISGGAHR MCGRTCVFGE LVLAQQADV
 51  DTAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
101  FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
151  TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

              10      20      30      40      50      60
m664.pep      VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGGRAVCVFGELVLAQQADVFDAAHGAAGAV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664           VIHPPHFRAFFINGHGVEIVHLLISGGAHRMCGRTCVFGEVLVLAQQADVFDTAHGAAGAV
              10      20      30      40      50      60

              70      80      90      100     110     120
m664..pep     AGKFLVAEHGQPFLLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVKGDELG
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664           AGKFLVAEHGQPFLLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG
              70      80      90      100     110     120

              130     140     150     160     170     180
m664.pep     VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVFXTPRQSRPWACPLRWCK
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664           VKDVQTLVFHRTHEIAHGDDHENIQVVFQTEARFVPLHCVFXAIPRQSRPWACPLRWCK
              130     140     150     160     170     180

m664.pep     TRFX
              |||
a664          TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
  1  atgaagtGg acgaaacgcg cttcgGgttg GAAtatgact tggatatttt
 51  CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101  GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACCGCC
151  ACCGATACCG ATTTCGAAGG CATTGAATCC GTGGTCGGAC ACGAATATTT
201  CCACAACCTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251  CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
301  CGCGCCGGCC GCGCCGTGCG CCGCATCGAG AACATCCGCC TGCTGCGCCA
351  GAACCACTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCcccg
401  TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451  GCGCGCGAAG TGGTGCGGAT GTATCATAAC CTGCTCGGCG AAGAGGGCTT
501  CCAAAAAGGC ATGAAGCTAT ATTTcCaacg CCACGACGGA CAGGCAGTGA
551  CTGCGACGTA TTCCGCGCGG GCGatggcgg ATGCGAACGG CATCAATCTC
601  GACCACTTCG CCTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGGAAGC
651  CGAAGGCCGT CTGAAAAACA ATGTTTTCGA GTTAACCATT AAACAAACCG
701  TGCCGCCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751  AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
801  GGGCAAACGC GCAACCGAAG CCGTGTGCTT GATGACCGAA GCCGAACagg
851  CCTTCCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
901  GGGTTCAGCG CGCCAGTGTA TCTGAACAT CCGTACAGCG ACGACGACCT
951  GCTGCTCCTG CTCGCCCACG ACAGCGACGC TTTCACGTGC TGGGAAGCCG

```

```

1001 CCCAAACGCT CTACCGTCGC GCCGTCGCCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTGCGCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAA ctGTGGGACG GCACGAAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
1251 CttcctgcCG AAATGGCACG AATTGGaccg tcaggcggcg aagCaggaaa
1301 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCCG
1351 AACGTCTGCC GCGCCTtcgt cctGCGCGCC GACCCCGCGC acatcgAAAC
1401 TGTTGCCGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGAcAA gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTGCGC CTTATCGGCT CAAGccggcg cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
1651 GCCCGTTGCG TCATCGGCAG CTTAGCCGCG AACGTCCCGC ATTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA cCCGCAggtc gccGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTgGTGAAAC AAGAATTGCA
1851 GTGCATTGCG GCGCAGGAAG GATTGTCGAA AGacGTGGGC GAaatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

g665.pep

```

1 MKWDETRFGL EYDLDFIMV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPTAHP VRPVSYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNVFELTI KQTVPPTPDM ADKQPMIPV
251 KVGLLNRNGE AVAFDYQGKR ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYLYN PYSDDDL LLL LAHSDAFTC WEAAQTLYRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDL LDNAFKA LLLGVPSAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDRAQA KQENQSYEYS PETADWRTLRL
451 NVCRAFLVLR DPAHIETVAE KYGEMAQNT HEWGILSAVN GNESTRNCL
501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQQVQALQAL PKFSLENPNK
551 ARSLIGSFSR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

m665.seq

```

1 ATGAAATGGG ACGAAACGCG CTTGCGTTTG GAATACGACT TGGATATTTT
51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAACAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACC GCC
151 ACCGATACCG ATTTGGAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCG TGCTGCGCCA
351 GCACCAAGTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCCCG
401 CCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TAGTGCGGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCCGTTA
551 CTTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCAAGTTCG CCTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCCCAC GCCCGATATG ACGGATAAAC AGCCGATGAT GATTCCGCTC
751 AAGGTCGGGC TGCTGAACCG CAACGCGGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CTTTCTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGCTGCA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CCCAAACGCT CTACCGCCGC GCCGTCGCCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTTCA
1251 CTTCTGCGG AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGGCG CACGCTGCGC

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1059

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1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTCGGCT CAAGCCGCGC CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTTCGAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
1651 GCCCGTTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGAGGTC GCCGCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTGGTGAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
1  MKWDETRFGL EYDLDFIMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
51  TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNIFELTV KQTVPTPDM TDKQPMIPV
251 KVGLLLNRNGE AVAFDYQGKR ATEAVLLLTE AEQTFLLLEV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDL LLL LAHDSDAFTR WEAQTLYRR AVAANLATLS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQAA KQENQSYEYS PEAAGWRTL R
451 NVCRAFLVRA DPAHIETVAE KYGEMAQNT HEWGILSAVN GNESDTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGSFSSR NVPHFHAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

	10	20	30	40	50	60
m665.pep	MKWDETRFGL EYDLDFIMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES					
g665	MKWDETRFGL EYDLDFIMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES					
	10	20	30	40	50	60
	70	80	90	100	110	120
m665.pep	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
g665	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQNF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m665.pep	PEDAGPTAHPVRPASYEEMNFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG					
g665	PEDAGPTAHPVRPVSYEEMNFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m665.pep	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPTPDM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m665.pep	TDKQPMIPVKVGLLLNRNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEVTEAVVPSLLR					
g665	ADKQPMIPVKVGLLLNRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300

1060

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEEAQTLYRRAVAANLATLSDGVELPKHEK					
g665	GFSAPVYLNYPYSDDDLLLLLAHDSDAFTCWEAAQTLYRRAVAANLAALSDGIGLPKHEK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
g665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNROAAKQENQSYEYSPEAAGWRTLNRVCRAFVLRADPAHIETVAEKYGEMAQNMT					
g665	KWHELDROAAKQENQSYEYSPETADWRTLNRVCRAFVLRADPAHIETVAEKYGEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
g665	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
g665	PKFSLENPNKARSLIGSFSRNVPHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILD					
g665	CNKLEPHRKNLVKQELQCIRAQEGLSKDVGEIVGKILGX					
	610	620	630			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

```

a665.seq
1  ATGAAGTGGG  ACGAAACGCG  CTTGCGTTTG  GAATACGACT  TGGATATTTT
51  CATGGTCGTC  GCCGTGGGCG  ATTTCAATAT  GGGTGCGATG  GAAAACAAGG
101 GTTTGAACAT  CTTTAACACC  AAGTTCGTCC  TTGCCGACAG  CCGTACCGCC
151 ACCGATACCG  ATTTTGAAGG  CATCGAATCC  GTGGTCGGAC  ACGAATATTT
201 CCACAACCTGG  ACGGGCAACC  GCGTGACCTG  CCGCGACTGG  TTCCAGCTTT
251 CGCTGAAGGA  AGGGTTGACC  GTGTTCCGCG  ACCAAGAATT  TTCCGGCGAC
301 CGCGCCAGCC  GCGCCGTGCG  CCGTATCGAA  AACATCCGCC  TGCTGCGCCA
351 GCACCACTTC  CCCGAAGACG  CAGGTCCGAC  CGCACATCCG  GTGCGCCCGG
401 CCCGATATGA  GGAGATGAAC  AATTTCTACA  CCATGACCGT  TTATGAAAAA
451 GCGCGCGAAG  TGGTGCGGAT  GTATCACACC  TTGCTCGGCG  AAGAGGGCTT
501 CCAAAAAGGT  ATGAAGCTCT  ATTTCCAACG  CCACGACGGA  CAGGCTGTTA
551 CCTGCGACGA  TTCCGCGCG  GCGATGGTGG  ACGCGAACGG  CATCAACCTC
601 GACCAATTCG  CCTTGTGGTA  CAGCCAAGCA  GGTACGCCGG  TTTTAGATGC
651 TCAAGGGCGT  CTGAAAAACA  ATGTGTTTGA  GTTAACCATC  AAACAAACCG
701 TGCCGCCAC  GCCCGATATG  GCGGACAAAC  AGCCGATGAT  GATTCCCGTC
751 AAAATCGGGC  TGCTGAACTG  CAACGGCGAA  GCGGTGGCAT  TTGATTATCA
801 GGGCAAACGC  GCGACCGAAG  CCGTGTGCT  GCTGACCGAA  GCCGAACAGA
851 CCTTCCAGTT  CGAAAGCGTA  ACCGAAGCCG  TCGTTCCTC  GCTGCTGCGC
901 GGGTTCAGCG  CGCCGGTGCA  TCTGAACTAT  CCGTACAGCG  ACGACGACCT
951 GCTGCTTCTG  CTCGCCCATG  ACAGCGACGC  CTTACGCGCG  TGGGAAGCCG
1001 CACAAACGCT  CTACCGCCGT  GCCGTCGCG  CCAACCTTGC  CGCGCTTTCA
1051 GACGGCGTCG  AGTTGCCGAA  ACACGAAAAA  CTGCTTGCCG  CCGTCGAAAA
1101 AGTCATTCA  GACGACCTCT  TAGACAACGC  TTTCAAAGCC  CTGCTTTTGG
1151 GTGTGCCGTC  TGAAGCCGAG  CTGTGGGACG  GCGCGGAAAA  CATCGACCCG
1201 CTGCGCTACC  ATCAGGCGCG  CGAAGCCTTG  TTGGATATAC  TTGCCGTCGG
1251 CTTTCTGCCG  AAATGGCAGC  AATTGAACCG  TCAGGCGGCG  AAGCAGGAAA
1301 ACCAAAGCTA  CGAGTACAGC  CCCGAAGCCG  CCGGTTGGCG  CACGCTGCGC
1351 AATGTCTGCC  GCGCCTTCGT  CCTGCGCGCC  GATCCGCGCG  ACATCGAAAC

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1061

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCGCTCGC TCATCGGCAG CTTAGCCGC AACGTCCCGC ATTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCCGCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTGGTGAAC AAGCATTCGA
1851 GCGCATTCGG GCGCAGGAAG GATTGTGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

```

a665.pep
1  MKWDETRFGL EYDLDFMVV AVGDFNMGM ENKGLNIFNT KFLVADSRTA
51  TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPPTPDM ADKQPMPIPV
251 KIGLLNCNGE AVAFDYQGR ATEAVLLLTE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNQAA KOENQSYEYS PEAAGWRTLK
451 NVCRAEVLRA DPAHIETVAE KYAEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRSRSD LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPFHAEDEG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQRIK AQEGLSKDVG EIVGKILD*

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m665/a665 97.3% identity in 638 aa overlap

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              10      20      30      40      50      60
m665.pep      MKWDETRFGLEYDLDFMVVAVGDFNMGMENKGLNIFNTKFLVADSRTATDTDFEGIES
              |||
a665           MKWDETRFGLEYDLDFMVVAVGDFNMGMENKGLNIFNTKFLVADSRTATDTDFEGIES
              10      20      30      40      50      60

              70      80      90      100     110     120
m665.pep      VVGHEYFHNWNTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
              |||
a665           VVGHEYFHNWNTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
              70      80      90      100     110     120

              130     140     150     160     170     180
m665.pep      PEDAGPTAHPVRPASYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
              |||
a665           PEDAGPTAHPVRPARYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
              130     140     150     160     170     180

              190     200     210     220     230     240
m665.pep      QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPTPDM
              |||
a665           QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDAQGRKNNVFELTIKQTVPPTPDM
              190     200     210     220     230     240

              250     260     270     280     290     300
m665.pep      TDKQPMPIPVKVGLLNRNGEAVAFDYQGRATEAVLLLTEAEQTFLEGVTEAVVPSLLR
              |||
a665           ADKQPMPIPVKIGLLNCNGEAVAFDYQGRATEAVLLLTEAEQTFQFESVTEAVVPSLLR
              250     260     270     280     290     300

              310     320     330     340     350     360
m665.pep      GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEAAQTLYRRAVAANLATLSDGVELPKHEK
              |||
a665           GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEAAQTLYRRAVAANLAALSDGVELPKHEK
              310     320     330     340     350     360

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	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLGVPSEAEWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNAFKALLGVPSEAEWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
a665	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
a665	HEWGILSAVNGNESDTRNRLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRIAQEGLSKDVGEIVGKILDX					
a665	CNKLEPHRKNLVKQALQIRIAQEGLSKDVGEIVGKILDX					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAACGC CTGCCTACCG
51  CATTTCTGAA ACCGAAGTGC ATTTTCGACAT TGCCGAACCG CAAACCGTCG
101 TGAAGTCGCG TTGACGGTC GAGCCGCAGA GGGCGGGCGA GCCGCTGGTG
151 TTGGACGGTT CGGCAAAAC TTTGTCCGTC AAAATCAACG GCGCGGGCGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAACACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATCTGTTTA CCCAGTGCAG
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG AAAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GGCGAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTCGC GGGCGATTG GCGGTAACGG AAGACCGTTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAACC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGGTTGGAA TATGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTAGGCGATT TCAATATGGG CGCGATGGAA AACAAAGGTT TGAACATTTT
801 TAACACCAAG TTCGTCTCTG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGGCGACCGC GCCGGCCGCG
1001 CCGTGCGCCG CATCGAGAAC ATCCGCCTGC TGCGCCAGAA CCAGTTCCCC
1051 GAAGACGCAG GCCCGACCGC CCATCCGTG CGCCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC CGGGAAGTGG
1151 TGCGGATGTA TCATACCTTG CTCGCGCAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG GCAGTGACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGAAGCCGA AGGCCGCTCTG
1351 AAAACAATG TTTTCGAGTT AACCATTAAG CAAACCGTGC CGCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA GTCCGGCTTC
1451 TGAACCGCAA CGCGAAGCG GTGGCATTCT ATTATCAGGG CAAACGCGCA
1501 ACCGAAGCCG TGTTGCTGAT GACCGAAGCC GAACAGGCCT TCCCGCTCGA
1551 AGGTGTAAAC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGTATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCACGACA GCGACGCTTT CACGTGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGTCGCGCC GTCGCCGCA ACCTTGCCGC GCTTTCAGAC GGCATCGGGT

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1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCTT CAAAGCCCTG CTTTGGGCG TGCCGTCCGA
1851 AGCCGAACTG TGGGACGCGA CGGAAACAT CGACCCGCTG CGCTACCATC
1901 AGCGCGCGGA AGCCTTGTTG GATACGCTT CCGTCCGCTT CCTGCCGAAA
1951 TGGCACGAAT TGGACCGTCA GCGGCGGAAG CAGGAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCGG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCCGCGCACA TCGAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGCTG GCGCAGTTTG
2201 CCACAAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCCGCCCTT
2251 ATCGGCTCAA GCCGCGCAG CGACACCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AATTTCAGTC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCG GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAAGCTCG
2501 AGCCGACCCG CAAAACTTG GTGAAACAAG AATTGCAGTG CATTGGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pep

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSERFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSIDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDRFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YDLDFMVVA
251 VGFNFMGAME NKGLNIFNTK FVLADSRAT DTDFTGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR AGRVRRRIEN IRLLRQNFPP
351 EDAGPTAHPV RPSYEEEMNN FYTMTVYKEG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPTPDMA DKQPMPIPVK VGLNLRNGEA VAFDYQKRA
501 TEAVLMTTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLYNP YSDDDLLLLL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNFAFKL LLGVPSEAEW WDGTEINIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROAAK QENQSYEYSP ETADWRTLRLN VCRAFLVRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSRRSDDL QVQVQALQHP KFSLENPNKA RSLIGSFSRN VPHEHAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVGE IVGKILG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAAA ACCGATTATC ATTTTGATAT TAATGAACCG CAAACCGCTG
101 TGAAGTCGCG TTTGACGGTT GAGCCGCAGA GGGTAGGGGA GCCGCTGGTG
151 TTTGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGCGGCG
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGCTCG
251 AACGCTTCAC GTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAACACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATTGTGTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACCACCACC ATCGTCGCGC AAAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTC CAAACCGAGC TATCTGTTTG
551 CTTTGGTCCG GGGCGATTG GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTATC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGA TACGACTTGG ATATTTTCAT GGTGCTCGCC
751 GTGGGCGATT TCAATATGGG CGCGATGGAA AACAAGGTT TGAACATCTT
801 TAACACCAAG TTCGTCCTTG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GCGAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGGCGCG CATCGAAAAC ATCCGCTGTC TGCGCCAGCA CCAGTTCCCC
1051 GAAGACGCAG GCCCGACCGC CCATCCGGTG CGCCCCGCCA GCTATGAGGA
1101 GATGAACAA TTCTACACCA TGACCGTTTA TGAAGGAGGC GCGGAAGTAG
1151 TCGGGATGTA TCACACCTG CTCGGCGAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTATCCT GCGACGATTT
1251 CCGCGCGCGG ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGAAGCGGA AGGTCTGCTG
1351 AAAAAAATA TTTTCAGTT GACCGTCAAA CAAACCGTGC CGCCACGCGC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCCGTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTTC ACTATCAGGG CAAACCGCGC

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1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
1551 AGGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CCGTGCACTCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGCCGCGCC GTCGCGGCCA ACCTTGCCAC GCTTTCAGAC GGCCTTGAGC
1751 TGCCGAAACA CGAAAACTG CTTGCCGCGG TCGAAAAAGT CATTTTCAGAC
1801 GACCTCTTAG ACAACGCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA
1851 AGCGGAGCTG TGGGACGGCG CAGAAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATACGCTTG CCGTCCACTT CCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGGCGAAG CAGGAAAAAC AAAGCTACGA
2001 ATACAGCCCC GAAGCCGCGG GCTGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTTGTCTT GCGCGCGGAC CCGCGGCACA TCGAAACCGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGCA TCCTGTCCCG
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGCCCTC
2251 GTCGGCTCAA GCCCGCGCAG CGACACCTG CAACAGGTTG GAACCGCCTT
2301 GCAGCATCCG AAATTCAGCC TCGAAAAACC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2401 GGTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCG GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAGCTCG
2501 AGCCGCAACG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTGGGCGG
2551 CAGGAAGGAT TGTGAAAGA CGTGGCGGAA ATCGTCGGCA AAATTTTGGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSERFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS YLFALVAGDL AVTETYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDFW QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRQHQP
351 EDAGPTAHVP RPASYEEMNN FYMTVYERK AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNIFELTVK QTVPPPTDPT DKQPMPIPVK VGLLNRNGEA VAFDYQKRA
501 TEAVLLLTEA EQTFLEGLVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVELPKHEKL LAAVEKVIDS
601 DLLDNAFKAL LLGVPSEAEI WDGAENIDPL RYHQAREALL DTLAVHFLPK
651 WHELNQAAK QENQSYEYSP EAGWRTLRN VCRFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNRL AQAADKFSDD ALVMDKYFAL
751 VGSSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVG EIVGKILD*

```

m665-1/g665-1 96.1% identity in 866 aa overlap

	10	20	30	40	50	60
m665-1.pep	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTVVKSRLTV	EPQRVGEPLV	LDGSAKLLSV
g665-1	MSKTVRYLKD	YQTPAYRIE	LETLHFDIAE	PQTVVKSRLT	VEPQRAGEPL	VLDGSAKLLSV
	10	20	30	40	50	60
m665-1.pep	KINGAAADYV	LEGETLTIAG	VPSERFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
g665-1	KINGAAADYV	LEGETLTIAD	VPSERFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
	70	80	90	100	110	120
m665-1.pep	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDGRHWV	KWEDPFSKPS
g665-1	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDGRHWV	KWEDPFSKPS
	130	140	150	160	170	180
m665-1.pep	YLFALVAGDL	AVTETYFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGL
g665-1	YLFALVAGDL	AVTETRFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGL
	190	200	210	220	230	240
m665-1.pep	YDLDFMVVAV	GDVFNMGAMEN	KGLNIFNTK	FVLADSRAT	DTFEGIESV	VGHEYFHNWT
g665-1	YDLDFMVVAV	GDVFNMGAMEN	KGLNIFNTK	FVLADSRAT	DTFEGIESV	VGHEYFHNWT
	250	260	270	280	290	300

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
g665-1	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
g665-1	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
g665-1	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
g665-1	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
g665-1	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
g665-1	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
g665-1	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
g665-1	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
g665-1	790	800	810	820	830	840
m665-1.pep	850	860				
g665-1	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTAC  ATTTGATAT  TAACGAACCG CAAACCATTG
101 TGAAGTCGCG TTTGACGGTC  GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT  CTTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGCG  AGACGCTGAC GATTGCGGAC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG  GAAACCGAAA TCCTGCCGGC GGAAACAAAA
301 TCGCTGATGG GGCTGTATGC  GTCCGCCGGT AACCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA  TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC  ATCGTCGGG  ACAAACACG  CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA  AATCGACGGC GGCGAGTATT CAGACGGCGG

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501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
 551 CTTTGGTTCG GGGCGATTTC GCGGTCACGG AAGACTATTT CACCACCATG
 601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
 651 CAAGGTCGGC TTTGCCGTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
 701 AAACGCGCTT CGGTTTGGA TACGACTTGG ATATTTCAT GGTCGTCGCC
 751 GTGGGCGATT TCAATATGGG TCGATGGAA AACAAAGGTT TGAACATCTT
 801 TAACACCAAG TTCGTCCTTG CCGACAGCCG TACCGCCACC GATACCGATT
 851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTCCA CAACTGGACG
 901 GGCAACCGCG TGACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
 951 GTTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
 1001 CCGTGGCGCG TATCGAAAAC ATCCGCCTGC TCGCCAGCA CAGTTCCCC
 1051 GAAGACGCAG GTCCGACCGC ACATCCGGTG CGCCCCGCC GATATGAGGA
 1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGC GCGGAAGTGG
 1151 TGCGGATGTA TCACACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
 1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCTGTACCT GCGACGATT
 1251 CCGCGCGCG ATGTTGGACG CGAACGGCAT CAACCTCGAC CAATTGCGCT
 1301 TGTGGTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
 1351 AAAACAATG TGTTTCGAGTT AACCATCAA CAAACCGTGC CGCCACGCC
 1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA ATCGGGCTGC
 1451 TGAATGCAA CGGCGAAGCG GTGGCATTTC ATTATCAGG CAAACGCGCG
 1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCAGTTCGA
 1551 AAGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
 1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
 1651 GCCCATGACA GCGACGCTT CACGCGTGG GAAGCCGAC AAACGCTCTA
 1701 CCGCGTGC GTCGCGGCA ACCTTGCCG GCTTTCAGAC GCGCTCGAGT
 1751 TGCGGAAACA CGAAAACTG CTTGCCGCG TCGAAAAAGT CATTTAGAC
 1801 GACCTCTTAG ACAACGCTTT CAAAGCCCTG CTTTGGGTG TGCCGTCTGA
 1851 AGCCGAGCTG TGGGACGGCG CGGAAAACAT CGACCCGCTG CGTACCATC
 1901 AGGCGCGCGA AGCCTTGTG GATATACTTG CCGTCCGCTT TCTGCCGAA
 1951 TGGCAGCAAT TGAACCGTCA GCGGCGAAG CAGGAAAACC AAAGCTACGA
 2001 GTACAGCCCG GAAGCCGCGG GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
 2051 CCTTCGTCTT GCGCGCCGAT CCCGCGCACA TCGAAACCGT TGCCGAGAAA
 2101 TACGCCGAAA TGGCGCAAAA CATGACCCAC GAATGGGCA TCCTGTCCCG
 2151 CGTCAACCGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTTG
 2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTGCCCTC
 2251 GTCGGCTCAA GCCGCCGAG CGACACCTG CAACAGGTTT AAACCGCTT
 2301 GCAGCATCCG AAGTTCAGCC TCGAAAATCC CAACAAAGCC CGCTCGCTCA
 2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
 2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTTAACC
 2451 GAGGTCGCG CCCGCGCTGG TGCAGGCGTT CAACCTCTGC AACAGCTCG
 2501 AGCCGCACCG CAAAACCTTG GTGAAACAAG CATTGCAGCG CATTGGGCG
 2551 CAGGAAGGAT TGTGAAAGA CGTGGCGGAA ATCGTGGCA AAATTTGGA
 2601 TTGA

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pep

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV
 51 LDGSAKLLSV KINGVAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
 101 SLMGLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
 151 LLSNGNKIDG GEYS DGRHWV KWEDPFAKPS YLFALVAGDL AVTETYFTTM
 201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YDLDFIMVVA
 251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTD FEGIESV VGHEYFHNWT
 301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRHQHFP
 351 EDAGPTAHVP RPARYEEMNN FYTMTVYERK AEVVRMYHTL LGEEGFQKGM
 401 KLYFQRHDGO AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAQGRL
 451 KNNVFELTIK QTVPTPDMA DKQPMPIVK IGLLNCNGEA VAFDYQGKRA
 501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
 551 AHDSDAFTRW EAAQTLYRRA VAANLAALSD GVLPKHEKL LAAVEKVIDS
 601 DLLDNAFKAL LLGVPSEAEI WDGAENIDPL RYHQAREALL DILAVRFLPK
 651 WHELNROAAK QENQSYEYSP EAAGWRTLRLN VCRAFVLRAD PAHIETVAEK
 701 YAEMAQNMTH EWGILSAVNG NESDTRNRL AQAADKFSDD ALVMDKYFAL
 751 VGSSRRSDTL QVQVQALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
 801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQRIRA
 851 QEGLSKDVG EIVGKILD*

a665-1/m665-1 97.2% identity in 867 aa overlap

	10	20	30	40	50	60
a665-1.pep	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTIVKSRLTV	EPKRVGEPLV	LDGSAKLLSV
m665-1	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTIVKSRLTV	EPKRVGEPLV	LDGSAKLLSV
	10	20	30	40	50	60
	70	80	90	100	110	120

a665-1.pep	KINGVAADYVLEGETLTIADVPSERFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
m665-1	KINGAAADYVLEGETLTIAGVPSEFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
	70 80 90 100 110 120
a665-1.pep	130 140 150 160 170 180
m665-1	FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS
	FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEFS DGRHWVKWEDPFSKPS
	130 140 150 160 170 180
a665-1.pep	190 200 210 220 230 240
m665-1	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGF AVESLKNAMKWDETRFGLE
	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGF AVESLKNAMKWDETRFGLE
	190 200 210 220 230 240
a665-1.pep	250 260 270 280 290 300
m665-1	YDLDFIMVVAVGDFNMGAMENKGLNIFNTK FVLADSRATD TDFEGIESVVGHEYFHNWT
	YDLDFIMVVAVGDFNMGAMENKGLNIFNTK FVLADSRATD TDFEGIESVVGHEYFHNWT
	250 260 270 280 290 300
a665-1.pep	310 320 330 340 350 360
m665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV
	310 320 330 340 350 360
a665-1.pep	370 380 390 400 410 420
m665-1	RPARYEEMNNFYTMVYKGAEVVRMYHTLLGEEGFQKGMKLYFQRH DGOAVTCDDFRAA
	RPASYEEMNNFYTMVYKGAEVVRMYHTLLGEEGFQKGMKLYFQRH DGOAVTCDDFRAA
	370 380 390 400 410 420
a665-1.pep	430 440 450 460 470 480
m665-1	MVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTVPPTPD MADKQPMMPVK
	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPTPDMDTKQPMMPVK
	430 440 450 460 470 480
a665-1.pep	490 500 510 520 530 540
m665-1	IGLLNCGEAVAFDYQGKRATEAVLLLTEAEQTFQFESVTEAVVPSLLRGFSAPVHLNYP
	VGLLNRNGEAVAFDYQGKRATEAVLLLTEAEQTFLEGVTEAVVPSLLRGFSAPVHLNYP
	490 500 510 520 530 540
a665-1.pep	550 560 570 580 590 600
m665-1	YSDDDLLLLLAHDSDAFTRWEAAQTL YRRAVANLAALSDGVLPKHEKLLAAVEKVISD
	YSDDDLLLLLAHDSDAFTRWEAAQTL YRRAVANLATLS DGVLPKHEKLLAAVEKVISD
	550 560 570 580 590 600
a665-1.pep	610 620 630 640 650 660
m665-1	DLLDNAFKALLGVPSEAE LWDGAENIDPLRYHQAREALLDILAVRFLPKWHELN RQAAK
	DLLDNAFKALLGVPSEAE LWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELN RQAAK
	610 620 630 640 650 660
a665-1.pep	670 680 690 700 710 720
m665-1	QENQSYEYSPEAAGWRTL RNVCFVLRADPAHIETVAEKYAEQAQNM THEWGILSAVNG
	QENQSYEYSPEAAGWRTL RNVCFVLRADPAHIETVAEKYGEQAQNM THEWGILSAVNG
	670 680 690 700 710 720
a665-1.pep	730 740 750 760 770 780
m665-1	NESDTRNRLLAQFADKFSD DALVMDKYFALVGSSRRSDTLQQVQTALQHPKFSLENP NKA
	NESDTRNRLLAQFADKFSD DALVMDKYFALVGSSRRSDTLQQVRTALQHPKFSLENP NKA
	730 740 750 760 770 780
a665-1.pep	790 800 810 820 830 840
m665-1	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL
	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL

1068

```

          790      800      810      820      830      840
          850      860
a665-1.pep VKQALQRIRAQEGLSKDVGEIVGKILD
|||||
m665-1     VKQALQRIRAQEGLSKDVGEIVGKILD
          850      860

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2171>:

```

g666.seq
1   ATGCTTTGTA TGAATTATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTAGC
51  TAAACATAT TTATTGACTG CATTGATAAT GTCTATGGTA ATCTCCGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTAA TTCTGCTGTC
151 ATCGCAGGTG CAGACGCTCA CACGCCTGAA CATGTAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT AGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTGTGTGT GTATTGGGAC AATACCGCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCAGAATTAT TTTTGGATAA AGATGGTTAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGCT CGGTAGGTAC GCCTGCTATC CCTAAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2172; ORF 666.ng>:

```

g666.pep
1   MLCMNYQSNS GEGVLVAKTY LLTALIMSMV ISGCQVIHAN QGKVNTNSAV
51  IAGADAHTPE HVTGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GREAPMRAT
151 PELFLDKDGX PLKFMEAVVA RXVRLLSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2173>:

```

m666.seq
1   ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTGGC
51  TAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTGTGTGT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2174; ORF 666>:

```

m666.pep
1   MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTNSAV
51  ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GREAPMRAT
151 PELFLDKDGQ PLKFMEAVVV VARWVRLSL N*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m666/g666 93.9% identity in 181 aa overlap

```

          10      20      30      40      50      60
m666.pep MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTNSAVITGADAHTPE
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g666     MLCMNYQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTNSAVIAGADAHTPE
          10      20      30      40      50      60
          70      80      90     100     110     120
m666.pep HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGSAAADAMVAVQTTL
SLVEPQSSGL

```

```
a666.seq
  1  ATGCTTGTGA  TGAATCATCA  ATCAAAGTCA  GCGAAGGAG  TGCTTGTGGC
51  TAAACATAT  TTATTGACTG  CATTGATAAT  GTCTATGACA  ATCTCTGGAT
101  GTCAAAGTCAT  CCATGCCAAT  CAAGGTAAGG  TTAATACTCA  TTCTGCTGTC
151  ATCAGAGGTG  CAGACGCTCA  CACGCTGAA  CATGCAACGG  GACTGACCGA
201  ACAAAGCAG  GTGATTGCAA  GTGATTTTAT  GGTAGCGTCA  GCCAATCCAT
251  TAGCAACACA  AGCTGGCTAT  GATATCTTAA  AGCAAGGCGG  TAGCGCTGCA
301  GATGCGATGG  TGGCGGTGCA  GACGACACTA  AGCTTGGTAG  AGCCACAGTC
351  GTCAGGCTTG  GGCAGTGGT  CATTTGTGTT  GTATTGGGAT  AATACCGCCA
401  AACATTGAC  CACATTTGAT  GGGCGTGAGA  CGGCACCGAT  GCGTGGCAGC
451  CCGGAATTAT  TTTTGGATAA  AGATGGTCAA  CCATTGAAAT  TTAGGAAGC
501  GGTGGTCGTG  GTCGCTCGGT  GGGTACGCCT  GCTATCCCTA  AACTGA
```

```
a666.pep
  1  MPCMNHQSNS  GEGVLVAKTY  LLTALIMSMT  ISGCQVIHAN  QGKVNTHSAV
51  ITGADAHTPE  HATGLTEQKQ  VIASDFMVAS  ANPLATQAGY  DILKQGSAA
101 DAMVAVQTTL  SLVEPQSSGL  GGGAFVLYWD  NTAKTLTTFD  GRETAPMRAT
151 PELFLDKDQG  PLKFEAVVVV  VARVVRLLSL  N*
```

		10	20	30	40	50	60
m666.pep		MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
a666		MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
a666		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLYWDNTAKTLTTFDGREAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL					
a666		GGGAFVLYWDNTAKTLTTFDGREAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL					
		130	140	150	160	170	180
m666.pep	NX						
a666	NX						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
1   atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51  tttccAtttg gtattcgctc gcgtcgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAAttgcy
151 GAtttccttc agcgtgcccgc cgtgGAacgc ttcccacact ttgctgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTcgCcat atcgtccagC
251 GGCACATTcg ccttcggctG GTAAAGCGCG AGCAAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCGCGC GCGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCCGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATACAG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651 GCTGCGCGAA CAGCACCCTG TCGTCATCCG GCAGGAAGA CGGCAAGTCA
701 TACAACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTA TTCATGGCAg tACCTTGCAT tcaAAAACAG ActTGCGCCT
801 ATTgTgtcaT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
1   MRFVFC LGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAAVE IAVARIPIAR GVDVYQGAV MQYGQVETAA
151 VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMLVLPP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHHEFVIRQR RQVIQRTDTL HIGYGFNIES
251 QNRHGSTLH SKTDLRLLLCH *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
1   ATGCGGCTTT TCCCGGCTT GTGCGGACAG GTAATTCGCG ATCCGTTTGA
51  TTTCCATTTC GTATTCGTCC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTGCGCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GCGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCCGCC
451 GTTCCAATG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TAGCAATGAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCCT TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
1   MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFALIA
51  DFLQPARMEC LPNLAHVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
101 VALVITADV VPLEIAAAVE IAVAHIPIAR GVDVYQGAV MQYQIETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHLN
201 MKMMLHKIAA RLSTAFVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

          10      20      30      40      50      60
m667.pep  MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFALIAADFLQPARMEC
          ||:  | |::  | ||:||||:| |||||:| | : : ||||| | | | | |
```

```
a667.seq
1  ATGCGGTTTG TCTTCTGTTT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51  TTTCCATTTT GTATTCTGCTG GCGTCGAATC TGCCGCTGAC CAGACAGAAA
101 CCGCATATACA TCAGATAGGT ATTTACCGCA TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG CGTGGAAACG CTCCCAACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAAC
251 GGCACATTCC CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 ATGACGTTGG TGGTAGCGCG TGATGTAGTT GTTCCACTTG AAATCGCGCG
351 TGTGCGCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GGCGTTGATG
401 CCGTGTAGCA GCGAACGGTA ATGCAGAAC GGCAGGTCGA AACCGCGGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT
501 TGGCGATAAC CACTTCTCTC CCGTCATCCA TCTCGCCGAT TGTACCACA
551 TGGACTTTAT CCTGCCCCCA ACGCATGCAG CAGAAATCG CCACAATCTG
601 ATGAAGATGA TGCTGCATAA AATCCCCACC CGTCTGAGCA CGGCGTTTTT
651 GCTGGGCAA CAGCACCAC TCATCGTCGG GCAGCGAGGA CGGCAAGTCA
701 TACAGCGTAC GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCTG GTCATGACAG CACCTTGAT TAAAA. CAG ACTTGCCT
801 ATTGTGTCAT TAA
```

```
a667.pep
1  MRFVFCLGGE  IVSDPLDFHF  LRVCKESAAD  QTETQIHQIG  IYRIGFAIIA
51  DFLQPARVER  LPHLAAVHTQ  LARKTAQFRH  IVQRHIRPRL  VKREQIHQIA
101 MTLVVAADV  VPLEIAAAVE  IAVAHIPIAR  GVDVAV*QRTV  MQNRQVETAA
151 VPTDQLRRMF  FNQLEKFGDN  HFLAVIHLAD  CTDMDFILPP  THAARNRHNH
201 MKMMLHKIPT  RSLTAFLLGK  QHHFIVGQRG  RQVIQRTDTL  HIGYGFNISS
251 QNRGHDSTLY  LKXDLRLLLC  *
```

```

          10          20          30          40          50          60
m667.pep  MRLFPGLCGQVIPHFFDFHFVVFVRIQPAADQTETQVHQISVCRVGFATIADFLQPARMEC
a667      ||: | ||:: |:||||| :: |||||:|:|:| |:|||||:|:|:|
          10          20          30          40          50          60
          70          80          90          100         110         120
m667.pep  LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREIQIHQIAVALVITADVVPLEIAAAVE
a667      ||:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
          70          80          90          100         110         120
          LPHLAAVHTQLARKTAQFRHIVQRHIRPRLVKREIQIHQIAMTLVVAADVVPLEIAAAVE

```

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	70	80	90	100	110	120
	130	140	150	160	170	180
m667.pep	IAVAHIPIARGVDVAVYQGAVMQYGGIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD					
	: : : : :					
a667	IAVAHIPIARGVDVAVXQRTVMQNRQVETAAVPTDQLRRMFFNQLEKFGDNHFLAVIHLAD					
	130	140	150	160	170	180
	190	200	210	220		
m667.pep	GADMYFILPPHTAARNRHNLMKMMLHKIAARLSTAFVLGNQHHL					
	: : : : : :					
a667	CTDMDFILPPHTAARNRHNLMKMMLHKIPTRLSTAFLLGKQHHFIVGQRGRQVIQRTDTL					
	190	200	210	220	230	240
a667	HIGYGFNIESQNRGHDSTLYLKXDLRLLLCHX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2183>:

```

g669.seq
1  ATGCGCCGCA TCGTTAAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2184; ORF 669.ng>:

```

g669.pep
1  MRRIVKKHQP VNAPHIVLEI RIMKLHRAV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2185>:

```

m669.seq
1  ATGCGCCGCA TCATTAAAAA ACACCAGCCC ATAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACAGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2186; ORF 669>:

```

m669.pep
1  MRRIKKHQP INAPHIVLEI RIMKLHRAV FLGRKRPHHH DSSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m669/g669 96.2% identity in 106 aa overlap

	10	20	30	40	50	60
m669.pep	MRRIKKHQPINAPHIVLEIRIMKLHRAVFLGRKRPHHHDRSLRRQHGI					
	: : : : :					
g669	MRRIVKKHQPVNAPHIVLEIRIMKLHRAVFLGRKRPHHHDRSLRRQHGI					
	10	20	30	40	50	60
	70	80	90	100		

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```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
|||||||:|||||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1  ATGCGCCGCA TCATTAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51 TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1  MRRIKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
51 EGMGDFDKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

              10      20      30      40      50      60
m669.pep    MRRIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHHHDSLRRQHGIEMGDFDKQI
|||||||:|||||||
a669        MRRIKKHQPVNAPHIVLEIRIMKLHRAFVFLGRKRPHHHDRSLRRQHGIEMGDFDKQI
              10      20      30      40      50      60

              70      80      90      100
m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
|||||||:|||||||
a669        FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1  ATGACTTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTTCG GGTGGTGAA
51 AAACGCTTCC GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTGAGGTG
451 GGCTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1  MTCCRNLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
51 IIVMPLSAKS FITFNTSPTI SGSSAEVGS NSITRGSIAS PRAIATRCCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNTVRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1  ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTTCG GGTGGTGAA
51 AAACGCTTCG GCGGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTTCGTCA AACACATTA

```

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```

251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTCAAGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1 MTCCRNLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151 G*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
               |||||||
g670           MTCCRNLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep      FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
               |||||||:|||||
g670           FITFNTSPTISGSSAEVGSSNSITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep      SSIAFFSACS AFCPLTFIGARVMFSNTVRCGX
               |||||||:|||||
g670           SSIAFFSACS AFCPLTFIGARVMLSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1 ATGACCTGTT GCAGGAAGTCT CTTGGCGCGT TCGTGTTCG GGTGGTAAA
 51 AAACGCTTCC GCGTTCGT CTTCGAGGAT TTGCCCTTA TCGACGAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 CCCGACCATT TCGGGGTGCA GTGCGGAGGT CGGTTCTGCA AACACATTA
251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGTTCATCG CTTTTTCTC TGCCTGTTCC GCATTTTGAC
401 CTTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTCAAGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1 MTCCRNLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151 G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
               |||||||
a670           MTCCRNLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```

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```

              70      80      90      100      110      120
m670.pep    FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
a670         FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK
              70      80      90      100      110      120

              130      140      150
m670.pep    SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX
              ||||||||||| ||||||||||| |||||||||||
a670         SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX
              130      140      150

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

```

g671.seq
1  ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC
51  GCCCAAAATG CGGTTGGCAA AGCCCAGACC GACCGCCGAA ACTGCGCCGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAATG ACAGagccaa TGCAAAACAgg cggggTTGGA ACgagGCAAA
201 GGCGAGGTcg gcgaaggGTG CGGCaaAGAG TTTggcaaAA AAGaaggAAA
251 ccaccCATGC cACCATCgaa ccTGCTTCCG CAATCACGCC GCGCATCGTG
301 GAAATGACGA TGCAGGCGGC GATGACGGcg gAGGCGAGGA GGTCGGCAAT
351 GGGGAGGCTA TTCATTGTT ACCTGGCCGG CGATGCCGTG CACGCGCAGT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

```

g671.pep
1  MISRVTIKTP FNAPNTPPKM RLAKPRPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKGAAKSLAK KKETTHATIE PASAITPRIV
101 EMTMQAAMTA EARRSAMGRL FIRYLAGDAV HAQFVQIAFG IPCVFIVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

```

m671.seq
1  ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTTGGCAA AGCCCAAAACC GACCGCCGAA ACTGCGCTGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAACG ACAGAGCCAA TGCAAAACAGG CGGGGTTGGA ACGAGGCCAAA
201 GGCGAGGTCTG GCGAAGGAGG CGGCAAGAG TTTGGCGAAA AAGAAGGAAA
251 CCACCCATGC CGCCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGACGGCG GAGACGAGGA GGTCGGCAAT
351 GGGGAGGCTA TTCATTGTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

```

m671.pep
1  MTSRVTIKTP FNAPNTPPKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEAAKSLAK KKETTHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

```

              10      20      30      40      50      60
m671.pep    MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
              | ||||||||||| ||||||||||| ||||||||||| |||||||||||
g671         MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDRANANR
              10      20      30      40      50      60

              70      80      90      100      110      120
m671.pep    RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL

```



```
a671.seq
1  ATGACCAGCA GGGTAATAAT CAAATGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAATG CGGTTGGCAA AGCCCAAACC GACCGCGGAA ACTGCCCCGG
101 TCAGCAGCGA CGGGAGTATT TTCTGGATCA GACAGGCAAT GACGAATAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTGGAA ACGATGCAAA
201 GGCATGTCTG GCGAAGGGTG CCGCAAAGAG TTTGGCGAAA AAAAAGGCAA
251 CCACCCATGC CGCCATTGAG CCAGCTCCG CAATCAGGCC GCGCATCGCG
301 GATAGCAGCA TGCAGGCGCG CATGATGGCG GAGACAGGGA GGTCCGCAAC
351 GGGGAGGTTA TTCATTCTGT AGGTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAATG CGCGTTTCGG ATCCCTTGCG TTTTATAGT TGCTTGA
```

a671.pep

1	MTSRVIIKMP	FNAPTPPKM	RLAKPKPTAE	TAPVSSERSI	FWIRQAMTNR
51	EMNDRANANR	RGWNDAKAMS	AKGAAKSLAK	KKATTHAAIE	PASAITPRIA
101	DSTMQAAMMA	ETRRSATGRL	FIRYLTGDTV	YAOFVQIAFG	IPCVFIVA*

		10	20	30	40	50	60
m671.pep		MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
a671		MTSRVIKMPFNAPNTPPKMRLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
		10	20	30	40	50	60
		70	80	90	100	110	120
m671.pep		RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL					
a671		RGWNDAKAMSAKGAAKSLAKKKATTHAAIEPASAITPRIADSTMQAAMMAETRRSATGRL					
		70	80	90	100	110	120
		130	140	149			
m671.pep		FIRYLTGDTVYAQFVQIAFGIPC VFIVAX					
a671		FIRYLTGDTVYAQFVQIAFGIPC VFIVAX					
		130	140				

```
g672.seq
1  ATGAGGAAAA  TCCGCACCAA  AATCTGCGGC  ATCACCACAC  CGGAAGACGC
51  ACTGTATGCC  GCCACGCGCG  GCGCAGACGC  ATTGGGACTG  GTTTTTTACC
101 CCCAAAGCCC  CCGCGCATAC  GACATCATT  AAGCACAAAA  AATCGCGCGC
151 GCATCTGCCG  CGTTTGTCAG  CGTTGTCGCG  CTTTTCGTCA  ACGAAAGCGC
201 GCAAAACATC  CGCCGCATCC  TTGCCGAAGT  CCGGATACAC  ATCATCCAAT
251 TCACAGCGGA  CGAAGACGAT  GCATCTGCGC  GGCAGTTCGA  CCGCCCTAT
301 ATTAAAGCCA  TTCGTGTTCA  GACGGCATCA  GACATCCGAA  ACGCCGCCAC
351 GCGCTTCCCC  AACGCTCAGG  CATGCTGTT  CGATGCCTAT  CACCCTTCGG
401 AATACGGCGG  CACCGGACAC  CGCTTCGact  GGacgttgtt  ggcggAATAT
451 TCGGGCAAGC  CGTGGGTGCT  TGCCGGCGGG  CTGACCCCTG  AAAACGTCGG
501 CGAAGCCGTC  CGCATCACC  GACCGGAAGC  GGTGACGTA  TCCGGCGGCG
551 TGAAGCGTCT  TAAAGGCAAA  AAGAGCCCCG  CCAAAGTCGC  CGCCTTTATC
601 GCAACCGCCA  ACCGCCTATC  CCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```

g672.pep
  1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATRF NAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAEVDV SGGVEASKGK KDKPAKVAEFI
201 ATANRLSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```

m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCG GCGCCAAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GCGCGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAATC GGTCGATGTA TCCGGCGGTG
551 TGGAAGCGTC TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACCGCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```

m672.pep
  1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQGSSRAV DIARAKKITA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATRF DAQALLFDAY HPSEYGGTGN RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDKAAKVAEFI
201 ATANRLSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICGITTTPEDAAAAAAGADAVGLVFFQGSSRAVDIARAKKITAALPPFVSVVA					
	: : : : : : : : :					
g672	MRKIRTKICGITTTPEDALYAAHAGADALGLVFYQSPRAIDIKAQKIAAALPPFVSVVA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m672.pep	LFVNESAQNIRRILAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATRF					
	: : : : : : : :					
g672	LFVNESAQNIRRILAEVPIHIIQFHGDEDDAFCRQFDRPYIKAIRVQTASDIRNAATRF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m672.pep	DAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLAGGLTPENVGEAVRITGAESVDV					
	: : : : : : : : :					
g672	NAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLAGGLTPENVGEAVRITGAEVDV					
	130	140	150	160	170	180
	190	200	209			
m672.pep	SGGVEASKGKKDKAAKVAEFIATANRLSRX					
	: : : : : : :					
g672	SGGVEASKGKKDKPAKVAEFIATANRLSRX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

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```

1  ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCCCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
101 CCCAAAGCCC CCGCGCTGTC GACATCATT AAGCACAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCTAG CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAGGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
351 CCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGACT GGACGCTGTT GGCAGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGA
501 CGAAGCCATC CGCATCACCG GAGCGGAAGC GGTGATGTA TCCGGCGGCG
551 TGGAAGCGTC TAAAGGCAAA AAAGACCCAG CCAAAGTTGC CGCCTTTATC
601 GCAACCGCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

```

a672.pep
1  MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAV DIIKAQKITA
51  ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFRCQFHRPY
101 IKAIRVQTAS DIRNAADRFP DAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAAFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

```

              10      20      30      40      50      60
m672.pep  MRKIRTKICGITTPEDAAGADAVGLVFFQGSSRAVDIARAKKITAALPPFVSVVA
          |||||
a672      MRKIRTKICGITTPEDALYAAHAGADALGLVFYQSPRAVDIKAQKITAALPPFVSVVA
              10      20      30      40      50      60

              70      80      90      100     110     120
m672.pep  LFNESAQNIRILAEVPIHIIQFHGDEDDAFRCQFHRPYIKAIRVQTASDIRNAATREFP
          |||||
a672      LFNESAQNIRILAEVPIHIIQFHGDEDDAFRCQFHRPYIKAIRVQTASDIRNAADRFP
              70      80      90      100     110     120

              130     140     150     160     170     180
m672.pep  DAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLGGGLTPENVGEAVRITGAESVDV
          |||||
a672      DAQALLFDAYHPSEYGGTGHREFDWTLLEAYSGKPWVLGGGLTPENVDEAIRITGAEAVDV
              130     140     150     160     170     180

              190     200     209
m672.pep  SGGVEASKGKKDAAKVAAFIATANRLSRX
          |||||
a672      SGGVEASKGKKDPAKVAAFIATANRLSRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

```

g673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51  TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGCGC
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CGGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGTGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GGCGATGCGC CTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGATCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGTGC
501 GAAACACGGT TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCGAAAG CGTACCGATG TATCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGGT GAAAACTCT TCCGCTATTT

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```

651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAATAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRINQ NVTEALGGVD
101 VVVFVVEAMR LTDADRVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE LPYAMNVEVE QFEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GGCGATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGT
451 GCCCAAGTGC GCGCCGAATT TGAATTGCG GCGGCGGAGG CGGTACGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRINQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVLK QLPKHTPVIL VVINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE LPYAMNVEVE QFEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

          10      20      30      40      50      60
m673.pep MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
          |||||
g673      MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
          10      20      30      40      50      60

          70      80      90     100     110     120
m673.pep YDDTAQFVFVDTPGFQTDHRNALNDRINQNVTEALGGVDVVVFVVEAMRFTDADRVLK
          |||||

```

1080

```

g673      YTDDTAQFVFDTPGFQTDHRNALNDRNLQNVTALGGVDVVVFVVEAMRLTDADRVVLK
           70          80          90          100          110          120

           130          140          150          160          170          180
m673.pep  QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELL
           130          140          150          160          170          180

           190          200          210          220          230          240
m673.pep  KPYPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g673      KPYPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           190          200          210          220          230          240

           250          260          270          280          290          300
m673.pep  IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR
           :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g673      IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDNKVFLKVWVKVKS GWADDIR
           250          260          270          280          290          300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51  TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTGTGTTT GTCGATACGC CCGGTTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CCGCGTGGAT
301 GTGGTGGTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGCTTTGTT
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CCGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51  QTTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRNLQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFDT KVFVKVWVK VKSGWADDIR
301 FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

           10          20          30          40          50          60
m673.pep  MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a673      MDIETFLAGERAADGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           10          20          30          40          50          60

```

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	70	80	90	100	110	120
m673.pep	YTD	DDTAQFV	FVDT	PGFQTD	HNRNALN	DRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK
a673	YTD	DDTAQFV	FVDT	PGFQTD	HNRNALN	DRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTP	VILV	VN	KIDK	DKAKDRY	ALEAFVAQVRAEF
a673	QLPKHTP	VILV	VN	KIDK	DKAKDRY	ALEAFVAQVRAEF
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPES	VPMYP	EDMVT	DKSAR	FLAMEIV	REKLF
a673	KPYLPES	VPMYP	EDMVT	DKSAR	FLAMEIV	REKLF
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVL	VDKES	QKAIL	IGK	GGERL	KKISTEARLDMEKLF
a673	IYIAVL	VDKES	QKAIL	IGK	GGERL	KKISTEARLDMEKLF
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCCC
201 GCTGCTCGAC AGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCAGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TGCAGCAGAG TATATCCGAC AAATCCGCCC
201 GCTACTTGAC AGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL

```

51 FFGTQTNAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	::					
g674	YIQKIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq

1	ATGAAACAG	CCGCCGCGG	TTCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCCGCGCC	CGAGATTGCT	AAAAACATCC
101	GCGAAATGCC	CGACTTTGCC	AAGGCAGACG	AAGAATTGTT	CAACAACTT
151	TTCTTCGGCA	CGCAAACCAA	TGCGGCAGAG	TACATCCGAC	AAATCCGCCC
201	CCTGCTCGAC	CGCGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTCC
251	TGCTGACCGC	CTGCCACGAG	CTGTCCGCCA	TGCCCGAAAC	GCCCTACCCC
301	GTCATCATCA	ACGAAGCCAT	CGAAGTAACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCGTCACG	GCATCCTCGA	CAAACGCGCC	GCCCAAATCC
401	GTCCCGACGA	GCCCAAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMPDFA	KADEELFNKL
51	FFGTQTNAE	YIRQIRPLLD	RDEKDLNPIE	RAVLLTACHE	LSAMPETPYP
101	VIINEAIEVT	KTFGGTDGHK	FVNGILDKLA	AQIRPDEPKR	R*

m674/a674 99.3% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

g675.seq

```
1  ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcacgctc
151 gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAAC TTGC
201 CTCTTCGAA AAATTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTCGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301 GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351 CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

1084

g675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCTRLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
 101 GRVALDYNIP IANAVLTEN DAQAIERIGE KASDAKVAV ECANLVNLLL
 151 EEQFEDEE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq
 1 ATGAACACCA TCGCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
 51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
 101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
 151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
 201 CTCTTCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
 251 GCGAAACCTA CCATTTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
 301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
 351 CACGAAAAAC GACGCGCAGG CAATCGAAGC GATTGAAGAA AAAGCCTCGG
 401 ATGCCGCCAA AGTCGCGGTC GAATGCGCCA ACCTCGTCAA CCGTCTGCTC
 451 GAAGAACAGT TTGAAGACGA AGAATAA

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV
 101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAKVAV ECANLVNLLL
 151 EEQFEDEE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCTRLQELGVADENITVATVPGALEIP					
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCTRLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFELVANESGAGIGRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIGEKASDAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq
 1 ATGAACACCA TCGCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
 51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
 101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
 151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
 201 CTCTTCTGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
 251 GCGAAACCTA CCATTTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
 301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
 351 CACGAAAAAC GACGCACAGG CAATCGAAGC GATTGAAGAA AAAGCCTCGG
 401 ATGCCGCCAA AGTCGCGGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
 451 GAAGAACAGT TTGAAGACGA AGAATAA

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV

1085

```

101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAKVAV ECANLVNLLL
151 EEQFEDEE*

m675/a675    100.0% identity in 158 aa overlap

              10      20      30      40      50      60
m675.pep     MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCTRLQELGVADENITVATVPGALEIP
              |||||
a675          MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCTRLQELGVADENITVATVPGALEIP
              10      20      30      40      50      60

              70      80      90     100     110     120
m675.pep     IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN
              |||||
a675          IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN
              70      80      90     100     110     120

              130     140     150     159
m675.pep     DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX
              |||||
a675          DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX
              130     140     150

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

```

g677.seq
1   ATGCCGCAGA TTTTGGTGCG GATTTCCTC ATTCGGTATT CCTTTATTg
51  ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTC AATT TCCTCACGGC CTTCGGCGCT
151 GTTCAAAACC ACTTCGTCGC CTTCGCGCGC TTTAATCAGG CAACGCGCCA
201 ACGGCGAAAT CCAAGAAATT TTGTTTTCGC CGGTATCGAT TTCATCGACG
251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
301 GGTGCGCGCG AAAAATACTT GGTGCGTCGC TTCGCGCAAT TCGGGATCGA
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTCTG
401 ATTCGCGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTGCTGCG
451 GTCGCCGTTG CCTGCCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GCGTAATGT AGTTTGTGGT TTCGCTACTC ATATTGTGTG CGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

```

g677.pep
1   MPQILVRIFL IRYFSIWETV RLCRFRHSR SVDFDVDRK DFNFLTAFR
51  VQNHFAFAR FNQATRRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT
101 GRAEKLVRG FAQFGIDDDG SLQTFGOETD AAVDFAHAF AVKIVAVFDA
151 VAVACRPVDD LDDFGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

```

m677.seq
1   ATGCCGCAGA TTTTGGTGCG GATTTCCTC ATTCGGTATT CCTTTATTG
51  GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTC AATT TCCTCACGCC CTTCGGCGCT
151 GTTCAAAACC ACTTCGTCGC CTTCGCGCGC TTTAATCAGA CAACGAGCCA
201 GCGGCGAAAT CCAAGAAATT TTGTTTTCGC CGGTATCGAT TTCATCGATG
251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCGAC
301 CGTCGCGCGG AAAAACACTT GGTGCGTCGC TTCGCGCAAT TCGGGATCGA
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTCTG
401 ATTCGCGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTGCTGCG
451 GTCGCCGTTG CCTGCCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTGTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GCGTAATGT AGTTTGTGGT TTCGCTACTC ATATTGTGTG CGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

```

m677.pep
1   MPQILVRIFL IRYFSIWETA RLCRFRHSR SVDFDVDRK DFNFLTPFR

```

1086

```

51  VQNHVFARFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQQSD
101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHATF AVKIVAVFAA
151 VAVACRPVDD LDDFGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

```

      10      20      30      40      50      60
m677.pep  MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVDRKDFNFLTFFRRVQNHVFARFAR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g677      MPQILVRIFLIRYSFIWETVRLCRFRHRSVDFDVDRKDFNFLTAFRRVQNHVFARFAR
          10      20      30      40      50      60

      70      80      90      100     110     120
m677.pep  FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
          |||:| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g677      FNQATRQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTDRRAEKHLVGRFAQFGIDDDG
          70      80      90      100     110     120

      130     140     150     160     170     180
m677.pep  SLQTFGQETDAAVDFAHATFAVKIVAVFAAVACRPVDDLDDFGAFFVDQLIKLVFQCL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g677      SLQTFGQETDAAVDFAHATFAVKIVAVFAAVACRPVDDLDDFGAFFIDQLIKLVFQCL
          130     140     150     160     170     180

      190     199
m677.pep  PSGGRNVVFGFGTHIVCGX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g677      PSGGRNVVFGFGTHIVCGX
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

```

a677.seq
1  ATGCCGCGAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTTG
51  GGAAACGGCG CGTTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCGGGCGT
151 GTTTAAACC ACTTCGTCGC CTTACGCGC TTTAATCAGA CAACGAGCCA
201 GCGGCGAAAT CCAAGAAATT TTGTTTTCGC CGGTATCGAT TTCATCGATG
251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
301 GGTCGCGCCG AAAAACACTT GGTCGGTCGC TTCGCGCAAT TCGGGATCAA
351 CGACGACGGC GGCTTCCAAA CGCTTGGTCA GGAAACGGAT GCGGCGGTTCG
401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGG TAGTCGCCGT TTTGCTGCG
451 GTCGCGGTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTATTAAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GCGGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

```

a677.pep
1  MPQILVRIFL IRYFSIWETA RLRCFRHRSR SVDFDVDRK DFNFLTFFRR
51  V*NHFVAFTR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVAAQQTD
101 GRAEKHLVGR FAQFGINDDG GFQTLGQETD AAVDFAHATF AVKVVAVFAA
151 VAVACRPVDD LDDFGAFFIN QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

```

m677/a677 93.4% identity in 198 aa overlap

```

      10      20      30      40      50      60
m677.pep  MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVDRKDFNFLTFFRRVQNHVFARFAR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a677      MPQILVRIFLIRYSFIWETARLRCFRHRSVDFDVDRKDFNFLTFFRRVXNHVAFTR
          10      20      30      40      50      60

      70      80      90      100     110     120

```

1087

```

m677.pep  FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
a677       FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQTDGRAEKHLVGRFAQFGINDDG
              70      80      90      100     110     120

              130     140     150     160     170     180
m677.pep  SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRFVDDLDFFGAFFVDQLIKLVFQCL
a677       GFQTLGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRFVDDLDFFGAFFINQLIKLVFQCL
              130     140     150     160     170     180

              190     199
m677.pep  PSGGRNVVFGFGTHIVCGX
a677       PSGGRNVVFGFGTHIVCGX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTccgCCG TCATCGCCGC
51 CTGCATCGTC ATTTCCACGA TCGCGGCGGT GATTGCGGAA GCaggttcGA
101 TGGTgGCATG ggtggTTTcc tTCTTTTttg ccAAACTCTt tGCCGCACcc
151 ttcgcccACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCattggc
201 tCTGTCATTc ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCGGC GCAGTTTCGG CGGTCGGTCT GGGCTTTGCC
301 AACCGCATTt TGGGCGGTGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTTT TCGTATCGCT TTCCGAAGCG
451 GTGTTAAACC ataccgaCAA CGCaccgaa tCCctcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1  MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGVLIIVTLL IMLASKTDLP DTEEWQSYT VPPFVSLSEA
151 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TCGCGGCGGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTCTT TGCCGCCTCC
151 TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCgcCTGT TTGCATTGGC
201 TCTGTCTGTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCAGC GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATTt TGGGCGGCGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1  MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLTTS AVSAVGLGFA
101 NRILGGVFGA LKGVLIIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

		10	20	30	40	50	60
m678.pep		MNSLP	IADLLV	SAVIAA	CIVLSA	MGRGVIAE	AGSMAA
		:	:	:	:	:	:
g678		MNSLP	IADLLA	SAVIAA	CIVIST	MRGVIAE	AGSMVA
		:	:	:	:	:	:
		10	20	30	40	50	60
		70	80	90	100	110	120
m678.pep		PRLFAL	ALSFIS	LFVIA	CLIQK	MLRSL	LLTSA
		:	:	:	:	:	:
g678		PRLFAL	ALSFIS	LFVIA	CLIQK	MLRSL	LLTGAV
		:	:	:	:	:	:
		70	80	90	100	110	120
		130	140	150	160		
m678.pep		VMLASK	TDLPD	TEEWR	QSYTL	PFFVSL	SEAVLN
		:	:	:	:	:	:
g678		IMLASK	TDLPD	TEEWQ	QSYTV	PFFVSL	SEAVLN
		:	:	:	:	:	:
		130	140	150	160		

```
a678.seq
  1  ATGAATAACC  TCCCCGTTGC  CGACCTCCTC  GTCTCCGCCA  TCATCGCCGC
51  CTGCATCGTG  CTATCCGCGA  TGCGCGGCGT  GATTGCGGAG  GCTGGGCTCAA
101 TGGCGGCATG  GGTGGTTGCG  TTTT'TTTCG  CCAAACCTCT  TGCCGCACCC
151 TTCGCCGACA  TCGCCTTGCC  ATCGTTCCAA  CCCCgcctGT  TTGCATGGC
201 TCTGTCGTT  ATT'TCCCTAT  TCGTcATTGC  CTGTCTGATC  CAGAAAATAC
251 TCCGCTCGCT  GCTGACCGGG  GCAGTTTCGG  CGGTcGGTTT  GGGCTTTGCC
301 AACCGCATT  TGGGCGGCGT  ATTCGGTGCA  TTGAaAGGCA  TTTTGATTAT
351 TACCCTGCTG  GTCATGTCTC  CTTCAAaAAC  CGACCTGCCC  GATACCGAAG
401 AATGGCGGCA  ATCTTACACA  CTGCCGTTTT  TCGTATCGCT  TTCGGAAGCC
451 GTGTTGAACC  ATAGCGCCGG  CACGCGGAA  ACTCGGAAG  ACGATTGA
```

a678.pep

1	<u>MNNLPVADLL</u>	<u>VSIIIAACIV</u>	<u>LSAMRGVIAE</u>	<u>AGSMAAWVVA</u>	<u>FFFAKLF AAP</u>
51	<u>FADIAFASFQ</u>	<u>PRLPALALSF</u>	<u>ISLFVIACLI</u>	<u>QKILRSLLTG</u>	<u>AVSAVGLGFA</u>
101	<u>NRILGGVFGA</u>	<u>LKGILIIITLL</u>	<u>VMLASKTDLP</u>	<u>DTEEWQSYT</u>	<u>LPFFVSLSEA</u>
151	<u>VLNHSGGTAE</u>	<u>TPEDD*</u>			

	10	20	30	40	50	60
m678.pep	MNSLP	FIADLLVS	AVIAACIVLS	SAMRGVIAE	AGSMAAWVVS	FFFFAKLF
	AA	AS	FAD	LAF	AS	FQ
	: : :	: : :	: : :	: : :	: : :	: : :
a678	MNNLP	PVADLLVS	AIACIVLS	SAMRGVIAE	AGSMAAWVVS	VAFFFFAKLF
	AA	AP	FAD	IA	FA	SFQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLF	ALALSF	ISLFVIA	CLIQKMLR	SLTS	SAVS
	AV	GLGFAN	RILGGV	VFGALK	GV	LIV
	: : :	: : :	: : :	: : :	: : :	: : :
a678	PRLF	ALALSF	ISLFVIA	CLIQKILR	SLT	GAVS
	AV	GLGFAN	RILGGV	VFGALK	GIL	IIT
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLAS	KTDLPD	TEEW	QSYTL	PFFV	SLSE
	AV	LNH	SGGT	AET	PED	DX
	: : :	: : :	: : :	: : :	: : :	: : :
a678	VMLAS	KTDLPD	TEEW	QSYTL	PFFV	SLSE
	AV	LNH	SGGT	AET	PED	DX
	130	140	150	160		

```
g680.seq
      1  ATGACGAAGG  GCAGTTCGGC  GATGTCAGC  CCACGCGCGG  CGATATCGGT
     51  GGCGACGAGG  ACGCGCAGGC  TGCCGTCTTT  GAAGGCGTTG  AGTGTTCGA
    101  GCCTGCTTTG  TTGGGAACGG  TCGCCGTGTA  TCGCTGTGC  GGACAGGTTG
```

1089

```

151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCTG
451 TCGATAAAC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTTG TTAAACTGA TGTTTTCTG TTTACATGG TCGAGCAGCC
551 GTCCGACGGT GGCGACGACT ATTTCGCAGC CGGCACGCAG GTCGGCGGTT
601 TGTTTGTTCCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
1 ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
51 GGCGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTGCA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTTTTGCGC GGCGACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCTG
451 TCGATAAAC CCATATCCAG CACACGGTCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTCTG TTTACGTGG TCGAGCAGCC
551 GTCCGACGGT GGCGACGACG ATTTCGCAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVFCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPKN TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||
g680       MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSRLRFKXMVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          |||
g680       TLCLVLQKTI TWFICRSTISRSSRLRFWKVSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW

```

1090

```

|||||
g680      ASLRIGA EKVAEKSRVWRWRG SICMILRMSSINPISNMRSASSRTTISALEFKLMFFCFTW
          130      140      150      160      170      180

          190      200      210      220
m680.pep  SSSRPTVATTISQPARRSAVCLSI FIPNKT VWRSGRFLMX
          |||||
g680      SSSRPTVATTISQPARRSAVCLSM LTPPKRT VCRSGRFLMX
          190      200      210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2241>:

```

a680.seq
1  ATGACGAAGG GCAGTTCGGC AATATCCAGC CCCC GCGCGG CGATATCGGT
51  GCGCAGCAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTG CACGCTTTGTT TGGTTTTCGA
201 GAACACGATG ACCTGGTTCA TATGCAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTCTTGCGC GCGCACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTGC
451 TCGATAAAAC CCATATCCAG CATA CGGTGCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTGG TTCAAATGGA TGTTTTTCTG TTTCACGTGG TCGAGCAGCC
551 GTCCGACGGT GCGCAGCAGC ATTCG CAGC CGGCACG CAG GTCGGCGGTC
601 TGTTTGTTCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTGTATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2242; ORF 680.a>:

```

a680.pep
1  MTKGSSAISS PRAAISVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51  RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVSCAATS TVSGAFMKSC ASLRIGA EKVA EKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPNKT TVWRSGRFLM *

```

m680/a680 98.6% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||||:|||||:|||||:|||||:|||||:|||||
a680      MTKGSSAISSPRAAISVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSRLRFKXMVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          |||||:|||||:|||||:|||||:|||||:|||||
a680      TLCLVLQNTMTWFICKSTISRSSRLRFKXMVSTAMMCCSTLALVVSCAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGA EKVA EKSRVWRWRG SICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW
          |||||:|||||:|||||:|||||:|||||:|||||
a680      ASLRIGA EKVA EKSRVWRWRG SICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW
          130     140     150     160     170     180

          190     200     210     220
m680.pep  SSSRPTVATTISQPARRSAVCLSI FIPNKT VWRSGRFLMX
          |||||:|||||:|||||:|||||
a680      SSSRPTVATTISQPARRSAVCLSI FIPNKT VWRSGRFLMX
          190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2243>:

```

g681.seq
1  ATGACGACGC CGATGGCAAT CAGTGGCTCA AATTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTCAAGCGC GCCGGGTACG GTGGcgacgg

```

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```

101  tgatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTG GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGCCgt cgaggttgGG GCGCATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CCGCGGTTTC AGGGTTGGTT
401  TTGGTGATGT CCGCGAGGCT GACGATGCTG AAGTTGTCGG GGTGTCGGT
451  GTATTCTCGT GTTTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501  CAAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTGTTG
551  GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651  TTTTACCACG ATTCCCGCGT TGTCCGCAGA CGGCGGCGGT TTGGTGGTAC
701  AATGTGCGCC GTTTCAGGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751  AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

```

g681.pep
1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVNGLEEC AVFGKLPRAA FGLGKQCGGF RVFGDVGGEA DDAEVVGVVG
151 VFVGFVAEE TPAAVVFKNG GFAVKEADGP VLFGDVGVDG AAVECRGKCL
201 CKCVHCGNTL GGGKLADFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
251 KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

```

m681.seq
1  ATGACGACGC CGATGGCAAT CAGTGCGTCA AACTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTG CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GCGCATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CCGCGGTTTC AGGGTTGGTT
401 TTGGCGATGT CCGCGAGGCT GACGATGCTG AAGTTGTCCG GATCGTCGGT
451 GTATTCTCGT GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTGTTG
551 GCGACGGTGT TGGTGGCGAT ACAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATTT
651 TACCACGATT CGTGCGTTGT CGGCAGACGG CCGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGAAA
751 CGCATTCGGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

```

m681.pep
1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGDGLEC AVFGKLPCAA FGLGEQCGGF RVFGDVGGEA DDAEVVRIIVG
151 VFVGLVAEE TPAAVVFKNG GFAVEEADGP VLFGDVGVDG TAVECRGKCL
201 CKCVHYGNTL GXKLDTFTT RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

          10      20      30      40      50      60
m681.pep  MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
          |||||
g681      MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV
          10      20      30      40      50      60

```


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	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVG DGLECAVFGKLPCAA					
g681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGNGLECAVFGKLPRAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGFVDVGEADDAEVVRIVGVFVGLVAAEETPAAVVFKNGGFAVEEADGP					
g681	FGLGKQCGGFRVGFVDVGEADDAEVVGVGVFVGFVAAEETPAAVVFKNGGFAVKEADGP					
	130	140	150	160	170	180
	190	200	210	220	230	239
m681.pep	VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGX-KLTDFTTIRALSADGGGLVVQCAPFAA					
g681	VLFGDGVGGDAAVECRGKCLCKCVHCGNTLGGGLADFTTIPALSADGGGLVVQCAPFAA					
	190	200	210	220	230	240
	240	250	260			
m681.pep	LRCFCIFGVWKRIRAVFCGRRX					
g681	LRCFCIFGVWKRIRAVFCGRRX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1  ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCCAA
51  GTTCATCAGC GCGATGGGGA TTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTC GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTGGG GCGATGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
301 AGGTTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCT GCCAATTCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CCGCGGTTTC AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCGTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTGCTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCTG GTTTTGTGTT
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTGCGG GAATACGTT. GGGGAAAC TTGCGGATTT
651 TACCACGATT CTTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTCGGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1  ITPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQCGGF RVGFGDIGEA DDAEVVRVVG
151 VFVGLVAAEE TPAAVVFKNG GFAVEEADGL VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTX GGLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

	10	20	30	40	50	60
m681.pep	MTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
a681	ITTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVG DGLECAVFGKLPCAA					
a681	KRACTMPMRRCLPSRLGAMVFIECPLVFGGFGMPSEGSVLRLPVG DGLECAVFCQFPRAA					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKNGGFAVEE	ADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVR	VGVFVGLVAAEET	PAAVVFKNGGFAVEE	ADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHYGN	TLGXKLTDTTIRALS	ADGGGLVVQCAPFAAL		
a681	VLFGDGVGGDAAVE	CRGKCLCKCVHCGN	TXGGKLADFTTILALS	ADGGGLVVQCAPFAAL		
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIRAV	FCGRRX				
a681	RCFCIFGVWKRIRAV	FCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAAT GCCGCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTGTATG GCAGGATTTA TTCGCTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWQTAFCM AGFIREFTDR
101 PILTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTG
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
301 CCCATTTCGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDFTVWVS YGKWRKNWDIR YCLLHLIHL STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY.. EMAMPSEP DWIQTAFCM YGFIREFTDR
101 PIRTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||:|||||:||||| |||:|| ||||| ||||| ||||| ||||| ||||| |||||
g682      MRDFAVWVPYGERRKNWDIRYCLPHLIRLSPTLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110
m682.pep  PILILIDY-----EMAMPSEPDWIIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFR
          ||||| |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g682      PILILIDYICVNDEIKMPSEPDWIIQTAFDMA-GFIRFPTDRPILTRQSGVVRISPRTGFR
          70      80      90      100     110

      120     130
m682.pep  YPTRSLPKSKKAYGX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g682      YPTRSLPKSKKAYGX
          120     130

```

```

a682.seq
  1  ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCACCCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGCTCG
151 ATTACGCCCG ATTTGACGAT GCATACTGTG CCTATTTTGA TTTTAATTGA
201 ATAT.....
251 .....TATA TTCGGTTTCC AACTGACCGA
301 CCCATCTCGA CAAGGCCGAC AGGCGTTGTT CGGATTTTCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

```
a682.pep
  1 MRDFTVWVSY GKWRKNWDIR YCLLHLIHLs STRLRKCGRI LSGICEPFCL
51 ITPDLTMHYC PILILIEY.. ..... ..YIRFPTDR
101 PILTRPTGVV RISPRTGFRY PTRSLPKSKK AYG*
```

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||||
a682      MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||||

      70      80      90      100     110     120
m682.pep  PILILIDYEMAMPSEPDWIIQTAFCMAYGFIREFPTDRPIRTRQSGVVRISPTGFRYPTRS
          |||||:|
a682      PILILIEY-----YIREFPTDRPIRTRPTGVVRISPTGFRYPTRS
                      70      80      90      100

      130
m682.pep  LPKSKKAYGX
          |||||
a682      LPKSKKAYGX
          |||||
      110

```

```

9683..seq
1      ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTACT
51     CCCTATTTTG ATAACCGCCT GCAGCAACC GGACAAGTCT GCCCGATGGG
101    AAAATATCGG CACAATCTCA AAGGGCAATA TTCATACATA TATTAATAAA
151    GACAGTGTGA GAAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201    TGTTACCAAT CTGAAACAAG AACGTTTTCG CAACACCCCC GCATAAAGA
251    CTGCCATTGC CGAGTGGGAA ATCCACTGAC ACAACAAAC ATACCGCTTA
301    AGTTCGCTAC AGTTATTTGA TACAAAAAC ACGGAAATT CCACACAAA
351    CTACACAGCC TTCTCCCTCC GCCCGATGAG CATCCTGTCC GGGCATATA

```

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683>:

g683.pap

1 MIKETLMRPI FLSEVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKQYET VCGKKL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTTACCAAT CTAAAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pap..

1 MIKETLMRPI FLSEVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pap	MIKETLMRPIFLSEVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
g683	MIKETLMRPIFLSEVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
m683.pap	70	80	90	100	110	120
	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
m683.pap	130	140				
	SSLRPMSILSGTLTEKQYETVCGKKLX					
g683	SSLRPMSILSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
201 TGTTACCAAT CTAAAAACAAG AACGTTTTCG CNACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pap

1 MIKETLMRPI FLSEVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVTN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL

101 SSLQLFDTKN TEISTQXYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

```

      10      20      30      40      50      60
m683.pep  MIKETLMRPILFSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
          |||
a683      MIKETLMRPILFSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
m683.pep  IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA
          |||
a683      IFQDKKVVTNLKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA
          |||
      70      80      90     100     110     120

      130     140
m683.pep  SSLRPMISLSGTLTEKQYETVCGKKLX
          |||
a683      SSLRPMISLSGTLTEKQYETVCGKKLX
          |||
      130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

g684.seq

```

1  ATGCGCCTTT TCCCCATCGC CGCCGCCCTG ACGCTTGCCG CCTGCGGTAC
51  TGTGCAAAGC ACACAATATT TCGTGTGTCG CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGGCGGCGAA ACCGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCATCAACAC
201 CGCACAAAAC CATGTTTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGACA GCACACGCAC CTTGTTCCT
301 GCCTCAGCA GCGGCAGTAC CGACAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CCATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

g684.pep

```

1  MRLFPAAAL TLAACGTVQS TQYFVLPDSR YIRPATQGE TAVEVRLAEP
51  LKRGGLVYQT DRYRLNTAQN HWADTLDDM LEAALSNAFN RLDSTRFVP
101 ASRSGSTDKW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD
151 GYAAMTALE QGLKQAAQM VE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

m684.seq

```

1  ATGCGCCTTT TCCCGATTGC CGCCGCCCTG TCGCTTGCCG CCTGCGGTAC
51  TGTGCAAAGC ACACAATATT TCGTGTGTCG CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGGCGGCGAA ACTGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCCTCAACAC
201 CGCACAAAAC CACGCTCTGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGACA GCACACGCAT CTTGTTCCT
301 GCCTCAGCA GCGGCAGTAC CGAAAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CGATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

m684.pep

```

1  MRLFPAAAL SLAACGTVQS TQYFVLPDSR YIRPATQGE TAVEVRLAEP
51  LKRGGLVYQT DRYRLNTAQN HWADTLDDM LEAALSNAFN RLDSTRIFVP
101 ASRSGSTEXW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD

```

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m684.pep	MRLFP	IAAALS	LACGT	VQSTQYFVLPDSRYIRPATQGGETAVEVR	LAEP	LKRGGLVYQT
	:	:	:	:	:	:
g684	MRLFP	IAAALT	LACGT	VQSTQYFVLPDSRYIRPATQGGETAVEVR	LAEP	LKRGGLVYQT
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQN	HVWADTLD	DMLEAALSNAFNRLDSTRIFVPASRSGSTEKWT	VYIDAFOGS		
	:	:	:	:	:	:
g684	DPYRINTAQN	HVWADTLD	DMLEAALSNAFNRLDSTRIFVPASRSGSTD	KWT	VYIDAFOGS	
	70	80	90	100	110	120
	130	140	150	160	170	
m684.pep	YTGKT	LISGYAVL	PDGTRNPFHIE	TQQGDGYAAMTAAL	EQGLKQA	AQMVE
	:	:	:	:	:	:
g684	YTGKT	LISGYAVL	PDGTRNPFHIE	TQQGDGYAAMTAAL	EQGLKQA	AQMVE
	130	140	150	160	170	

```
a684.seq
1  ATGCGCCTCT TCCCGATTGC CGCGCGCCTG ACGCTTGCCG CCTGCGGTAC
51  TGTGCAAAAG ACACAATATT TCTGTTGTGC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGCGCGCGAA ACGTCCGTCG AAGTCCGCTT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCCCTAACAC
201 CGCACAACAA CACGTCCTGG GACAGACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGACA GCACACGCAT CTTTGTCTCT
301 GCCTCACGCA CGGGCAGTAC CGAAAAATGG ACGGTCTATA TCGACGCTAT
351 CCAAGGCAGC TACACGGGCA AAACCCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CGCAGCGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CCATGACCCG CGCATCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG TCGAGTAA
```

a684.pap

1	MRLFP	IAAAL	TLAAC	GTVQS	QYFVL	PDSR	YIRPAT	QGGE	TAVEV	RLAEP
51	LKRGG	LVIYT	DPYRL	NTAQN	HVWAD	TLDLM	LEAALS	NAFN	RLDSTR	IFVP
101	ASRSG	STEKW	TVYIDA	FQGS	YTGKTL	ISGY	AVLPDG	TNRP	FHIETE	QQGD
151	GYAAM	TAALE	QGLKQ	AAQOM	VE*					

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

	10	20	30	40	50	60
m684.pep	MRLFP	IAAALS	LAACGT	VQSTQY	FVLPDS	RYIRPATQ
a684	MRLFP	IAAALT	LAACGT	VQSTQY	FVLPDS	RYIRPATQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRL	NTAQNH	VWADTL	DDMLEA	ALSNAF	NRLDSTR
a684	DPYRL	NTAQNH	VWADTL	DDMLEA	ALSNAF	NRLDSTR
	70	80	90	100	110	120
	130	140	150	160	170	

```

m684.pep      YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQQMVEX
               |||||
a684          YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQQMVEX
               130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2267>

```

g685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TCGGGCGTGG TTTCTGCAGG
51  TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCAC
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCCGGCCGCC
151 TGTTGCGCCG AACCTGCCGC CGAAAAAACT GTATccgCCG CATCCCAAGC
201 CGCATCCACA CCTGTCGCCA CGCTGACCGT GCCGACCGCG CGGGCGGATG
251 CCGTTGTGCC GAAGAATCCC GAACgcgctcg ccgtgtAcga CtggCGGCGG
301 TtggATACGC TGACCGAGCC GGGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTG GACTATTTCG AGCCTGCATT TGACAAGGCG GCAACGGTGG
401 GGACGCTGTT TGAGCCCGAT TGCGAATCCC TGCACCGCCA CAATCCGCAG
451 TTTGTCATTA CCGGCGGGCC GGTGCGGAA GCGTATGAAC AGTTGGCGAA
501 AAACCGGACC ACCATAGATT TGACGGTGA CAACGGCAAT ATCCGCACCA
551 GCGGCGAGAA GCAGATGGAG ACCCTGTCGC GGATTTTCGG TAAGGAGCG
601 CGCGTGGCGG AATTGAATGC GCAGATTGAC GCGCTGTTTCG CCCAAAGCG
651 CGAAGCCGCG AAAGGCAAAG GACGCGGGCT GGTGCTGTCG GTTACAGGCA
701 ACAAGGTGTC CGCCTTCGGC ACGCAATCGC GGTGGCAAAG TTGGATACAC
751 GCGGACATCG GCCTGCCGCC CGTGGACGAA TCTTTACGCA ACGAAGGCA
801 CGGGCAGCCC GTTTCCTTCG AATACATCAA AGAGAAAAAC CCCGGCTGGA
851 TTTTATCATC CGACCGCACC GCGCCATCG GGCAGGAAG GCGGCTGCC
901 GTGGAAGTGT TGGATAACGC GCTGGTATGC GGCACGAACG CTTGGAAGCG
951 CAAGCAATC ATCGTCATGC CTGCCGCGAA CTACATTGTC GCGGGCGGCG
1001 CGCGGCAGTT GATACAGGCG GCGGAACAGT TGAAGCGGCG GTTTGAAAAG
1051 GCAGAACCCG TTGCGGCGCA GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685 >:

```

g685.pep
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLPAA
51  CSPEPAEKT VSAASQAAS PVATLTVPPTA RGDVVPKPN ERVAVYDWA
101 LDTLTPGVN VGATTAPVRV DYLPAPFKA ATVTGLFEPD CESLHRHNPQ
151 FVITGGPGE AYEQLAKNAT TIDLTVDN GN IRTSGEKQME TLSRIFGKEA
201 RVAELNAQID ALFAQKREA KKGKRGRLVLS VTGNKVSAGF TQSRLASWIH
251 GDIGLPPVDE SLRNEGHHGP VSFEYIKEKN PGWIFIIDRT AAIQOEGPAA
301 VEVLDNALVC GTNAWKRKQI IVMPAANYIV AGGARQLIQA AEQLKAAFEK
351 AEPVAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2269>:

```

m685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TCGGGCGTGG TTTCTGCAGG
51  TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCAC
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTGCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCGG CATCCGCATC
201 TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCAG ACGCGTCGCC GTGTACGACT GGGCGCGCTT GGATACGCTG
301 ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG TCGCGGTGGA
351 TTATTTCGAG CCTGCATTTC ACAAGGCGGC AACGGTGGGG ACGCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCATTACC
451 GCGGGCGCGG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGACCAC
501 CATAGACTCG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGCGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCGCC CAAACGCGCG AAGCCGCCAA
651 AGGCAAGGGA CGCGGGCTGG TGCTGTGCGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGCG
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG
851 ACCGTACCGC CGCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAAAGCGA AGCAAAATCAT
951 CGTCATGCCT GCCGCGAAGT ACATTGTGCG GGGCGGCGCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGCGGCGT TTAAGGAGGC AGAACCCGTT
1051 GCGCGGGGGA AAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>:

m685.pep

1099

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLO PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPAGAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAGFTQSR LASWIHGDIG
251 LPPVDESRLN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQL KAAFKKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

              10      20      30      40      50      60
m685.pep    LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
              |||||||
g685         LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPPEPAAEKT
              10      20      30      40      50      60

              70      80      90      100     110
m685.pep    VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
              |||||
g685         VSAASQAASTPVTATLTVPTARGDAVVPKNPERVAVYDWAALDTLTEPGVNVGATTAPVRV
              70      80      90      100     110     120

              120     130     140     150     160     170
m685.pep    DYLPAPFDKAATVGTLEFPDYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGN
              |||||||
g685         DYLPAPFDKAATVGTLEFPDCESLHRHNPQFVITGGPGAEAYEQLAKNATTIDLTVDNGN
              130     140     150     160     170     180

              180     190     200     210     220     230
m685.pep    IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKRGRLVLSVTGNKVSAGF
              |||||||
g685         IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKGKRGRLVLSVTGNKVSAGF
              190     200     210     220     230     240

              240     250     260     270     280     290
m685.pep    TQSRLASWIHGDIGLPPVDESRLNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAA
              |||||||
g685         TQSRLASWIHGDIGLPPVDESRLNEGHGQPVSEFYIKEKNPGWIFIIDRTAAIGQEGPAA
              250     260     270     280     290     300

              300     310     320     330     340     350
m685.pep    VEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAAGKKX
              |||||||
g685         VEVLDNALVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFEKAEPVAAQX
              310     320     330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTTGCC GTATCGGGAA TTTTGCCTTT TGC GCGCTGG TTTCTGCAGG
51 TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TGC GCGTGA
351 TTATTTGCAG CCTGCATTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCC
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCAATTACC
451 GCGGGGCCGG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGC GAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGCA AGGAAGCGCG CGCGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCGGCCAA
651 AGGCAAGGA CGCGGCGTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCGG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```


1100

```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAAAGCGCA AGCAAATCAT
951 CGTCATGCGT GCCGCGAACT ACATTGTCGC GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

```

a685.pep
  1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
 51  CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101  TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151  GGPGEAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201  LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAFGTQSR LASWINGDIG
251  LPPVDESILRN EGHGQPVSE YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301  DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQ KEAFKAEPV
351  AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

m685/a685 98.9% identity in 355 aa overlap

	10	20	30	40	50	60
m685.pep	LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT					
a685	LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m685.pep	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
a685	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m685.pep	PAFDKAATVGTLEFEPDYEALHRYNPQLVITGGPGAEEYQLAKNATTIDLTVDNGNIRTS					
a685	PAFDKAATVGTLEFEPDYEALHRYNPQLVITGGPGAEEYQLAKNATTIDLTVDNGNIRTS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m685.pep	GEKQMETLARIIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAFGTQSR					
a685	GEKQMETLARIIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAFGTQSR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m685.pep	LASWINGDIGLPPVDESILRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
a685	LASWINGDIGLPPVDESILRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
	250	260	270	280	290	300
	310	320	330	340	350	
m685.pep	DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQKAAFKKAEFVAAGKKX					
a685	DNALVRGTNAWKRKQIIVMPAANYIVAGGSRQLIQAAEQKAEFEKAEFVAAGKEX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

```

g686.seq (partial)
  1  ..AATTCCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
 51  TGAAGGCTTC ggcgGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101  GTGGCGCGGT TGAATCCGTC GCCTACTCCT TGCCTCAGCA TAGCGCCGGC
151  ATTGTGGAAA CGGTCGGCAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201  GGTGAGGCGG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251  TCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301  GCCGTCGGCG GGATGGTGT CGTATCCGTC CCAATGGATG CGGTAAAGGC
351  TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686 >:

g686.pep (partial)
 1 ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
 51 IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
 101 AVGGMVVFVS PMDAVKAESV NGTTGFVRIG M*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

m686.seq..
 1 ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGGTTTTGGC
 51 GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
 101 TCTCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA
 151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGCTG TATCGGGTGG
 201 CGCGTTTGAA TCCGTCGCCT ACTCCTTGCG TCAGCATACT ACCGGCATTG
 251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
 301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
 351 TCGCCCTTT GGGAGCGGGA TAGCCGCCG CCTGTGGCCC GTCATAGCCG
 401 TCGGCGGGAT GGTGTTGTA TCCGTCCCA TGGATGCGGT AAAGGCTAAA
 451 TCCGTCAACG GGAATACCG CTTCATCAGA ATCGGAATGT GA

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

m686.pep
 1 MMLKKFVLGG IAALVLAACG GSEGGSGAXX XNFSCSADD VFNDICSAVE
 51 GFGGIARSVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
 101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGGMVFV SVPMDAVKAK
 151 SVNGTTGFIR IGM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

g686.pep				10	20	30
				NFSCRADDVFDDICSAVEGFGGIARSVQLG		
m686	LKKFVLGGIAALVLAACGGSEGGSGAXX	XXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG				
	10	20	30	40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYSLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
m686		AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
	70	80	90	100	110	120
g686.pep		100	110	120	130	
		GIAAALWPVIAVGGMVFVSVPMDAVKAESVNGTTGFVRIGMX				
m686		GIAAALWPVIAVGGMVFVSVPMDAVKAKSVNGTTGFIRIGMX				
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

a686.seq (partial)
 1 ..AATTCTCCT GCCGCGCCGA TGATGTTTT GACGATATCT GCAGTGCCGT
 51 TGAAGCTTC GCGGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
 101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGCTCAGCA TACTACCGGT
 151 ATTGTGGAAG CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
 201 GGTGAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
 251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
 301 GCCGTCGCGG GGATGGTGT CGTATCCGTC CCAATGGATG CGGTAAAGGC
 351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N meningitidis*:

```

              10      20      30      40      50      60
m686.pep    LKKFVLGGIAALVLAACGGSEGGSGAXXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
              |||  ||||:|||||:|||||
a686         NFSCRADDVFDDICSAVESFGGIARSVQLG
              10      20      30

              70      80      90      100     110     120
m686.pep    AVSGGAFESVAYSRLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
              |||  ||||:|||||:|||||
a686         AVSGGAFESVAYSRLRQHTTGIVETVDKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
              40      50      60      70      80      90

              130     140     150     160
m686.pep    GIAAALWPVIAVGGMVFVSVPMDAVKAKSVNGTTGFIRIGMX
              |||  ||||:|||||:|||||
a686         GIAAALWPVIAVGGMVFVSVPMDAKESVNGTTGFIRIGMX
              100     110     120     130

```

```

g687.seq
1  ATGAAATCCA  GACACCTCGC  CCTCGCCCTC  GGCCTTGCCG  CCCTGTTCGC
51  CTTTGGCGCG  TGGCAGACGA  AAGTGCAAAC  CAGCGTCCCC  CGCAGACGCG
101 CGCCTGCCGC  TTGGCGAGCC  GCCGCCCCGG  CAGCACTGGT  GCGAGGGCAG
151 AACTACACCG  TCCTTGCCAA  CCGGATTTCC  CAACAGCAGG  CAGGCAAGGT
201 TGAAGTGCTT  GAGTTTTTCG  GCTATTTTTC  TCCGCATGCG  GATCGCTCTg
251 AACCTGTTTT  GACCAAAAC  GCCAAGTCTT  TTAAGACGA  TATGTACCTT
301 CGTACCGAAC  ACGTCGCTGT  GCAGAAAGAA  ATGCTGCCGC  TGGCACGCct
351 cGCCGCCCGC  TCGATATG  GTGCCGCGGA  AAGCAAAGAT  GTGGCGAACa
401 GCCATATTTT  CGATCGCATG  CTCACCAACA  AAATCAAGCT  GCAAGGCGCG
451 GAAGTCTCTA  AAAAATGGCT  GGGCGAACa  ACcgctTTG  ACGGCAAAAA
501 AGTCTCTTGC  GCCTACGAAT  CCCCCGAAAG  TCAGCGCCGC  CCGcgAAAA
551 TGCAGGAGCT  GACCGAAACC  TTCCAATTCG  ACGGTAGCGC  CAGGTTATC
601 GTCGGCGGCA  AATATAAAGT  CGAATTTGCC  GACTGGGAGT  CCGGTATGAA
651 CACCATCGAC  CTTTGTGGCG  ACAAGTAGC  TGAAGACAA  AAAGCCCGCG
701  AGTAG

```

g687.pap

1	MKSRHLALAL	GVAALFALAA	CDSKVQTSVP	ADSAPAASAA	AAPAGLVEGO
51	NYTVLANPIP	QQQAGKVEVL	EFFGYFCFHC	ARLEPVLSKH	AKSFKDDMYL
101	RTEHVVVQKE	MLPLARLAAA	VDMAAASKD	VANSHIFDAM	VNQIKLQEP
151	EVLKKWLGEQ	TAFDGGKVID	AYESPESQAR	AGKKQELTET	FQIDGTPTVI
201	VGGIKKVEFA	DWESGMTNTI	LLADKVRREEQ	KAAQ*	

```
m687.seq
1  ATGAAATCCA GACACCTTGC CCTCgGCGTT GCCGCCCTGT TCGCCCTTGC
51  CGCGTGCAC AGCAAAGTCC AAACCAGCGT CCGCGCCGAC AGCGCGCTGT
101 CGGTTTCGGC AGCGCGCGCC CGCGGAGGGC TGGTCTGAAG GCAAACACTA
151 ACCGTCCTTG CCAACCCGAT TCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCGCGA CTGCGCCCACT CTCGAACCTG
251 TTTTAAGCAA ACGCGCAAG TCTTTTAAAG ACGATATGTA CCTCGGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCTTCGCCGC
351 CGCGCTCGAT ATGGGTCGCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC AAAAAATCAA AGCTGCAAAA TCCGGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAAACGCC TTTGACGGCA AAAAAGTCCT
```

1103

```

501 TGCCGCTAC GAGTCCCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGTAAATATA AAGTTGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA AAAAAAGCC GCGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2282; ORF 687>:

```

m687.pep
  1 MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
 51 TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWVQKEML TLARLAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNEV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFO IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

```

m687/g687 97.0% identity in 234 aa overlap

      10      20      30      40      50
m687.pep MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAA PAGLVEGQNYTVLANPIP
          |||||
g687      MKSRHLALGVAALFALAACDSKVQTSVPADSAPAASAAAA PAGLVEGQNYTVLANPIP
          10      20      30      40      50      60

      60      70      80      90     100     110
m687.pep QQQAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTHEHVWVQKEMLTLARLAAA
          |||||
g687      QQQAGKVEVLEFFGYFCPHCARLEPVLSKHAKSFKDDMYLRTHEHVWVQKEMPLARLAAA
          70      80      90     100     110     120

      120     130     140     150     160     170
m687.pep VDMAAADSKDVANSHIFDAMVNQKIKLQNEVLKKWLGEQTA FDGKKVLAAYESPESQAR
          |||||
g687      VDMAAASKDVANSHIFDAMVNQKIKLQNEVLKKWLGEQTA FDGKKVLAAYESPESQAR
          130     140     150     160     170     180

      180     190     200     210     220     230
m687.pep ADKMQELTETFOIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          |||||
g687      AGKMQELTETFOIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

```

a687.seq
  1 ATGAAATCCA AACACCTCGC CCTCGGCGTT GCCGCCCTGT TCGCACTTGC
 51 CGCGTGCGAC AGCAAAGTCC AAACCAGCGT CCGCGCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGCAGGGC TGGTCGAAGG GCAAACTAT
151 ACTGTCCTTG CCAACCCGAT TCCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTCGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAGA GCCGGAAGTC
451 CTCAAAAATG GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT
501 TGCCGCTTAC GAATCTCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGCAAATATA AAGTCGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA AAAAAAGCC GCGCACTAA

```

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

```

a687.pep
  1 MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
 51 TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWVQKEML TLARLAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNEV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFO IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N. meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

	10	20	30	40	50	60
m687.pep	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAAASAAAAPAGLVEGQNYTVLANPIPQQ					
a687	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAAASAAAAPAGLVEGQNYTVLANPIPQQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m687.pep	QAGKVEVLEFFGYFCPHCAHLEPVLKSHAKSFKDDMYLRTEHVWVQKEMLTARLAAAVD					
a687	QAGKVEVLEFFGYFCPHCAHLEPVLKSHAKSFKDDMYLRTEHVWVQKEMLTARLAAAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m687.pep	MAAADSKDVANSHIFDAMVNQIKLQNEVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
a687	MAAADSKDVANSHIFDAMVNQIKLQNEVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m687.pep	KMQLTETFTQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX					
a687	KMQLTETFTQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAHX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

1	GTGCTACACT	AGACATCCCG	ATTGTCACAG	AAAGGTTCTC	CCGTGAACAA
51	AACCTCATC	CTCGCCCTTT	CGCCCTGTT	CAGCCTGACC	GCGTGCAGCG
101	TCGAACGCGT	CTCGCTGTTT	CCCTCCTACA	AACTCAAAT	CATCCAAGGC
151	AACGAACTCG	AACCGCGCGC	CGTTGCCGCC	CTGCGCCCGC	GCAATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAACCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCCCTCC	AAAATGCCGC	CGAAGCCCTC	CGCGCGAAAC
401	AAAACGCAGA	CAAACAATAA			

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688>:

g688.pep

1	VLH*TSRFAQ	KGSPVNKTLI	LALSALFSLT	ACSVERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DALQNAAEAL	RAKQNAADKQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

1	GTGTTACACT	ACCCATCCCG	ATTGTCACAG	AAAGGCATT	CCGTGAACAA
51	AACCTCATC	CTCGCCCTTT	CGCCCTCCT	CGGCCTTGCC	GCGTGCAGTG
101	CCGAACGCGT	TTCATGTTT	CCCTCGTACA	AACTCAAAT	CATACAGGGC
151	AACGAACTCG	AACCGCGCGC	CGTTGCCGCC	CTCCGCCCGC	GCAATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCATTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAATCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCTCTGC	AAAACGCTGC	CGAAGCCCTC	AAAGACCGCC
401	AAAACACAGA	CAAACCATAA			

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

1	VLHYSRFAQ	KGISVNKTLI	LALSALLGLA	ACSAERVSF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DVLQNAAEAL	KDRQNTDKP*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

```
m688/g688    90.6% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep     VLHYPSRFAQKGISVNKTLILALSALLGLAACSAERVSFLFPSYKLKIIQGNELEPRVAA
              ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688          VLHXTSRFAQKGSPVNKTLILALSALFSLTACSVERVSLFPSYKLKIIQGNELEPRVAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m688.pep     LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIISKERSNLTVYFENGVLVRTEG
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688          LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIISKERSNLTVYFENGVLVRTEG
              70      80      90      100     110     120

              130     140
m688.pep     DVLQNAAEALKDRQNTDKPX
              ||||| ||||| ||||| |||||
g688          DALQNAAEALRAKQNADKQX
              130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

```
a688.seq
1  GTGTACTACT ACCCATCCCG ATTTGCACAG AAAGGCATT CCGTGAACAA
51 AACCTCATC CTCGCCCTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGCG
101 TCGAACGCGT TTCACTGTTC CCCTCGTACA AACTCAAAAT CATACAGGGC
151 AACGAACTCG AACCTCGCGC CGTCGCCTCC CTCGCCCCCG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAAACGGCG TGCTCGTCCG
351 CACCGAAGGC AACGCCCTGC AAAATGCCGC CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

```
a688.pep
1  VLHYPSRFAQ KGISVNKTLI LALSALLGLA ACSVERVSFL PSYKLKIIQG
51 NELEPRAVAS LRPGMTKDQV LLLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KDRSNLTVYF ENGVLRVTEG NALQNAAEAL RVKQNADKQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

```
m688/a688    93.5% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep     VLHYPSRFAQKGISVNKTLILALSALLGLAACSAERVSFLFPSYKLKIIQGNELEPRVAA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688          VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFPSYKLKIIQGNELEPRAVAS
              10      20      30      40      50      60

              70      80      90      100     110     120
m688.pep     LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIISKERSNLTVYFENGVLVRTEG
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688          LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIISKERSNLTVYFENGVLVRTEG
              70      80      90      100     110     120

              130     140
m688.pep     DVLQNAAEALKDRQNTDKPX
              ::||| ||||| ||||| |||||
a688          NALQNAAEALRVKQNADKQX
              130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

g689.seq (partial)

```

1  ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTCCAT CGATGCCCTAC CTGCCCCGCGA
101 TTCCCCGAAAT GCGCGAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGTATTGTT CGGCACGGCG TTCGGGCAAG TGGCCGGCGG
201 CGCGGTGTCC GACATCAAAG GCGCAAACC CGTCGCCCTG ACCGGTTTGA
251 TTGTATATTG CCTTGCCTGT GCCGCCATCG TATTGTCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGCGCAG GCATGGCTGT
351 AGTCATCGTc ggtgcgatgg tgcgcgatTA TTATCCGGA CGCAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCATCATTC TGATGGTTGT GCCGCTGGCC
451 GCACCCATGG TCGGCGCATT GTTGACGGGA TTGGGCGGAT GCGGGGCGAT
501 TTTCGTTTTT ttggcGgcgT ATTGCGCGGT GCTGCCCGGT TTGGTACAGT
551 ATTTCTGTCC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTC
601 GGGCTGGTGG CGGGCGCGTT CAAGCGCGTA TTGAAAACCC GTGCCCGGAT
651 GGGTtatCTG TTTTTTCAGG CATTACGCTT CGGTTTCATG TTCGCCTTTC
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCAGT TACGCCGCAC
751 CCGTACGCAT GGGTGTTCG ACTCAACATC ATCAGCATGA TGTTTTCAG
801 CCGCGTTACC GCGTGGCGGC TTAACACCG CGCGCATCCG CAAAGCATCC
851 TGCTGCGGGG GATTGTCGTC CAATTTGCCG CCAACCCGTC CCAACTCGCC
901 GCCGTGCTGT TTTTCGGGTT GCCCCCGTTT TGCTGCGCG TCGCGTGCCT
951 GATGTTTTTC GTCGGTACGC AGGGCCTGGT CGGTGCGGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAA GAAGAGGGCG GCAGCGCGAA CGCCGTGTCTG
1051 GGTGTATTCC GGTCTTAAT CGGCGCGGGC GTGGTCATGG CGGCAACCGT
1101 GATGGCGGCA ACCATGACCG CGTCCGCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGAAGGAAA ACGAAAAAA GCGAATACTT

```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689>:

g689.pep (partial)

```

1  ..SPPLPMSGK LMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51  SLSLFMFSTA FGQVAGGAVS DIKGRKEVAL TGLIVYCLAV AAVVFASSTE
101 QLLNLRAVQA FGAGMAVVIV GAMVRDYSG RKAQMFIIL GIILMVPLA
151 APMVGALLQG LGGWRAIFVF LAAYSPVLPG LVQYFLPNPA VGGKIGRDVF
201 GLVAGRFKRV LKTRAAMGYL FFQAFSFGSM FAFLTESSEF YRQLYHVTPH
251 RYAWVFALNI ITMMFFSRVT AWRLKTGAHP QSILLRGIV QFAANPSQLA
301 AVLFFGLPPE WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

m689.seq

```

1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCT GTTTGTGCCG GTGTGTTAAA ATTTCCCGT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGCGG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCCC ATTATCTGA AATGAGCGAA AAATGATGG CGGTTTTGAT
201 CGCGATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
301 CAGAGTTTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCCG
351 CCGTTCCGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCCTTGCC GTTGCCGCCA TCGTATTTGT TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGACG GCATTCCGTG CCGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCGCGA TTATTATTCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGACG GGCTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCC TCCCAAGCCC GCCGTGCGCG GCAAAATCGG ACGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAA CCCGTGCTGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTGCGTTTC ATGTTGCGCT
851 TTCTGACCGA ATCTTCTTTC GTGTACGAG AGCTCTACCG TGTACGCTT
901 CATCAATACG CTTGGGCGTT TGCACCTAAC ATCATACGA TGATGTTTTT
951 CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CGGCGTGAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTG CCGCAACCT GTCCCAACTC
1051 GCCCGCGTGC TGTTTTTTCG GTTGCCCGCG TTTTGGCTGC TGGTCGCTG
1101 CGTGATGTTT TCCGTCGCTA CGCAGGCGTT GGTGCGTGA AACACGACG
1151 CGTGTGTTAT GTCCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCGGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTTGAC GACGGTTTCG CAACCGTGAT GCGGCAACG ATGACCGCGT
1301 CCACCTCTTG CCGCATTCG CTTCTGTGGC TCTGCTGCA TCGTGGTGG

```

1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA

This corresponds to the amino acid sequence <SEQ ID 2294; ORF 689>:

m689.pep
 1 LLIHIVPVR PVLPGLLLP VCAGVLKFSV SAYCVFERRA VCLRIGREFM
 51 PSAHYPEMSE KIMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
 101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLIVYCLA VAAIVFVSSA
 151 EQLNLNRVVO AFGAGMTVVI VGAMVRDYS GRKAAQMFAL IGIILMVVPL
 201 VAPMVGALLQ GLGGWQAIIV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
 251 FGLVAGRFKR VLKTRAAMGY LFFQAFSFGS MFAFLTESSF VYQQLYRVTP
 301 HQYAWAFALN IITMMFFNRV TAWRLKTGVH PQSILLWQIV VQFAANLSQL
 351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
 401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
 451 KENGQSEYL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

	30	40	50	60	70	80
m689.pep	CAGVLKFSVSAYCVFERRAVCLRIGREFMPSAHYPEMSEKIMAVLMAMLVTLMPFSIDA					
g689	SPPLPPMSGKLMAVLMAVLVALMPFSIDA					
		10	20	30		
	90	100	110	120	130	140
m689.pep	LPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLA					
g689	LPAIPEMAQPLNADIHRIEXSLSLFMFGTAFGQVAGGAVSDIKGRKPVALTGLIVYCLA					
	40	50	60	70	80	90
	150	160	170	180	190	200
m689.pep	AAIVFVSSAEQLNLNRVQAFGAGMTVVIVGAMVRDYSGRKAAQMFALIGIILMVVPLV					
g689	AAIVFASSTEQLNLNRVQAFGAGMAVVIVGAMVRDYSGRKAAQMFALIGIILMVVPLA					
	100	110	120	130	140	150
	210	220	230	240	250	260
m689.pep	APMVGALLQGLGGWQAIIVFLAAYSLVLLGLVQYFLPKPAVGGKIGRDVFGVLVAGRFKRV					
g689	APMVGALLQGLGGWRAIFVFLAAYSPLVGLVQYFLPNFVAVGGKIGRDVFGVLVAGRFKRV					
	160	170	180	190	200	210
	270	280	290	300	310	320
m689.pep	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMMFFNRVT					
g689	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYRQLYHVTPHRYAWVFALNIITMMFFSRVT					
	220	230	240	250	260	270
	330	340	350	360	370	380
m689.pep	AWRLKTGVHPQSILLWQIVVQFAANLSQLAAVLFFGLPPFWLLVACVMFSVGTQGLVGAN					
g689	AWRLKTGAHPQSILLRGIVVQFAANPSQLAAVLFFGLPPFWLVPVACVMFSVGTQGLVGAD					
	280	290	300	310	320	330
	390	400	410	420	430	440
m689.pep	TQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLHDGSATVMAATMTASTSCGIAL					
g689	TQACFMSYFKEEGGSANAVSGVFRSLIGAGVMAAT-----VMAATMTASASCGIAL					
	340	350	360	370	380	
	450	460				
m689.pep	LWLCSHRAWKENGQSEYLX					
g689	LWLCSHKAWKENKKRIL					
	390	400				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

```
a689.seq
1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCGCT GTTGTGCGCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAAGTATGCG CGGTTTTGAT
201 GGCATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCCG
251 CGATTCCCGA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCACG GCGTTCGGAC AGGTGGTCCG
351 CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGGCCGCTCTA CTGCCTTGCC GTTCCCGCCA TCGTATTTGC TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCTGTCAG GCATTCGGTG CGGGCATGAC
501 GTTGGTCATC GTCGGCGCAA TGGTGCAGCA TTATTATCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCCGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCTT GCCAAGCCC GCCGTCGGCG GCAAATCGG CAGGGATGTG
751 TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAAA CCCGTGCCCG
801 GATGGGTTAT CTGTTTTTTC AGGCATTAG CTTCGGTTCG ATGTTGCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCA CGTTACGCCG
901 CACCAAGTACG CTTGGGCGTT TGCATCAAC ATCATCACA TGATGTTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAC CCGCGTGCA CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACTC GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTTCG GTTGCCCCCG TTTTGGCTGC TGGTCCGCTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTCCGGTGA AACACGCAGG
1151 CGTGTGTTAT GTCTTATTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGCGGAC
1251 CTTCTTGACG GACGGTTCGG CAACCGTGAT GCGGCAACC ATGACCGCGT
1301 CTACCTCTTG CGGCATTGCG CTTTGTGGC TCTGCTCGCA TCGTCCGTGG
1351 AAAGAAACG GCAAAGCGA ATACCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

```
a689.pep
1  LLIHIVPVR PVLPGLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
151 EQLNLNRVQ AFGAGMTVVI VGAMVRDYS GRKAAQMFAL YGIIIMVVPL
201 VAPMVGALLQ GLGGWQALFV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGREKR VLKTRAAMGY LFFQAFSFGS MFAFLTESSF VYQQLYHVT
301 HQYAWAFALN IITMFFNRI TAWRLKTGVH POSILLWGIV VQFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
451 KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

```
m689/a689 99.1% identity in 459 aa overlap

      10      20      30      40      50      60
m689.pep  LLIHIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
          |||
a689      LLIHIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
          |||

      10      20      30      40      50      60
m689.pep  KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
          |||
a689      KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
          |||

      70      80      90      100     110     120
m689.pep  SDIKGRKPVALTGLIVYCLAVAAIVFSSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYS
          |||
a689      SDIKGRKPVALTGLAVYCLAVAAIVFASSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYS
          |||

      130     140     150     160     170     180
m689.pep  GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQALFVFLAAYSLVLLGLVQYFLPKP
          |||
a689      GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQALFVFLAAYSLVLLGLVQYFLPKP
          |||
```

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```

|||||
a689      GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSLVLLGLVQYFLPKP
          190      200      210      220      230      240

          250      260      270      280      290      300
m689.pep  AVGGKIGRDVFGVLVAGRFRKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTP
          |||||
a689      AVGGKIGRDVFGVLVAGRFRKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYHVT
          250      260      270      280      290      300

          310      320      330      340      350      360
m689.pep  HOYAWAFALNIITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLF FGLPP
          |||||
a689      HOYAWAFALNIITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLF FGLPP
          310      320      330      340      350      360

          370      380      390      400      410      420
m689.pep  FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLG VFGSLIGAGVGM AATFLH
          |||||
a689      FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLG VFGSLIGAGVGM AATFLH
          370      380      390      400      410      420

          430      440      450      460
m689.pep  DGSATVMAATMTASTSCGIALLWLC SHRAWKENGQSEY LX
          |||||
a689      DGSATVMAATMTASTSCGIALLWLC SHRAWKENGQSEY LX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

```

g690.seq (partial)
1  ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCGCGCGT TCCCGGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTTCCTCAAC CGATTTGCAA
151 CCGGCCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCCTGC ACCCGCCGCG CGGCATTGGC GATCTCATAC
251 AGCAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 AACGAACTGG AAACCGTTT CGGCTTACCC GCGCGCGGCT ATGACAACAT
351 ACAGCGGCTG CTgtttCCCG ACATCCGCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGccgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAAACCGG GgACAAGCGG
551 AGGAACCGAA ACGCGCACGT TATTTTGAAG TTTCGGCAAC ATctgCCtat
601 TTgaaccggc ACAACAacGG ACTTggcgGC AATTTCCAAT ACATCGGCCA
651 ATTGCCCGGC TATCTGAAAA TGCACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCAGC CGTATTGTCT TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

```

g690.pep (partial)
1  MKNKTSLLPL WLAAIMLAAR SPSKEDKKE NGASAASSSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQQAIEHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSOKTR GQGEPEKRRAR YFEVSATSAY
201 LNRHNNGLGG NFOYIGQLPG YLKMHGEMLE NQSLFRLSNR ERNPKPFPLD
251 IHFDENGKIT RIVVYEKNY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

```

m690.seq..
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTGCAT
101 CCGCTGCTTC GTCCTCCGCG TCATCAGCTC CTTCCTCAAC CGATTTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCG
201 GTCAAATTGC ACCAGCCTGC ACCCGGCCAC CGGCATTGAC GATCTCATGC
251 AGCAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 CACGAACTGG AAACCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAC GCGCACGATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACCCGC GGACAAGCGG

```

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```

551 AGGAGCCGAA ACGCACGCGT TATTTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTTCCAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTGTAGAC
751 ATCCATTTT ACGAAAATGG CAAAATCAG CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCAATCCAA ACACGGGGCG AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
  1 MKNKTSLLL WLTAIMLTAC SPSKDDKTKE VGASAASSA SSAPSQTDLQ
 51 PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQQIAEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQKIILAI EDLRYGKRTI
151 SRQAQNALME QERRLREATL LLIQGSQETR GQGEEPKRTR YFEVSATPAY
201 SSRHNNGLGG NFQYISQLPG YLKIHGEMLE NQSLFRLSNR ERNPDKPFLLD
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

```

m690/g690      89.3% identity in 408 aa overlap

      10      20      30      40      50      60
m690.pep  MKNKTSLLLWLTAIMLTACSPSKDDKTKEVGASAASSSASSAPSQTDLQPTASAPDNVK
          |||:||||:| |||:|||| |||:|||| |||:|||| |||:||||
g690      MKNKTSLLPLWLAAIMLAARSPSKEDKTKEVGASAASSSASSAPSQTDLQPAASAPDNVK
          10      20      30      40      50      60

      70      80      90      100     110     120
m690.pep  QAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNIQRL
          |||:||||:| |||:|||| |||:|||| |||:|||| |||:||||
g690      QAESAPLXNCTGLHPAAGIGDLIQQIAEHIDSDCLFALSHHELETRFGLPGGGYDNIQRL
          70      80      90      100     110     120

      130     140     150     160     170     180
m690.pep  LFPDIRPEDPDYHQKITLAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQETR
          |||:||||:| |||:|||| |||:|||| |||:|||| |||:||||
g690      LFPDIRPEDPDYHQKIMLAIEDLRYGTRTISRQAQDAIMEQERRLREATLMLTQGSQKTR
          130     140     150     160     170     180

      190     200     210     220     230     240
m690.pep  GQGEEPKRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLENQSLFRLSNR
          |||:||||:| |||:|||| |||:|||| |||:|||| |||:||||
g690      GQGEEPKRARYFEVSATSAYLNRHNNGLGGNFQYIGQLPGYLMHGEMLENQSLFRLSNR
          190     200     210     220     230     240

      250     260     270     279
m690.pep  ERNPDKPFLLDIHFDENGKITRIVVYEKNIYFNPNTGRIX
          |||:||||:| |||:|||| |||:|||| |||:||||
g690      ERNPDKPFLLDIHFDENGKITRIVVYEKNIY
          250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.seq
  1 ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
 51 GACCGCGTGT TCCCGGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTCT GTCCACGGCA TCCCGCGCTT CGTCTTCCGC GCCCCAAACC
151 GATTGCAAC CGGCCGCATC CGCCCTGAT AACGTCAAGC AGGCAGAAAG
201 CGTGCCGCCG TCAAATTGCA CCGACCTGCA CCCCGCCACC GGCATTGACG
251 ATCTCATGCA GCAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCCGTTTC GGCTTACCCG GCGCGCGCTA
351 TGACAACATA CAGCGGCTGC TGTTTCCCGA CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAATCATA CTGGCAATTG AAGACTTGCG TTACGGAAAG
451 CGCACGATCA GCCGGCAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGGCAGTCAA GAAACCCGCG
551 GACAAGGCGA GGAGCCGAAA CGCACGCGTT ATTTTGAAAT TTCGGCAACC
601 CCTGCCTATT CGAGCCGGCA CAACAACGGA CTTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGGCT ATCTGAAAT ACACGGAGAA ATGCTTGAAA

```

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701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
 751 TTTTATAGACA TCCATTTTGA CGAAATGGC AAAATCACGC GTATTGTCGT
 801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep
 1 MKNKTSLLL WLAAMLTAC SPSKEDKKE NGASAASSTA SAASSAPQT
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA
 101 LSHHELETRF GLPGGGYDNI QRLFPDIRP EDPDYHQKII LAIEDLRYGK
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRGQGEEPK RTRYFEVSAT
 201 PAYSSRHNNG LGGNFQYIGQ LPGAUKIHGE MLENQSLFRL SNRERNPDKP
 251 FLDIHFDENG KITRIVVYEK NIYFNPGLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

m690.pep	10	20	30	40	50
	MKNKTSLLLWLTAIMLTACSPSKDDKTKEVGASAASSASSAPS---	QTDLPQTASAPD			
a690	MKNKTSLLLWLAAMLTACSPSKDDKTKEVGASAASSASSAPS---	QTDLPQTASAPD			
	10	20	30	40	50
m690.pep	60	70	80	90	100
	NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI				
a690	NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI				
	70	80	90	100	110
m690.pep	120	130	140	150	160
	QRLFPDIRPEDPDYHQKII LAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQ				
a690	QRLFPDIRPEDPDYHQKII LAIEDLRYGKRTISRQAQDALMEQERRLREATLLLIQGSQ				
	130	140	150	160	170
m690.pep	180	190	200	210	220
	ETRGQGEPEPKRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGAUKIHGEMLNQSFLRL				
a690	ETRGQGEPEPKRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGAUKIHGEMLNQSFLRL				
	190	200	210	220	230
m690.pep	240	250	260	270	279
	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPGLGRX				
a690	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPGLGRX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq
 1 GTGCCGCTGC CTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTT
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCGGAA CGATTTCCTA CCGAACTGCG ACATACGCCG GCTCGGGCTG
 151 ACACAGGGTC AGCACAAATGA GCTGCGTAAA ATCCGCGCCG CCTTCAAAAT
 201 GCGGGCGGAC AGGCGCGGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
 251 GCGGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG
 301 GCGGCGGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTTGCGGT
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
 401 AGCAGCAAAT GTGGCTTCTT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep
 1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
 51 TQGHNELRK IRAAFKMGAD RARLKVHSE HSRRSVVEI ISSDVFNRE
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGGTAT GCATTCCGAA CACAGCCGCC
251 GCCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQGOHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691 97.2% identity in 144 aa overlap

      10      20      30      40      50      60
m691.pep VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQGOHNELRK
      |||
g691      VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQGOHNELRK
      |||

      70      80      90      100     110     120
m691.pep IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL
      |||
g691      IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL
      |||

      130     140
m691.pep EIQRFFHILTPQQQMWLS SCLKX
      |||
g691      EIQRFFHILTPQQQMWLS SCLKX
      |||
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGGTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQGOHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. meningitidis*:

m691/a691 97.2% identity in 144 aa overlap

```

      10      20      30      40      50      60
m691.pep VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDPQPCNDIRRLGLTQSQHNELRK
      |||
a691     VPLXAPCRFAKPAASFLSMALLSCQLSHAATAYIPLNDFQPCNDIRRLGLTQSQHNELRK
      10      20      30      40      50      60

      70      80      90     100     110     120
m691.pep IRTAFKMAGDRARLKVHSEHSRRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL
      |||
a691     IRTAFKMAGDRARLKVHSEHSRRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL
      70      80      90     100     110     120

      130     140
m691.pep EIQRHFFHILTPQQQMWLSSCLKX
      |||
a691     EIQRHFFHILTPQQQMWLSSCLKX
      130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2309>

```

g692.seq
1  GTATCGCACA CACGCTGTCG CTGTTCCGAA TCGAtacGCC GGATTGCGCG
51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATGCGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGT ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTgacGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGCTCT TGGAACAGGG CTTCGGTCAG CTTATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTGCGCGCG
401 AGTTGTGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCCCG
451 GATGTGCGGT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAAACCAG TTCGTTACAG ATCACCAGG CGCGTGCGAA GTTGGAcggG
551 TcgtTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGTTTGCCC GGATACAGTC CCAAAGGCGC GGTGCGCACT TGAAGGCTT
651 CGGTGATGTC CAGGTTGTGT TCTTTTTTGA AATCGTCAAG ATAGGGTTTG
701 TGGTGCAGAA CGTTGATGTC CAACTCGCCC TCCGCCAATG CCAGATTCCG
751 GCGCACATAG TCggTAAATT cgaccaatTT gacgGTGTAg cTTTTTTTCT
801 CCAGCTCGGc tTGGATTTGT TCTTTGACCA TATcgccgaa gtcgcccacg
851 gTCGTGCCa agacgaTTT TTTTTCGCGc GcgcCGTTAT CGGCAGAAGG
901 GCGGCGGgca gaggctgcGG GCGCGCTGTC TTTTtgaccG ccgCAGGCTG
951 CGAGGATGAG CGCGAGtgcg gcggcggaag ggGTTTGAA GAAGGTTTc
1001 atATTTTCTc ctga

```

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692>:

```

g692.pep
1  VSHTRCRCSE SIRRIWRNGR EWRIKQKCR LNTDAVQTAS FYTTALEGCA
51  FIPCGRVFVA LEAFVRVGFE RVGVIGLVYV FKPLAVFVGG FDGRPVDIGK
101 ARLLLEQGFQ LHAAYGVVA VDDGKIHVGA AARQLCGFKL DDFDVFQVFR
151 DVGFGCGQRI DAVFEFDPTQ FVQHHQGACE VGRVVGGRYG AAVDFDFQRF
201 QFARIQSQR GRHLEGFGDV QVVFVEIVK IGFVLEDVDV QLALRQCQIR
251 AHIVGKFDQF DGVAFFLQLG LDLEFDHIAE VAHGRAEDDF FFRAVIGRR
301 GGGRCGRAV FLTAAGCEDE RECGGKGFE EGFHIFS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

```

m692.seq
1  GTGTTGCACA CGCTTTGTCG CTGTTCCGAA TCGATACGCC GGATTGCGCG
51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACAGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTCGGTCAG CTTATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGCG

```

m692.pap

```

1 VLHTLCRCSE SIRRIRNRG EWRIGQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCFRGFEV LEAFVRVGEV RVDGKILGYV FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAYVGVVA VVGQIHWGA ATROLGRGFKL DDFDVFQVLG
151 DVRFEGCGRI DAVEFDPQT FVEHHQDAGE VGRVVLRGGL AADEVFFQVL
201 QLARVQSQRH GRHLEDFDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AIVYGVKLDQF GDVAFFLLQG LDFLFDHIAE VADGRAEEDF FFRRAVVGGG
301 RSGCGGRADV LTAAGGEDER ECGGGKGFEF GHFHS*

```

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

m692/g692 91.1% identity in 338 aa overlap

	10	20	30	40	50	60
m692.pep	VLHTLCRCSESI	RRIRNRNGREWRI	KGQKCRLNTD	TQTASFYTTAL	FGCAFI	PCGRGFVA
g692	VSHTRCRCSESI	RRIRNRNGREWRI	KGQKCRLNTD	AVQTASFYTTAL	FGCAFI	PCGRGFVA
	10	20	30	40	50	60
m692.pep	70	80	90	100	110	120
g692	LEAFVRVGFER	VGIVGLGYVFK	PLAVFVGGFD	GRPVDIGKAR	FLEQGF	QQLHAAAYGVVA
	70	80	90	100	110	120
m692.pep	130	140	150	160	170	180
g692	VDDGKIHVGAA	TRQLRGFKLDD	FDVFQVLGDV	RFGGCQRIDAV	FEFDPTQFV	EHHQDAGE
	130	140	150	160	170	180
m692.pep	190	200	210	220	230	240
g692	VGRVVGGRGYG	AAVDFDFQRFQ	LARVQSQRGR	HLIEDFGDVQ	IVFFFEVVKI	GFVLEDVDV
	190	200	210	220	230	240
m692.pep	250	260	270	280	290	
g692	QLALSQCQIRAY	IVGKLDQFDG	VAFFLQLGLD	LFDDHIAEVA	DGRAEDDFFFR	RAVVG--
	250	260	270	280	290	300
m692.pep	300	310	320	330		
g692	GGRSGCGGRAV	FLTAAGGEDER	ECGGGKGFE	EGFHIFSX		
	300	310	320	330		
m692.pep	300	310	320	330		
g692	GGGRGCG-RAV	FLTAAGCEDER	ECGGGKGFE	EGFHIFSX		

a692.ssq

1 GTGTTGCACA CGCTTTGTCG CTGTTCGGAA TCGATACGCC GGATTCGGCG

```

51 GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTGCGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGC CTTCAGCTC GACGATTTG ATGTTTTC A GGTTTTCGGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTCGGCACT TGGAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGCAAG ATAGGGTTT
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGCACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGTCGGG TTGGATTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTTGT CCGCGCGGCG
901 AGAAGCGGAT GCGGCGGGCG CGCTATCTT TTGACCGCG CAGGCGGCGA
951 GGATGAGCG GAGTGCAGCG GCGGAAAGG TTTGAAGAA GGTTCCTATA
1001 TTTTCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

```

a692.pep
1 VLHTLCRCSE SIRRI RRNGR EWRIGQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGF E RVGVIGLYV FKPLAVFVG FDGRPDVIGK
101 ARFLEQGGFQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVFG
151 NVRFQCGQRI DAVFEFDPTQ FVEHHQDAGE VGRVVG RGYG AAVFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQQIR
251 AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVG
301 RSGCGGRAIF LTAAGGEDER ECGGKGFE EGFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

```

m692/a692 98.8% identity in 336 aa overlap

```

	10	20	30	40	50	60
m692.pep	VLHTLCRCSE	SIRRI RRNGR	EWRIGQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
a692	VLHTLCRCSE	SIRRI RRNGR	EWRIGQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
	10	20	30	40	50	60
m692.pep	LEAFVRVGF	ERVGVIGLYV	FKPLAVFVG	FDGRPDVIGK	ARFLEQGGFQ	LHAAAYGVVA
a692	LEAFVRVGF	ERVGVIGLYV	FKPLAVFVG	FDGRPDVIGK	ARFLEQGGFQ	LHAAAYGVVA
	70	80	90	100	110	120
m692.pep	VDDGKIHVGA	ATRQLRGFKL	DDFDVQVFG	GNVRFQCGQRI	DAVFEFDPTQ	FVEHHQDAGE
a692	VDDGKIHVGA	ATRQLRGFKL	DDFDVQVFG	GNVRFQCGQRI	DAVFEFDPTQ	FVEHHQDAGE
	130	140	150	160	170	180
m692.pep	VGRVVG RGYG	AAVFDFFQRF	QLARVQSQR	GRHLEDFGDV	QIVFFFEVVK	IGFVLEDVDV
a692	VGRVVG RGYG	AAVFDFFQRF	QLARVQSQR	GRHLEDFGDV	QIVFFFEVVK	IGFVLEDVDV
	190	200	210	220	230	240
m692.pep	QLALSQQIR	AHIVGKLDQF	DGVAFFLQLG	LDLFFDHIAE	VADGRAEDDF	FFRRAVVG
a692	QLALSQQIR	AHIVGKLDQF	DGVAFFLQLG	LDLFFDHIAE	VADGRAEDDF	FFRRAVVG
	250	260	270	280	290	300
m692.pep	RSGCGGRAIF	LTAAGGEDER	ECGGKGFE	EGFHIFS		
a692	RSGCGGRAIF	LTAAGGEDER	ECGGKGFE	EGFHIFS		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

g694.seq
 1 TCGGCATTG TGTGCCCCA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
 51 AACGTTTGCA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
 101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
 151 TTCATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCCGC ACCAACACTT
 201 CGGGCGCGGA CGCGCCTGCC GTTACGCCGA CTTTGCTTTT GCCTTCAAAC
 251 CACGTGCGTT GCaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
 301 GCGCGATGCC GCCACTTCGC GCAGGCGGTT GCTGTTGGAC GAATTGGGCG
 351 AACCGACCAC AATCACGATG TCGCACTGTT CCGCCAGCTC TTTGACGGCG
 401 GTTTGCGCGT TGGTCGTGCG ATAGCAGATG TCTTCCTTGT GCGGATTGCG
 451 GATATTGGGG AAACGCGCGT TCAGCGCGGC GATGATGTCT TTGGTTTCAT
 501 CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTC GGGGTTTCTG
 551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
 601 CGGTGCAAGC TGCCCCATCG TGCCTTCGAC CTCGGCGTGC CCCTTATGCC
 651 CGATCATGAT GATTTCACAG TCTTGGGCAT CCAGTCGGGC GACTTCCTTA
 701 TGCACTTTTC TCACCAGCGG GCAAGTCGCA TCAATAACCC GGAACCGCG
 751 CTCGCGCGCT TCCTGCTGCA CCGCCTTCGA TACGCCGTGT GCCGAATAAA
 801 CCAGTGTGCG GCCCGGCGGC ACTTCCGCCA AGTCTTCGAT AAACACCGCG
 851 CCTTTTTCGC GCAGGTTGTC CACGACGAAT TTGTGTGGA CGACTTCGTG
 901 GCGCACATAA ACCGGCGCGC CGAATTCTTC CAAAGCACGT TCGACAATAC
 951 TGATTGCCCC ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAGGATG
 1001 ATGGTTTTCG CGTTCATAAG TTTTGCATTC CGTGTTCAGA CGGCATTAC
 1051 GTTTTTCGCG TNNATCTTG CGATGGACGA TATTGTCAAG CACCGCCAAC
 1101 ACCGCACCGA CGCAGATAA

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694>:

g694.pep (partial)
 1 SAFVLPKHPM PALTPASTFA QIGFGFALAA QLLGQDEHDA FFRAPPFAGH
 51 FMPPSAYGCQ YFPHQHFGRG RACRYADFAF AFKPRALQVG RVVHHIRIDS
 101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGGLPVGRR IADVFLVRIA
 151 DIGETRVRQG DDVFGFIDRE RGLADIGEFV GVSDFEFCHI SDRFDQKHFA
 201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHRHQR ASRIKYPETA
 251 LRRELLHLRL YAVCRINQCR ARRHFRQVFD KHRAFFAQVV HDEFVVDDEV
 301 AHINRRAEFF QSTFDNTDCP IHTGAEEARI GKDDGFSVHK FCIPCSGDIH
 351 VFLLXLCDDR YCQAPPTPHR RR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

m694.seq
 1 TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
 51 GACGGCATTT GTGTTGCCA AACATTCAAC GCCTGCGTCA ACGTTTGAC
 101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
 151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
 201 ATCCCGGTAT GGTGCCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
 251 GCGCCTGCCG TTACGCCGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
 301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
 351 CCACTTCGCG CAAGCGGTTG CTGTTGACG AATTGGGCGA ACCGACCACA
 401 ATCAGCATGT CGCACTGTTT TGCCAACTCT TTGACGGCGG TTTGCCGGTT
 451 GGTGCTGCGA TAGCAGATAT CTTCTTGTG CGGATTGCGG ATATTGGGGA
 501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
 551 TTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTGAGTTT
 601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GGCACAAGCT
 651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCCC GATCATGATG
 701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
 751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
 801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGC
 851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTCACG
 901 CAGGTTGTCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
 951 TCGGCGCGCC GAACCTCTCC AAAGCACGTT CGACAATACT GATT GCCCGA
 1001 TCCACACGAG CGCAGAAAGC GCGCGGATTG GCAAGGATGA TGGTTTCTC
 1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
 1101 TGGGTTTAC GGTGGACGAT GTTGTCCAAC ACCGCCAACA CCGCACCGAC
 1151 GCAGATAA

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

m694.pep
 1 LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
 51 HNAFFRTLAF AYGFVPSPAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
 101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDHALF CQLFDGGLPV

1117

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151 GRRRIADIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPKR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVVD DFVAHINRRA ELFQSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

m694/g694 86.8% identity in 372 aa overlap

```

              10      20      30      40      50
m694.pep    LVSASGTRQKCR LKPVQTAFVLPKHS----TPASTFAQIGFGFALAAQLFGQDEHNAFFR
              :|||||  |||||||  |||||||  |||||||  |||||||
g694        SAFVLPKHPMPALTPASTFAQIGFGFALAAQLLGQDEHDAFFR
              10      20      30      40

              60      70      80      90     100     110
m694.pep    TLAFAYGFVPPSAYGCQYFPQHFGGRGRACRYADVFALKPCALQVACIIHHRIDSARC
              :|||:|||||  |||||||  |||||||  |||:|  |||:|  |||:|
g694        APPFAHGFMPPSAYGCQYFPQHFGGRGRACRYADFAFAFKPRALQVGRVVHHRIDSARC
              50      60      70      80      90     100

              120     130     140     150     160     170
m694.pep    RHFAQAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDV
              |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
g694        RHFAQAVAVGRIGRTDHNHDVALFRQLFDGGLPVGRRIADVFLVRIADIGETRVQRGDDV
              110     120     130     140     150     160

              180     190     200     210     220     230
m694.pep    FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPKRSFDLDVPLMPDHDDFT
              |||||||  |||||||  |||||||  |||||||  |||:|  |||:|
g694        FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARCKLPKRAFDLGVPLMPDHDDFT
              170     180     190     200     210     220

              240     250     260     270     280     290
m694.pep    VLGIQSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHR
              |||||||  |||||||  |||||||  |||||||  |||:|  |||:|
g694        VLGIQSGDFLMHFRHQRASRIKYPETALRRFLHRLRYAVCRINQCRARRHFRQVFNKHR
              230     240     250     260     270     280

              300     310     320     330     340     350
m694.pep    TFFTQVVHDEFVVDNFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGI
              :||:|||||  |||||||  |||||||  |||:|  |||:|  |||:|
g694        AFFAQVVHDEFVVDNFVAHINRRAELFQSTFDNTDCPIHTGAEAAARIGKDDGFSVHKFCI
              290     300     310     320     330     340

              360     370     380
m694.pep    SFSDGINIFLLGFYGGRCCTPPTPHRRRX
              |||:|  :  ||  :|||||
g694        PCSDGIHVFLXXLCDGRYQAPPTPHRRRX
              350     360     370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

```

a694.seq
1  TTGGTTTCGG CATCCGGCAC ACGGCAAAAA TGCCGCTCTGA AGCCTGTTCAC
51  GACGGCATTG TGTTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGCAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCGGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTTCGCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCCG TTACGCGGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCACCATGT CGCACTGTTT TGCCAACTCT TTGACGGCGG TTTGCCGGTT
451 GGTCTGTCGA TAGCAGATAT CTTCCTTGTT CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTCT GGGTTTCTGA CTTTCGAGTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTCGCCC GGCAGCAAGCT
651 GCCCATCATG TCCTTCGACC TCGACGTGCC CCTTATGCCC GATCATGATG

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1118

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701 ATTCACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGCCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

```

a694.pep
1  LVASGTRQK CRLKPVQTAFLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHR IDSARCRHEA QAVAVGRIGR TDHNDHVALF CQLFDGGLPV
151 GRIADIPLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVNV DFVAHINRRA ELFQSTFDNT DCPINTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

m694/a694 100.0% identity in 385 aa overlap

m694.pep	10	20	30	40	50	60
a694	10	20	30	40	50	60
m694.pep	70	80	90	100	110	120
a694	70	80	90	100	110	120
m694.pep	130	140	150	160	170	180
a694	130	140	150	160	170	180
m694.pep	190	200	210	220	230	240
a694	190	200	210	220	230	240
m694.pep	250	260	270	280	290	300
a694	250	260	270	280	290	300
m694.pep	310	320	330	340	350	360
a694	310	320	330	340	350	360
m694.pep	370	380				
a694	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```

g695. seq
1   TTGCCTCAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTTGTGATG GCCGCCCAGT
101 GTCAAAATTC TCAAAGATTT CAATCAAAAC CTGCCGAACG ATACGCCGGAT
151 TGTCCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGCTG
251 CCTCCTGTGC TTCCGTTTTC CCCGTTCCGG AGGCGAGCCG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACTCT
351 GCAAGACCGT TTGGACTATC TGGAAAGCAA AATCGTCCGG CTGTGGAACG
401 AAGTGGAAAT GTTAAACGGG AAAGTCAAAG CATTTGGAGCA TACGAAAATA
451 CACCCCTCCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAACGGC
601 AGGTTTTCTG CCGCAGCCGC CTTGTTGAAG GGGCGGACG GCGGAGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCCGAA GTCATATTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTACGCA AACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```

g695. pep
1   LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCONSQRF QSKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIWL SVSASCASVL PVPEGSRTM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRTYVQK LDDRKLKEHY LNTEGGSASA HTVETAONLY NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQKQDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```

m695. seq
1   TTGCCTCAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGCTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCCGGATCG TCAAAGATTT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGTCGG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG CAGGCGACCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGGAAAGCAA AATCGTCCGG CTGTGGAACG
401 AAGTGGAAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCCTCCG GCAGGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCT
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAGCGGC
601 AAGTTTTCTG CCGCTGCCTC CCGTTTGAAG GCGCGGACG GAGGCGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGGAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTC AATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTGCGCA AACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```

m695. pep
1   LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRRHPQRF QSKPAERPAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAONLY NQALKHYKSG
201 KFSAASALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQKQDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

m695/g695 90.8% identity in 305 aa overlap

	10	20	30	40	50	60
m695.pep	LPQTRPSRRHHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR					
g695	LPQTRPARRHHRQYFVERKGDARSGFXCAAQCQNSQRFQSKPAERYADCPHHPARRRR					
	10	20	30	40	50	60
m695.pep	LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR					
g695	FDPASEKIMKTKLPLFIIWLSVSASCASVLPVEGSRTEMPTQENASDGIPYPVPTLQDR					
	70	80	90	100	110	120
m695.pep	LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTEGGSASA					
g695	LDYLEGKIVRLSNEVETLNGKVKALEHTKIHPGRTYVQKLDLDRKLKEHYLNTEGGSASA					
	130	140	150	160	170	180
m695.pep	LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTEGGSASA					
g695	LDYLEGKIVRLSNEVETLNGKVKALEHTKIHPGRTYVQKLDLDRKLKEHYLNTEGGSASA					
	130	140	150	160	170	180
m695.pep	HTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGGSIQRSMYLLQLSRARMGNCS					
g695	HTVETAQNLYNQALKHYQNGRFSAAAALLKGADGGDGGGSIQRSMYLLQLSRARMGNCS					
	190	200	210	220	230	240
m695.pep	HTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGGSIQRSMYLLQLSRARMGNCS					
g695	HTVETAQNLYNQALKHYQNGRFSAAAALLKGADGGDGGGSIQRSMYLLQLSRARMGNCS					
	190	200	210	220	230	240
m695.pep	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
g695	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
	250	260	270	280	290	300
m695.pep	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
g695	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
	250	260	270	280	290	300
m695.pep	AVRKRKX					
g695	AVRKRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

a695.seq

```

1  TTGCCTCAAG CTTGTCCGGC AAGCGGCAT CATGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCAGC
101 GTCCGGCATCC TCAAAGATTT TAATCAAAAC CTGCCGACG ATACGCCGAT
151 TGTCCCATC ACCCTGCCCG TCGCGACGG TTTGACCTG CTTCTGAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCCGTATCCG
251 CCGCCTGTTT TCCCTGTGTT TCCGCAATA TTCAGGATAT GCGGCTCGAA
301 CCGCAGGCAG AGGCAGGTAG TTCGGACGCT ATTCCCTATC CCGTCCAC
351 TCTGCAAGAC CGTTTGATT ATCTGGAAG CACTCGTC CGCTGTGCA
401 ACGAAGTGA AACCTTAAAC GGCAAGTCA AAGCACTGA GCATGCGAAA
451 ACACACCTT CCAGCAGGC ATACGTCAA AAACGACG ACCGCAAGT
501 GAAAGAGCAT TACCTCAATA CCGAAGCGG CAGCGCATCC GCACATACCG
551 TCGAAACCGC ACAAACCTC TACAATCAG CACTCAAACA CTATAAAGC
601 GGCAGTTTT CTGCCGTGC CTCCTGTTG AAAGCGCGG ACGGAGGCGA
651 CGGCGGCAGC ATCGCGCAAC GCAGTATGTA CCTGTTGCTG CAAAGCAGGG
701 CGCGTATGGG CAACTGCGAA TCCGTATCG AAATCGGAG GCGTTACGCC
751 AACCGTTTCA AAGACAGCCC AACCGCGCT GAAGCCATGT TCAAATCGG
801 CGAATGCCAA TACAGGCTT AGCAAAAAGA CATTGCAAG GCGACTTGGC
851 GCAGCCTGAT ACAGACCTAT CCCGGCAGC CGGCGGCAA ACGCGCCGCC
901 GCAGCCGTGC GCAAACGATA G

```

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

a695.pep

```

1  LPOACPARRH HCHRQYFVER KGDARSGFR AARRHPQRF *SKPAERYAD
51  CPHHPARRRR FDPASEKIM TKLPLFIIWL SVSACSSPV SRNIQDMRL
101 PQAEAGSSDA IPYPVPTLQD RLDYLEGLTV RLSNEVETLN GKVKALEHAK
151 THPSSRAYVQ KLDLDRKLKEH YLNTEGGSAS AHTVETAQNL YNQALKHYKS
201 GRFSAASLL KGADGGDGGG IAQRSMYLLL QSRARMGNCE SVIEIGGRYA
251 NREKDSPTAP EAMFKIGECQ YRLQKDIAR ATWRSLIQTY PGSPAAKRAA
301 AAVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from *N. meningitidis*:

m695/a695 88.3% identity in 308 aa overlap

m695.pep	10	20	30	40	50	60
	LPQTRPSRRHHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR					
a695	LPQACPARRHCHQYFVERKGDARSGFRCAAQRRHPQRFQSKPAERYADCPHHPARRRR					
	10	20	30	40	50	60
m695.pep	70	80	90	100	110	
	LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQT---EMSTRENASDGIYPVPVPTL					
a695	FDPASEKIMKTKLPLFIIWLSVSAACSS--PVSRNIQDMRLEPQAEAGSSDAIPYPVPVPTL					
	70	80	90	100	110	
m695.pep	120	130	140	150	160	170
	QDRLDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYLNTTEGGS					
a695	QDRLDYLEGTLVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLD DRKLKEHYLNTTEGGS					
	120	130	140	150	160	170
m695.pep	180	190	200	210	220	230
	ASAHTVETAQNLNQLKHYKSGKFSAASLLKGADGGDGGGSIQRSMYLLQLSRARMGN					
a695	ASAHTVETAQNLNQLKHYKSGRFSAAASLLKGADGGDGGGSIQRSMYLLQLSRARMGN					
	180	190	200	210	220	230
m695.pep	240	250	260	270	280	290
	CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRS LIQTYPGSPAAR					
a695	CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRS LIQTYPGSPAAR					
	240	250	260	270	280	290
m695.pep	300					
	AAAAVRKRKX					
a695	AAAAVRKRKX					
	300					

The following partial DNA sequence was identified in *N. gonorrhoeae*

g696.seq: not found

This corresponds to the amino acid sequence < ORF 696.ng>:

g696.pep: not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2327>:

m696.seq

```

1  TTGGGTTGCC GGCAGCGGCG ATCCCATCAT TTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGCTGCGCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTCA AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GCGGCAGAA
251 GCCGCACTGT CTTAACATC GGACTCAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTTG GCTTCTTTCG AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>:

m696.pep

```

1  LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
101 LFFGLRTSC QGSRHHCNQ *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:

a696.seq

1122

```

1   TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGTCTGCCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GCGGCAGAA
251 GCCGCAGTGT CTTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTG GCTTCTTTCG AACAAAGCTG CAAGGCAGCC GCCATCATG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

```

a696.pep
1   LGCRQAASHH FCQGNKLFEG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRLN
101 LLFGFLRTSC QGSRHHCNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

```

m696/a696 100.0% identity in 120 aa overlap

      10      20      30      40      50      60
m696.pep LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
      |||
a696     LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
      10      20      30      40      50      60

      70      80      90     100     110     120
m696.pep ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRLNLLFGFLRTSCQGSRHHCNQ
      |||
a696     ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRLNLLFGFLRTSCQGSRHHCNQ
      70      80      90     100     110     120

m696.pep  X
          |
a696      X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

```

g700.seq
1   ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTTCCTA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTCG
151 CGCGTGGAGG ATTTGGGTTC GCGGTTGGGC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TAGGGGCGAA CTTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTTC GATGCCGTCT GAAAACGCGG
401 GTATGTAATG CCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTG CTTAACCGGC GGGGCATCCG
501 GCTGTCGGTT TGGTTTATAT TGTCTCTCTT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGATGGGTGTG TCGTGGACGA AAGGTTTGCG GATGGCTTCC
601 GGCTTCGGTT GGTATTCCTT CTCGGGTTTG GTAATGACCG AGGCTTACGG
651 GCGGGTATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTCC GGATGCGGCG
751 GTGGGGTTCG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGCGGGC GGTGTGGAAG TCGTGCCGGT AGCGGTGAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTTTC CACGCTGGG
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

```

g700.pep
1   MSSLMTLFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRIG DMALTVLWLF VCTVGANLLA LAVLGKLSPW RIGGKGKGV
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMP ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRGIRLSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```

m700.seq

m700.pap

m700/g700

		10	20	30	40	50	60
m700.pep		MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
		: : : :					
g700		MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLLIGVSLSRVEDLGSRLG					
		10	20	30	40	50	60
		70	80	90	100	110	120
m700.pep		DMALTVLWLFVCTVGANLLALAVLGKLFPPWRIKGGKGVSVGSGSVGQLGCVLLGFAFG					
g700		DMALTVLWLFVCTVGANLLALAVLGKLSPPWRIGGGKGVSVGSGSVRQLGCVLLGFVSG					
		70	80	90	100	110	120
		130	140	150	160	170	180
m700.pep		KLMRDIWMPSESAGMYCMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
g700		KLMCDIWMPSENAGMYCMLLVFLIGVQLKSSGVSLRQVLNRRGIRLSVWFILSSLSGG					
		130	140	150	160	170	180
		190	200	210	220	230	240
m700.pep		LLFAASTDGVSWTKGLAMASGFGWYSLSGVLMT EAYGAVWGSIMLLNDLARELFALAFIP					
g700		LLFAASADGVSWTKGLAMASGFGWYSLSGVLMT EAYGAVWGSIMLLNDLARELFALAFI					

1124

	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDA	AVGVGGAT	SMDFTLP	VIQAGGLE	VPVAVS	FGVVVNIAAPFLMVVFSALG
g700	LLMKRFPDA	AVGVGGAT	SMDFTLP	VIQAGGLE	VPVAVS	FGVVVNIAAPFLMVVFSTLG
	250	260	270	280	290	300
m700.pep	X					
g700	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

```

a700.seq
1  ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51  ATTTTATATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCTG
151 CGCGTGGAGG ATTTGGGTTT GCGGTTGGAC GATATGCGCT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
301 GTCGGTGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCATCCGGC AAACGTATGC GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTCTG
501 GTTGTCGGTC TGGTTTATGC TTTTCTCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCCGGC AGACGGTGTG TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTGATGACCG AGGCTTACGG
651 CGCGGTATGG GGCAGTATCG CGCTTTTGAA CGATTTGCCA CGAGAGCTGT
701 TCGCGCTGGC ATTTATTCCG CTGCTGATGA AGCGTTTCC CGATGCGGCA
751 GTGGGGGTCTG CCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTCG
801 GGGTGCGGGC GGCTTGGAAG CCGTACCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCTCCG TTTCTGATGG TGGTGTTTTC CGCTTTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

```

a700.pep
1  MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLPFW RIKGKGKGV
101 VGVSGSVGQL GCVLLGFASG KLMRDIWMP ENAGMYCLML LVXLXIGVQLK
151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASADGV SWVKGLAMAS
201 GFGWYSLSLG VMTEAYGAVW GSIALNNDLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSMD FTLPVIRGAG GLEAVPVAVS FGVVVNIAAP FLMVVFSALG
301 *

```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
a700	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPFWRIKGKGKGVSVGVSGSVGQLGCVLLGFAFG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLPFWRIKGKGKGVSVGVSGSVGQLGCVLLGFAFG					
	70	80	90	100	110	120
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPFWRIKGKGKGVSVGVSGSVGQLGCVLLGFAFG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLPFWRIKGKGKGVSVGVSGSVGQLGCVLLGFAFG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVXLXIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180

1125

	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYSLSGGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
a700	LLFAASADGVSWVKGLAMASGFGWYSLSGGLVMTEAYGAVWGSIALNDLARELFALAFIP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLPIVIGAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
a700	LLMKRFPDAAVGVGGATSMDFTLPIVIRGAGGLEAVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
a700	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2337>:

g701.seq

1	ATGTCTTGGC	ACATATTCCA	AGTTGCAGGG	ATACCGACCG	CTTCGATGGC
51	ACAATCTACG	CCGTCTTCGC	CGACGATGGC	GAAAACCTGT	TTGGAGACGT
101	CGCCGGAAGC	GGGGCTGATG	GTATGGGTCG	CGCCCAACTC	TTTCGCCGGT
151	TTCAAACGGT	TTTCGTCCAT	ATCGCACACG	ATAATGGCGG	CAGGGCTATA
201	CAGTTGGGCG	GTCACAAGG	CGGACATACC	GACAGGGCCG	GCACCTGCGA
251	TGAATACGGT	ATCGCCGGGT	TTACATCGC	CGTATTGCAC	GCCGATTTCG
301	TGGGCGGTCG	GTAAAGCGTC	GCTCAACAGC	AGGGCGATTT	CTTCGTTGAC
351	GTTGTCGTGC	GGCGGCACGA	GGCTGTTGTC	GGCATAA	

This corresponds to the amino acid sequence <SEQ ID 2338; ORF 701>:

g701.pep

1	MSWHIFQVAG	IPTASMAQST	PSSPTMAKTC	LETSPEAGLM	VWVAPNSFAG
51	FKRFSSISHT	IMAAGLYSWA	VNKADIPTGP	APAMNTVSPG	FTSPYCTPIS
101	WAVGKASLNS	RAISSLTLSG	GGTRLLSA*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2339>:

m701.seq

1	ATGTCTTGGC	ACATATTCCA	TGTAGCAGGG	ATACCGACGG	CTTCGATGGC
51	GCAATCCACG	CCGTCTTCGC	CGACGATGGC	AAAGACTTGT	TTGGATACTT
101	CGCCGGAAGC	AGGGTTAATG	GTATGGGTCG	CACCCAATTC	TTTCGCCAGT
151	TTCAAACGGT	TTTCGTCCAT	ATCGCAACAG	ATGATGGCGG	CGGGACTGTA
201	CAGTTGGGCG	GTCACAAGG	CGGACATACC	GACAGGGCCT	GCCCCAGCGA
251	TGAATACGGT	GTCGCCGGGT	TTGACATCGC	CGTATTGCAC	GCCGATTTCG
301	TGGGCGGTCG	GCAAAGCGTC	GCTCAACAAC	AGGGCGATTT	CTTCGTTGAC
351	ATTATCGGGC	AGCGGAACGA	GGCTGTTGTC	GGCATAA	

This corresponds to the amino acid sequence <SEQ ID 2340; ORF 701>:

m701.pep

1	MSWHIFHVAG	IPTASMAQST	PSSPTMAKTC	LDTSPPEAGLM	VWVAPNSFAS
51	FKRFSSISQT	MMAAGLYSWA	VNRADIPTGP	APAMNTVSPG	LTSPYCTPIS
101	WAVGKASLNN	RAISSLTLSG	SGTRLLSA*		

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with menB

ORF 701 shows 92.2% identity over a 128 aa overlap with a predicted ORF (ORF701.ng) from *N. gonorrhoeae*:

m701/g701

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTC	LDTSPEAGLMVWVAPNSFASFKRFSSISQT				
g701	MSWHIFQVAGIPTASMAQSTPSSPTMAKTC	LETSPEAGLMVWVAPNSFAGFKRFSSISHT				

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	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIP TGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG					
	: : : : : :					
g701	IMAAGLYSWAVNKADIPTGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISLTLSC					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
	:
g701	GGTRLLSAX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACGG CTCGATCGC
51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTG CGCCCACTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201 CAGTTGGGCG GTCGGAAGG CGGACATACC GACAGGAGCG GCACCTGCCA
251 TGAATACGGT GTCGCCGGT TTGACATCGC CGTATTGCAC GCCGATTTTCG
301 TGTGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351 GTTGTGCGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VWVAPNSFAS
51  FKRFSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101 CAVGKASLNN RATSSLTLSG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASF					
	: : : : :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPEAGLMVWVAPNSFASF					
	10	20	30	40	50	60

	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIP TGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG					
	: : : : :					
a701	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTLSG					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
	:
a701	SGTRLLSAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
1  ATGCCGTGtT ccaAAGCCAG TTGGACTTCG CCCGGAGtgg cAACGCCGGG
51  AATCAGGGGA ATGCCGCTGT TGCGGCCGGC TCTGGCGAGG GATTCGTGCA
101 AACCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGAT TGGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTC
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTCGAGGGT GGGGATGCCG CCTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAAt cgCCATCACA GGCACAAC TGCCGCGGGT
351 CAGGATTTCG cggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

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```

1  MPCSKASWTS PGVATPGIRG MPLLRLPALAR DSCKPGLMAK TAPASSTALS
51  CSQLVTVAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRARDKST
101 AVLKSSIAIT GTTAPAVRIS RGVs*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

```

m702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACTG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

```

m702.pep
1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSQLVTVAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

```

m702/g702
      10      20      30      40      50      60
m702.pep  MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSQLVTVAP
          |||||  |||||  |||||  |||||  |||||  |||||
g702       MPCSKASWTS PGVATPGIRGMPLLRLPALARDSCPKGLMAKTAPASSTALSCSQLVTVAP
          10      20      30      40      50      60

      70      80      90     100     110     120
m702.pep  TMALGTSIAIRRMASRPTGVRVISRVGMPPSTRAWDKSM AVLKSSIAITGTTAPAVKIS
          |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g702       MMALGISLAIRRMASPTGVRKVISRVGMPPSTRARDKSTAVLKSSIAITGTTAPAVRIS
          70      80      90     100     110     120

      130     140
m702.pep  RGVSLDISVLRVEWGILLRWDRILX
          |||
g702       RGVSX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

```

a702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACTG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

```

a702.pep
1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSQLVTVAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

```

      10      20      30      40      50      60

```

1128

```

m702.pep  MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVFAP
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702      MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVFAP
          10      20      30      40      50      60

          70      80      90      100     110     120
m702.pep  TMLGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702      TMLGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
          70      80      90      100     110     120

          130     140
m702.pep  RGVSLDISVLRVEWGILLRWDR LX
          ||||||||||||||||||
a702      RGVSLDISVLRVEWGILLRWDR LX
          130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

```

g703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAGCC GTTTACGACA ATATCAGCGG TTTTATATAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCGAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTGATGCCG
551 TTTTGAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCTT CTTTGGACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GCGGAACGG ATTGACCGTG CCGTctgTGc gcTGTgggt aaggCAACA
851 TCAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

```

g703.pep
1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
201 DGYVPLKDL E QGVPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
251 KVPSFDEMKG QIAGNLQAE R IDRVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

```

m703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 TAACGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAACA ATATCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GGCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

```

m703.pep
1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGYVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNDREV
251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

```

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVVNTVVQAEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVVNTVVQAEVKRLKLDRAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
g703	EAYALHIKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703	VYYVNDREVKVPSFDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACGAG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGCGAGGCGG TAAATATG
351 CTTGAACGCG GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGTTT
401 CCGAGCAGGA AGTAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATTCCTC AACGACCGTA CCAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

1130

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GGCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

```

a703.pep
1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGYVPLKDL E QGVPPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSDREV
251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

m703/a703 100.0% identity in 288 aa overlap

m703.pep      10      20      30      40      50      60
MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL
a703          10      20      30      40      50      60
MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL

m703.pep      70      80      90      100     110     120
LENEVVNTVVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG
a703          70      80      90      100     110     120
LENEVVNTVVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG

m703.pep     130     140     150     160     170     180
EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDKEENAKKAVADLKAKKG
a703         130     140     150     160     170     180
EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDKEENAKKAVADLKAKKG

m703.pep     190     200     210     220     230     240
FDAVLKQYSLNDRTKQTGAPVGYVPLKDLQGVPPLYQAIKDLKKGEFTATPLKNGDFYG
a703         190     200     210     220     230     240
FDAVLKQYSLNDRTKQTGAPVGYVPLKDLQGVPPLYQAIKDLKKGEFTATPLKNGDFYG

m703.pep     250     260     270     280     289
VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX
a703         250     260     270     280
VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

```

a704.seq
1  ATGAAAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA
51  TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT
101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC
151 AAACAACGCA CCGCCGACGC GCAAAAAACC GAGCTGCCGC CCAAGAAAT
201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTGT
251 TGGAAACCCA CGCGGGCAGC CGCGAGGCGG TTTAATGCT CGGCGGCATC
301 ACCTGCGCCG CCTGCGTCTG GCTGATCGAA CAGCAGCTTT TCGGTACAGA
351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG
401 TCTGGGACGA CGGCAAAATC CGCCTTTCGG ACATTCTGTT GAAATCAGG
451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCGC
501 CAACCAAAAA GAACGCAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC
551 TGGGGATGAT GCAGACGATG ATGTTTCGCG TGCCGACCTA CCTTTACGGC
601 GGCGACATCG AACCCGATT CTGCAAATC CTCCATTGGG GCGGCTTTTT
651 AATGGTGCTG CCCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGGCG
701 CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA

```

```

801 TGC GGGG CAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851 TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCGCGCGAGA GGCTGGTGAA GCTGATTCCT GCGTTTTGCC ATCATATGCC
951 CGATTACCCC GATACGCAGG AAACCTGCCA GGCAGCTGTC GTCAAATTGA
1001 AGCGGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCGTTGAC
1051 GGCACGGTGC TGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGGCGGC
1201 GGCACGCGAC TGTGCGACAT CGTCCGCGTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCCGTCT TCATCGGCTG GACGCTGTAC
1351 GCGGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCTTGC GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GCGCGCGGAA GGTATTTTAA TCGCGGAAA GCAGGCAATC
1501 GAAACCTTCG CCCAAACCAC CGACATCATC TTCGACAAA CCGGCACGCT
1551 GACCCAAGGC AAACCGCGCG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTCTCGCG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCCCTG CCCGCGCCAT CCTCAACTGC CGCATTTTCA ACGCAGCGCT
1701 CCCCACATC GCTATTAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGGCGAACT GACCGTCAAC GCGGAAACAC AGGTTTGGG ATTGGGCAGG
1801 GCATCCTATG TCGCGGAAAT TTCAGGTAAA GAACCGCAA CAGAAGGCGG
1851 CGGCGCGCG GTTACCTCG GCAGTCAAAG CGGTTTCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCGG CGGAGGCGGT GCGGCAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCTGGGTGT CGGCACTAC CGGCCCAAAG
2051 CCATGCCCGA GGACAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCGC CCGTTTTGGC
2151 GCAGGCAGAC GTATCCGCCG CCGCAGCGGG CGGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTTA TTGAACGAAG ATTTGCGTAC CGTCGCCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCCGCCAT ATTATCCGCG AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCACAAA CGGGGGAAAA TGCAGTCTGA
2451 AAAAATGCCG TCCGAACAA GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```

a704.pep
1 MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAQS IIDAGLGSYY
51 KORTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLIQ QLLRRTDGI V RIDLNYSTHR CRVWDDGKI RLSDILLKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMQTM MFALPTYLYG
201 GDIEPDLFIQ LHWGGFLMVL PVVFYCAVPF YQGALRDLKN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAEAEQYAS SFIFGELLLA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTDDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSSQSGFQ AVFYLDPLK DSAAEAQRQL
651 AGKNLTLHIL SGDRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAAAGGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRQNLIWAG AYNIIAVPLA VLGYPWPWIA ALGMSFSSLA
801 VLGNALRLHK RGMQSEKMP SEQ*

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m704/a704 99.8% identity in 823 aa overlap

```

          10      20      30      40      50      60
m704.pep MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVAQSIIDAGLGSYYKORTADAQKT
          |||
a704      MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVAQSIIDAGLGSYYKORTADAQKT
          10      20      30      40      50      60

          70      80      90     100     110     120
m704.pep ELPPQEILDQIRLYDLPEVQSDVFETHGGTREAVLMLGGITCAACVWLIQQLLRTDGI
          |||
a704      ELPPQEILDQIRLYDLPEVQSDVFETHGGTREAVLMLGGITCAACVWLIQQLLRTDGI

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1132

	70	80	90	100	110	120
m704.pep	130	140	150	160	170	180
a704	RIDLNYSTHRCRVVWDDGKIRLS	DILLKIRQIGYTAAPYDAQKIEA	ANQKERRQYIVRLA			
	130	140	150	160	170	180
m704.pep	190	200	210	220	230	240
a704	VAGLGMMQTMFALPTYLYGGDIE	PDFLQILHWGGFLMVLPVVFYCA	VPFYQGALRDLKN			
	190	200	210	220	230	240
m704.pep	250	260	270	280	290	300
a704	RRVGMDTPITVAIIMTFIAGVYS	LATNAGQGMFESIAMLFFLLGG	REMEHIARRKAGD			
	250	260	270	280	290	300
m704.pep	310	320	330	340	350	360
a704	AAERLVKLI PAFCHHMPDYPDTQ	ETCEAAVVKLKAGDIVLVPGETI	PVDGTVLEGSSAV			
	310	320	330	340	350	360
m704.pep	370	380	390	400	410	420
a704	NESMLTGESLPVAKMPSEKVTAG	TLNTQSPLIIRTDR	TGGGTRL	SHIVRL	LDRALA	QKPR
	370	380	390	400	410	420
m704.pep	430	440	450	460	470	480
a704	TAEAEQYASSFIFGELLAVPVFI	GWTLYADAHTALWITVALLVIT	CPCALS	SLATPTAL		
	430	440	450	460	470	480
m704.pep	490	500	510	520	530	540
a704	AASTGTLAREGILIGGKQAIETLA	QTTDII	FDKTGTLTQ	GKPAVRRIS	LLRGTDEAFVLA	
	490	500	510	520	530	540
m704.pep	550	560	570	580	590	600
a704	VAQALEQQSEHPLARAILNCRIS	DGVSVPDIAIKQRLNRIGEGV	GVAQLTVNGETQVWALGR			
	550	560	570	580	590	600
m704.pep	610	620	630	640	650	660
a704	ASYVAEISGKEPQTEGGGSAVYL	GSQSGFQAVFYLTDP	PKDSAAEAVRQ	LAKGNLTLHIL		
	610	620	630	640	650	660
m704.pep	670	680	690	700	710	720
a704	SGDRETAVAETARALGVAHYRAQ	AMPEDKLEYVKALQ	KEGKKVLMIGD	GINDAPVLAQAD		
	670	680	690	700	710	720
m704.pep	730	740	750	760	770	780
a704	VSAAAAGGTDIARDGADIVLLNE	DLRTVAHLLDQARRTRHI	IRONLIWAGAYNII	AVPLA		
	730	740	750	760	770	780
m704.pep	790	800	810	820		
a704	VLGYVQPWIAALGMSFSSLA	VLGNALRLHKGKMQSEKMPSEQX				
	790	800	810	820		

1	GTGTTCAATA	ATTTCCcttgC	CTCTCTGCGG	TTTATGACGG	AAACACGGCG
51	TGATATGCTC	ATCAGCGCGT	TTTGCCCATC	GGTTAAAGCC	GATTTTACAG
101	TGTCCTtgC	TTTGCGCATG	GCTTCTTTTCG	TATATGCGCAT	GGATTATTGCC
151	GTAGCCGTTG	CTTTGGTAAG	AATCATGCCT	TCCGGCGGTA	TTTTCCAAAA
201	ATGCTTTGGT	AAGCTGGTGG	AATTTTATAT	TTCCGTCGTT	CGCGGTACGC
251	CGCTGTGTGT	TCAGCTTTGT	ATTGTGTTTT	ACGGCGTGCC	TGCGGTCCGG
301	ATCTATATCA	ATCCGATTCC	CGCCGCCATC	ATCGGCTTTT	CGCTCAATGT
351	CGCGCGCATC	CGTCCGAAG	CCATACGCGC	GGCGATTTTG	TCCGTCGCCA
401	AAGGGCCAGT	GGAAGCAGGT	TTCTCCATCT	GTATGACCTA	TATGCAGACG
451	TTCCGCCGCA	TCGTCGCACC	GCAGGCATT	CGCGTCGCCG	TTCCGCCGTT
501	GAGCAACGAG	TTGATCCGCT	TGTTCAAAAA	CACCTCGGTT	CGCCCGCGTG
551	TAAACGGTAAC	GGAGCTTTTC	CGTGCGCAC	AGGAAACGGC	AAACCGCACT
601	TATGACTTTT	TGCCTGTCTA	TATCGAAGCT	GCATTGGTTT	ATTGGTGT
651	CTGTAAAGTG	CTGTTTTTGA	TTCAGGCGCG	TTTGGAAAAA	CGTTTCGACC
701	GTATTGTCGC	CAATAAA			

```

1 VFNFLASLP FMTETRADML ISAFWPMVKA GFTVSLPLAI ASFVIGMIIA
51 VAVALVRIMP SGGIFOKCLL KLVEFYISV V RGTPLLVQLV IVFYGLPSVG
101 IYINPIPAAI IGFSNLVNGE ASETIRAAIL SVPKQWEAF FSIGMTYMQT
151 FRRIAPQAAI RVAVPPLVSAY FIFGLFKNTSL AAHVGTZELF RVAQETANRT
201 YDELFPVYIEA ALVYWCFCVK LFLIQARLEK RFDRYVAK*

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1	GTGTTCAATA	ATTTCCTTGC	TTCGCTGCCG	TTTATGACGG	AAACACGGCG
51	CGATATGATT	TTGAGCGCGT	TTTTGGCCTAT	GGTCAAAGCT	GGCTTCGGCG
101	TC7CTCTGCC	TTGCGCGGCA	GCTTCTTTTCG	TATATCGGATC	GAGTATTGCG
151	GTAGCCGTGG	CTTTGGTGCG	GATTATGCCC	GCCGGCGGCA	TCGTGCGGAA
201	AA7CTCTGCT	AAATTGGTGG	AATTTTATAT	TTCCGCTATT	CGCGGTACGC
251	CGCTGTTGGT	TCAGCTTTGT	AAATGGCTTT	ACGGGCTGCC	TTCCGTCCGC
301	ATCTATATCG	ACCCGATTTC	TGCCGCCATC	ATCGGCTTTT	CGCTCAATGT
351	CGCGGCATAC	GCTTCGGAAG	CCATACGCGC	GGCAATTTTG	TCCGTACCTA
401	AAGGCGCAAT	GGAAGCGAAT	TTCTCCATCT	TGATGACCTA	TATCGACAGC
451	TTCCGCCGCA	TTGTGCGGCC	GCAGGCATTC	CGCGTTGCCG	TGCCGCCCTT
501	GAGCAACGAG	TTTATCGGTT	TGTTTAAAAA	CACCTCGCTC	CGCGGACGCT
551	TGACGGTAAAC	GGAAATTATC	CGCTTCCGCG	AGGAACAGGC	AAACCGCATC
601	TATGACTTTT	TGCCCGTCTA	TATCGAAGCC	GCTTTGGTTT	ACTGGTGGTT
651	TTCTAAAGTG	CTGTTCTCTGA	TTACGGCGCG	TTTGGAAAAA	CGTTTCGACC
701	GCTCAGTCCG	CAATAAA			

```

1  VFNFNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVQLV IVFYGLPSVG
101 IYIDPIPAAI IGFSNLNGAY ASETIRAIL SVPKQWEAG FSIGHTYMQT
151 FRRIAPQAF RVAVPPLSNE FIGLFRNTSL AAVVTQTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVK LFLIQARLEK RFDRYVAK*

```

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m705.pep	VFNNFLASLPFMTETRADMIVSAFLPMVKAGFVSLPLAASFVIGMMIAVAVALVRIMP					
g705	VFNNFLASLPFMTETRADMLISAFWPMVKAGFTVSLPLAIASFVIGMIIAVALVRIMP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m705.pep	AGGIVRKILLKLVEFYISVIRGTPLLVLVIVFYGLPSVGVIYIDPIPAAIIGFSLNVGAY					
	:	:	:	:	:	:

```

g705      SGGIFQKCLLKLVIFYISVVRGTPLLVQLVIVFYGLPSVGIYINPIAAIIGFSLNVGAY
              70          80          90          100          110          120

              130          140          150          160          170          180
m705.pep  ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
              |||
g705      ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
              130          140          150          160          170          180

              190          200          210          220          230          239
m705.pep  AAVVTVTELFRAQETANRTYDFLPVYIEAALVYWCFCVKVLFLLIARLEKRFDRYVAKX
              |||
g705      AAVVTVTELFRAQETANRTYDFLPVYIEAALVYWCFCVKVLFLLIARLEKRFDRYVAKX
              190          200          210          220          230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTTCAATA ATTCCTTGC TTCGCTGCCG TTTATGACGG AACACGCGC
51  CGATATGATT GTCAGCGCGT TTTGCGCTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTGGTGCG GATTATGCCC GCCGGCGGCA TCGTGCGGAA
201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCGTCATT CGCGGTACGC
251 CGCTGTTGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGCGGCATAT GCTTCCGAAA CCATACGCGC GGCAATTTG TCCGTACCGA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCGCC GCAGGCATTT CGCGTTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTGTGTTT ACTGGTGTTC
651 TTGTAAGTG CTGTTCTCTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLV IVFYGLPSVG
101 IYIDPIPAI IGFSNLVGAY ASETIRAIL SVPKQWEAG FSGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVKV LFLIARLEK RFDYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

a705/m705 100.0% identity in 238 aa overlap

```

              10          20          30          40          50          60
a705.pep  VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
              |||
m705      VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
              10          20          30          40          50          60

              70          80          90          100          110          120
a705.pep  AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAIIGFSLNVGAY
              |||
m705      AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAIIGFSLNVGAY
              70          80          90          100          110          120

              130          140          150          160          170          180
a705.pep  ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
              |||
m705      ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
              130          140          150          160          170          180

              190          200          210          220          230          239
a705.pep  AAVVTVTELFRAQETANRTYDFLPVYIEAALVYWCFCVKVLFLLIARLEKRFDRYVAKX
              |||
m705      AAVVTVTELFRAQETANRTYDFLPVYIEAALVYWCFCVKVLFLLIARLEKRFDRYVAKX
              190          200          210          220          230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq
 1 ATGAACCTCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
 51 CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTCCGG CTCGGCggaa
 101 ccgtCCTGTT CGCCACCGCA CTCGCCCGgc tACTCCACCT CCAacacggc
 151 gAATGGATAG GGAtgaCCGT CTTGTCGTC CTCGGCATGC TCCAGTTCCA
 201 AGGGcgatatt tActccaacg cggtgGAacg taTGctcggg acggtcatcg
 251 ggctgGGCGC GGGTTTGGgc gTTTATGGC TGAACAGCA TTAttccac
 301 ggcaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
 351 ctGGGCGGCG GTCGGCAAAA acggtacgt ccctatgctg GCGGGGctgA
 401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
 451 CTGATGCCCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATTGCCCG
 501 CGCCAAATG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
 551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
 601 AGGCGTATGA CGCGCGAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
 651 AATCAACGCA CGCATGGTCA AAAGCCGCAG CCACCTCGCC GCCACATCGG
 701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
 751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
 801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
 851 TCACACTGCT CCAAAACGAC CTGCAACAAA CCGCGCCCT CATCAACGGC
 901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
 951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGTCA
 1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCGTCATCCT GCTGCAACGC
 1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
 1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep
 1 MNSSQRKRLS GRWLSYERY RHRLIHAVR LGGTVLFATA LARLLHLQHG
 51 EWIGMTVFVV LGMLQFOGAI YSNAVERMLG TVIGLGAGLG VLWLNQHYFH
 101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCMLIG DNGSEWLD SG
 151 LMRAMNVLIG AAIATAAAL LPLKSTLMWR FMLADNLADC SKMIAEISNG
 201 RRMTRERLEQ NMVKMRQINA RMVKSRSILA ATSGESRISP SMMEAMQHAH
 251 RKIVNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTAAALING
 301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMROE ISALVILLQR
 351 TRRWLDAHE RQHLRQSLLE TREHG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq
 1 ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
 51 CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
 101 CCGTCCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
 151 GAGTGGATAG GGATGACCGT CTTGTCGTC CTCGGCATGC TCCAGTTTCA
 201 AGGGGCGATT TACTCCAAGG CGGTGGAACG TATGCTCGGC ACGGTCATCG
 251 GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACAGCA TTATTCCAC
 301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
 351 CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA
 401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
 451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCCG
 501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
 551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
 601 AGGCGCATGA CCCGCGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
 651 AATCAACGCA CGCATGGTCA AAAGCCGCAG CCATCTCGCC GCCACATCGG
 701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
 751 CGTAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
 801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
 851 TCACACTGCT CCAAAACGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
 901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
 951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGTCA
 1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCGTCATCCT GCTGCAACGC
 1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
 1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep
 1 MNTSQRNRLV SRWLSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
 51 EWIGMTVFVV LGMLQFOGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
 101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCMLIG DNGSEWLD SG
 151 LMRAMNVLIG AAIATAAAL LPLKSTLMWR FMLADNLADC SKMIAEISNG
 201 RRMTRERLEE NMAKMRQINA RMVKSRSILA ATSGESRISP AMMEAMQHAH
 251 RKIVNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTVALING

301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
 351 TRRKWLDAHE RQHLRQSLLE TREHG*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQNRNLVSRWLSYERYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
g706	MNSSQRKRLSGRWLSYERYRRLIHAVRLGGTVLFATALARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m706.pep	LGMLQFQGAISKAVERMLGTVIGLGAGLGVWLWNQHYFHGNLLFYLTVTGASALAGWAA					
g706	LGMLQFQGAISNAVERMLGTVIGLGAGLGVWLWNQHYFHGNLLFYLTIGTASALAGWAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m706.pep	VGKNGYVPMLAGLTMCLIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
g706	VGKNGYVPMLAGLTMCLIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m706.pep	FMLADNLADCSKMI AEISNGRRMTREERLEENMAKMRQINARMVKSRSLSLAATSGESRISP					
g706	FMLADNLADCSKMI AEISNGRRMTREERLEENMAKMRQINARMVKSRSLSLAATSGESRISP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m706.pep	AMMEAMQHAHRKIVNTTELLTTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
g706	SMMEAMQHAHRKIVNTTELLTTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTAAALING					
	250	260	270	280	290	300
	310	320	330	340	350	360
m706.pep	RHARRIRIDTAINPELEALA EHLHYQWQGF LWLSTNMRQEISALVILLQRTTRRKWLDAHE					
g706	RHARRIRIDTAINPELEALA EHLHYQWQGF LWLSTNMRQEISALVILLQRTTRRKWLDAHE					
	310	320	330	340	350	360
	370					
m706.pep	RQHLRQSLLETREHGX					
g706	RQHLRQSLLETREHGX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

```

1  ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51  CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATGACCGT CTTGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CCGTGGAACG TATGCTCGGC ACGGTCATCG
251 GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACCAGCA TTATTTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCTATGCTG GCGGGGCTGA
401 CGATGTGCAT GCTCATCGGC GACAACGGCA GCGAATGGTT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGCGGT TTCATGCTTG
551 CCGACAACCT GACCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCCGCGAACG CCTCGAAGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAATTTG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAACCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC

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1137

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901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACAGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACAGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

```

a706.pep
1  MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51  EWIGMTVFVV LGMLQFQGA IYSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWFD SG
151 LMRAMNVLIG AAIATAA AKL LPLKSTLMWR FMLADNLTDC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRS HLA ATSGESRISP AMMEAMQH AH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHS*

```

a706/m706 99.5% identity in 374 aa overlap

	10	20	30	40	50	60
a706.pep	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
m706	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a706.pep	LGMLQFQGA IYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
m706	LGMLQFQGA IYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
a706.pep	VGKNGYVPM LAGLTMCLIGDNGSEWFD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
m706	VGKNGYVPM LAGLTMCLIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
	130	140	150	160	170	180
	190	200	210	220	230	240
a706.pep	FMLADNLTDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRS HLAATSGESRISP					
m706	FMLADNLTDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRS HLAATSGESRISP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a706.pep	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD LQQTVALING					
m706	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD LQQTVALING					
	250	260	270	280	290	300
	310	320	330	340	350	360
a706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTRRKWLDAHE					
m706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTRRKWLDAHE					
	310	320	330	340	350	360
	370					
a706.pep	RQHLRQSLLETREHSX					
m706	RQHLRQSLLETREHGX					
	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

m707.seq

```

1   ATGGAAATTA TTAACGATGC AGAACTTATC CGTTCATGC AGCGTCAGCA
51  GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTTGGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTCTTT
201 TCTTCTTCT GTGCTCATGA AAGAAACAGC TTTTAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTTGAGC AGGCTACAAA AAGCGCGCA ACAGATACTG
301 ATCGTGCGTG GCTACCTCAC TTCCAAGCT ATTATCCAAC CACAGAATAT
351 GGATTCGGGA ATTCTGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCATAA ACAAAATTC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGGCG AGTGTAAAAA
551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTACAG
601 ATCAAAATGGC AGCAGAATAA ACCCATACGG TTCAGTATCG GTATAGATGA
651 TCGGGGCGGC AAAACGACCG GCAAAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTGT TTTATGTTTC ATATGGACGC
751 GGTGTGCGC ACAAAACGGA CTTGACTGAT GCCACCGTA CGGAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCATTA TTCGTGCCC GTAAAAAAT
851 GCGTGTTC TTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
901 GGTATTCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GGCGCGCGAG CGCATGCTTT GCGTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCCGCG CTCTGCAGGC TGGGAAGCCG AATTGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 CGCGGACCGG CATGCGCCAA AGTATGCCTG CACCGGAAGA AAACGGCGGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGA
1251 CGCAGCCGCC CCATTTATTT TAGGCAACA GCAGTTTTTC TACGCAACCG
1301 CCATTCAAG TCAATGGAAC AAAACGCCGT TGGTTGCCA AGATAAATG
1351 TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGG AGCAGAGTCT
1401 TTTCCGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGGG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTGG
1551 CTTTCAGAGG GGCATATAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTT
1601 CCGGCAAGCC GCTTCATAAA CCCAAGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```

1   MEIINDAELI RSMQRQQHID AELLTDANVR FEOPLEKNNY VLSEDETPCT
51  RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQIL
101 IVRGYLTSSA IIQPNMDSG ILKLRVSAGE IGDIREYKRR DGKSAEGSIS
151 AFNKKFPLYR NKILNLRDVE QGLENLRRLP SVKTDIQUIP SEEEKGSDLQ
201 IKWQONKPIR FSGIDDAGG KTTGKYQGNV ALSFDNPLGL SDFYVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGRHYHEATE
301 GYSVNYDYG KQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAE LRHRAY LNRWQLDGKL SYKRGTGMRQ SMPAPEENG
401 DILPGTSRMK IITASLDAEA PFILGKQOFF YATAIQAWN KTPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYWQNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGKQ LMGAVVGFRG GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```

1   NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51  GAGCAGGCTA CAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTG GGAATTCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCAATC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGCG
301 TTGGAAACCG TCGTCTGTTT GCCGAGTGTT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATTT ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTCACT ATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACGGCAAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NTTAAGCGAT TNGTTTTATG TTTCATATGG ACGCGGTTG GTGCACAAAA
551 CGGACTTGAC TGNTGCCACC GGTACGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

```

```
751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCGTAT GAAAATCATA ACCGCCGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTC AAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTTCG CGGATTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TCAACTTGA
1451 ATTACAGTTT CTAA
```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```
a707.pep
  1 XKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
 51 KLRVSAGEIG DIRYEKRDY KSAEGSISAF NKKXPLYRNK ILNRDVEQGG
101 LENLRLRPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ YQSSLAERM
251 LWXXFXXTS VXMKLWTRQT KYIDDAEIE VQRRRSAGWE AELRHRAYLX
301 RWQLDGKLSY KRGTMGRQSM PAPEENGGGT IPXXSRMKII TAGLDAAAPX
351 MLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*
```

a707/m707 95.3% identity in 486 aa overlap

```

                                     10      20      30
a707.pep                               XKETAFTKGMCLGSNNLSRLQKAAQQILIVR
                                     |||
m707      EDETPCTRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIVR
                                     50      60      70      80      90     100

                                     40      50      60      70      80      90
a707.pep      GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEKRDYKSAEGSISAFNKKXPLYRNKI
               |||
m707      GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEKRDGKSAEGSISAFNKKFPLYRNKI
               110     120     130     140     150     160

                                     100     110     120     130     140     150
a707.pep      LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
               |||
m707      LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
               170     180     190     200     210     220

                                     160     170     180     190     200     210
a707.pep      GKYQGNVALSXDNPLGLSDXFYVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK
               |||
m707      GKYQGNVALSFDNPLGLSDLFYVSYGRGLAHKTDLTDATGTETESGSRYSVHYSVPVKK
               230     240     250     260     270     280

                                     220     230     240     250     260     270
a707.pep      WLFNFHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWXXFXXTSVXMKLWTRQTY
               |||
m707      WLFNFHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWRNRLHKTSVGMKLWTRQTY
               290     300     310     320     330     340

                                     280     290     300     310     320     330
a707.pep      KYIDDAEIEVQRRRSAGWEAELRHRAYLXRWQLDGKLSYKRGTMGRQSMPEENGGGTI
               |||
m707      KYIDDAEIEVQRRRSAGWEAELRHRAYLNRWQLDGKLSYKRGTMGRQSMPEENGGDIL
               350     360     370     380     390     400
```


1140

	340	350	360	370	380	390
a707.pep	PXXSRMKIITAGLDAAAPXMLGKQOFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG					
m707	PGTSRMKIITASLDAAAPFILGKQOFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG					
	410	420	430	440	450	460
	400	410	420	430	440	450
a707.pep	EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRRGGHK					
m707	EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRRGGHK					
	470	480	490	500	510	520
	460	470	480			
a707.pep	VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX					
m707	VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX					
	530	540	550	560		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2373>:

g708.seq

```

1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAA
301 CCCGACAGTG CCGAAATCAA CAACAAC TAC GGTGGTTC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACCTA CCCGACCCT TATATTGCCA ACCTGAATAA AGGTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GCGCGGCAG TTGGCGGATG CCGATTACTA CTTTAAAAAA
601 TACCAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGTGCA GCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2374; ORF 708.ng>:

g708.pep

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSNPKNE LAWLVRAEIY QYLKVNDAQ ESFRQALSIK
101 PDSAEINNYY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFLGA EAYLKRS LAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNVQRAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2375>:

m708.seq

```

1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAA
301 CCCGACAGTG CCGAAATCAA CAACAAC TAC GGTGGTTC TATGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GCGCGGCAG TTGGCGGATG CCGATTACTA CTTTAAAAAA
601 TACCAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2376; ORF 708>:

m708.pep

1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQALSIE
101 PDSAEINNNY GWFLCGRNLN PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSALAA QPQFPFPAKE LARTKMLAGQ LGDADYYFFK
201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

m708/g708 99.2% identity in 253 aa overlap

      10      20      30      40      50      60
m708.pep MPFKPSKRISLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
|||||
g708      MPFKPSKRISLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
      10      20      30      40      50      60

      70      80      90     100     110     120
m708.pep DALKSDPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSAEINNNYGWFLCGRNLN
|||||
g708      DALKSNPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSAEINNNYGWFLCGRNLN
      70      80      90     100     110     120

      130     140     150     160     170     180
m708.pep PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPFPAKE
|||||
g708      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPFPAKE
      130     140     150     160     170     180

      190     200     210     220     230     240
m708.pep LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF
|||||
g708      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNVQAAYEYEAQLQANF
      190     200     210     220     230     240

      250
m708.pep PYSEELQTVLTGQX
|||||
g708      PYSEELQTVLTGQX
      250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCGACAGTG CCGAAATCAA CAACAAC TAC NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCGCCGAAT CTATGGCATA TTTGACAAA GCCCTGGCCG
401 ACCCCACNTA CCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTGCT TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQXLSIK
101 PDSAEINNNY XWFLCGRNLN PAESMAYFDK ALADPTYXP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSALAA QPQFPFPAKE LARTKMLAGQ LGDADYYFFK
201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLAGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLAGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDPKNELAWLVRAEIIYQYLVNDKAQESFRQXLSIKPDSAEINNYYWFLCGRLNR					
m708	DALKSDPKNELAWLVRAEIIYQYLVNDKAQESFRQALSIPKPSAEINNYYWFLCGRLNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
m708	PAESMAYFDKALADPTYTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

```

1  ATGTTTGCTT  TCAATCCTT  ACTCGATATG  CCGCGCGGTG  AGGCACTTGC
51  CGTCGTCGTC  GCTCTGATTG  CCGCAATGGG  CTATACCATC  ATTTCAATTGG
101 AGTGGCTGCC  GCATATGTCC  ATTATTGCCG  CCATCGTCGT  GCTGATTTTG
151 TACGGCTTGG  CGCGCGGTTT  GAAATACAAC  GATATGCAGG  CAGGGATGAT
201 AGGCGCGTTG  AATCAGGGTA  TGGGCGCGGT  TTACCTGTTT  TTCTTCATCG
251 GCGTGATGGT  CAGCGCGCTG  ATGATGAGCG  GCGCGATTCC  GACGCTGATG
301 TATTACGGTT  TCGGGCTGAT  TTCCCGGACT  TATTTTATT  TTTCCGCCCT
351 CGCGCTGTGT  TCCGTATCG  GCGTGTCAT  CCGCAGCAGC  CTGACCGCCT
401 CGGCCACTGT  CGCGCTTGCC  TTTATGGGGA  TGGCGGCGGC  GTTTCAGGCC
451 GATATGGCGA  TGACGcggg  cgcgattgTT  tccggtGTGT  TTTTCGGCGA
501 TAAATGTCC  CCGCTTCCG  ACACCACGGG  CATTTCGCG  TCCATCGTCG
551 GTATCGACCT  GTTTGAACAC  ATCAAAAACA  TGATGTACAC  CACCATCCCT
601 GCGTGGCTTA  TCAGCGCGGC  ACTGATGCTT  TGGCTTCTTC  CCAGCGTCGC
651 CGCGCAGGAT  TTGAACAGCG  TCGAATCCTT  CCGCAGCCAG  CTTGAAGCCA
701 CGGGATTGGT  GCACGGCTAT  TCGCTGATT  CGTTTGCACT  GTTGGTCGTT
751 TTGGCATTGA  TGCGCGTCAA  TGCCGTGGTC  GCCATGCTCT  TTACCGTCAT
801 TGCGCGCGTT  GCCGTAACGT  ATCTGCACAG  CACGCCCGAT  CTGCGTCAGC
851 TCGGCGCGTG  GTTTTATGGC  GGCTACAAAC  TCGAAGGCGA  AGCGTTTAAA
901 GACATTGCCA  AACTGATTTC  GCGCGGCGGC  TTGGAGAGTA  TGTCTTTTAC
951 GCAGACCATC  GTTATCCTCG  GTATGAGTTT  GGGCGGGCTG  CTGTTTGGCG
1001 TCGGTGTGAT  TCCTTCCTTG  CTGGAGGCCG  TCCGTACCTT  CTTGACGAAT
1051 GCCGGACGCG  CGACGTTTCA  CGTTGCCATG  ACTTCGGTCG  GGGTCAATTT
1101 CCTGATTGGA  GAGCAATATT  TGAGCATCCT  GCTTTCGGGA  GAAACGTTCA
1151 AATCCGTTTA  CGACAAATC  GGCCTGCATT  CGTGCAACCT  GTCGCGGACT
1201 CTGGAAGATG  CGGGGACGGT  GATTAACCCG  CTCGTGCCGT  GGAGCGTGTG
1251 CGGCGTATTT  ATCAGCCACG  CCCTTGGCGT  ACCCGTTTGG  GAATATCTGC
1301 CTTATGCCTT  TTTCTGTAT  TTGAGTTTGG  CTTTAACCC  GTTATTCGGC
1351 TGGACGGGGC  TGACTTTGAG  CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

```

1  MFAFKSLDM  PRGEALAVVV  ALIAAMGYTI  ISLEWLPHMS  IIAAIVVLIL
51  YGLARGLKYN  DMQAGMIGAL  NQGMGAVYLF  FFIGLMVSAL  MMSGAIPTLM
101 YYGFGLISPT  YFYFSAFALC  SVIGVSISS  LTACATVGA  FMGMAAFQA
151 DMAMTAGAIV  SGVFFGDKMS  PLSDTTGISA  SIVGIDLEH  IKNNMYTTIP
201 AWLISAALML  WLLPSVAQOD  LNSVESFRSQ  LEATGLVHGY  SLIPFALLVV
251 LALMRVNAV  AMLETVIAAV  AVTYLHSTPD  LRQLGAWFYG  GYKLEGEAFK
301 DIAKLISRG  LESMFTQTI  VILGMSLGL  LFLGVIPSL  LEAVRTFLTN

```

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETEKPVYDKL GLHSCNLSRT
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
451 WTGLTLSKK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq
1 ATGTTTCGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTTG AGGCACTTGC
51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTTCATTGG
101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGCGCGGAT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGGACT TATTTTATT TTTCTCCTT
351 CCGCGTGTGT TCCGTATCG GCGTGTCCAT CCGCAGCAGC CTGACCACCT
401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGCGGCG GTTTCAGGCC
451 GATATGGCGA TGACGGCGGG CCGGATTGTT TCGGCGCAT TTTTGGCGA
501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCCGCG TCCATCGTCG
551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
601 CCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTGCG
651 CCGCGAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTG CGTTTGCCTT GTTGGTCATT
751 TTGGCATTGA TCGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT
801 GGTGTCCGTT GCTGTAACGT ATCTGCACAG CACGCGCGAT CTGCGTCAGC
851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGCGCA AGCGTTTAAA
901 GATGTTGTCA AACTGATTTT CCGCGCGGCT TTGGAAGTA TGTTTTTCAC
951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTTGCCT
1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT
1051 GCCGGACGCG CGACGTTTCA CGTTGCCATG ACTTCGCTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTGCGGT GAAACGTCA
1151 AATCCGTTTA CGATAAGCTC GGTCTGCATT CCGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CCGGGACGGT GATTAACCCG CTCGTACCGT GGAGCGTATG
1251 CCGCGGTGTT ATCAGCCACG CGCTGGGCGT GCCGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCTT GTTATTTCGT
1351 TGGACGGGCG TGACTTTGAG CAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep
1 MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAIVVLIL
51 YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGILSPT YFYFSSFALC SVIGVSISSS LTTTCATVGA FMGMAAFQA
151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFEH IKNNMYTTIP
201 AWLISAALML WLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DVVKLISRGG LESMFFTQTI VILGMSLGLL LFALGVIPSL LEAIRFTLTN
351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETEKPVYDKL GLHSRNLST
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
451 WTGLTLSKK*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDDMPRGEALAVVV	ALIAAMGYTIISLEWLPHMS	IIAIVVLILYGLARGLKYN			
g709	MFAFKSLDDMPRGEALAVVV	ALIAAMGYTIISLEWLPHMS	IIAIVVLILYGLARGLKYN			
	10	20	30	40	50	60
	70	80	90	100	110	120
m709.pep	DMQQGMIGALNQGMGAIYLF	FFIGLMVSALMMSGAIPTLM	YYGFGILSPTYFYFSSFALC			
g709	DMQAGMIGALNQGMGAVYLF	FFIGLMVSALMMSGAIPTLM	YYGFGILSPTYFYFSAFALC			
	70	80	90	100	110	120
	130	140	150	160	170	180
m709.pep	SVIGVSISSSLTTCATVGV	AFMGMAAFQADAMTAGAIV	SGAFFGDKMSPLSDTTGISA			
g709	SVIGVSISSSLTACATVGV	AFMGMAAFQADAMTAGAIV	SGVFFGDKMSPLSDTTGISA			
	130	140	150	160	170	180
	190	200	210	220	230	240
m709.pep	SIVGIDLFEHIKNNMYTTIP	AWLISAALMLWLLPNVAAQD	LNSVESFRSQLEATGLVHGY			
g709	SIVGIDLFEHIKNNMYTTIP	AWLISAALMLWLLPSVAAQD	LNSVESFRSQLEATGLVHGY			
	190	200	210	220	230	240

1144

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLFVTVMVAVVTYLHSTPDRLQLGAWFYGGYKLEGEAFK					
	: : : : : : : : : : :					
g709	SLIPFALLVILALMRVNAVAVMLFTVIAAVVAVTYLHSTPDRLQLGAWFYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLSEMFQTIVILGMSLGGLLFALGVIPSLLEAIRTFLTNAGRATFSVAM					
	: : : : : : : : : : :					
g709	DIAKLISRGGLSEMFQTIVILGMSLGGLLFALGVIPSLLEAVRTFLTNAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEQLSILLSGETFKPVYDKLGLHSRNLRTLEDAGTVINPLVPWSVCGVF					
	: : : : : : : : : :					
g709	TSVGVNFLIGEQLSILLSGETFKPVYDKLGLHSCNLSRTLEDAGTVINPLVPWSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKKX					
	: : : : : : : : :					
g709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKKX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1  ATGTTTCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCGCTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTNGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGA TGGCGCGGAT TTACCTNTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGACT TATTTTATT TTTCCGCCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCACCT
401 GCGCCACTGT CGGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC
451 NANATGGNGN NGNNGNNGGN CNNGATTGTN NNGGNCGCAT TNTNNGGCN
501 CAAAATGTCN CCGCTTCCG ATACGNCGGG CATNTCCGCG TCCATTGTCTG
551 GTATCGACCT GTTTGAACAC ATCAAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACTGCTAT TCGTGATTTC CGTTTGCCT GTTGGTCGTT
751 TTGGCATTGA TGCGCGTCAA TGCCGTGGTC GCTATGCTCT TTACCGTCAT
801 TGCCGCGGTT GCCGTAACGT ATCTGCACAG CACGCCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTACGGC GGCTACAAAC TCGAAGCGA AGCGTNTANA
901 GACATTGCCA AACTCATTTT TCGCGGCGGT TTGGAAGTA TGTTTTTCAC
951 GCAGACCATC GTGATTCTTG GGATGAGCCT TGGCGGGCTG CTGTTTGCAC
1001 TGGGCGCGAT TCCTTCCTG CTGGATGCCG TCCGCGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTCAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTGNGGT GAAACGTTCA
1151 AACCTGTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTT ATCANCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGCG TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1  MFAFXSLDM PRGEALAVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQOGMIGAL NQMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGGLISPT YFYFAFALC SVIGVSIGSS LTTCATVGVA XMGXAXFXA
151 XMXXXXXXIV XXAXXGXKMS PLSDTXGXSA SIVGIDLFEB IKNMYYTTIP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLVV
251 LALMRVNAV AVMLFTVIA AVTYLHSTPD LRLQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMFFTQI VILGMSLGG LFLGAIPLS LDAVRSFLTN
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST

```

1145

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTSLKK*

a709/m709 91.1% identity in 459 aa overlap

	10	20	30	40	50	60
a709.pep	MFAFXSLDMPRGEALAVVVALIAAMGYTIIIXLEWLPHMSIIAAIVVLILYGLARGLKYN					
m709	MFAFXSLDMPRGEALAVVVALIAAMGYTIIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a709.pep	DMQQGMIGALNQGMGAIYLLFFFIGLMVSALMMSGAIPTLMYYGFGGLISPTYFYFSAFALC					
m709	DMQQGMIGALNQGMGAIYLLFFFIGLMVSALMMSGAIPTLMYYGFGGLISPTYFYFSSFALC					
	70	80	90	100	110	120
	130	140	150	160	170	180
a709.pep	SVIGVSIGSSLTTCATVGVAXMGXXXAFXAXMXXXXXXIVXXAXXGXKMSPLSDTXGXSA					
m709	SVIGVSIGSSLTTCATVGVAFMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
	190	200	210	220	230	240
a709.pep	SIVGIDLFEHIKNMYYTTIPAWLISXXLMLXLLPSVAAQDLNSVESFRSQLEATGLVHCY					
m709	SIVGIDLFEHIKNMYYTTIPAWLISAAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240
	250	260	270	280	290	300
a709.pep	SLIPFALLVVLALMRVNAVVAAMLFTVIAAVAVTYLHSTPDLRQLGAWFGYGGYKLEGEAXX					
m709	SLIPFALLVILALMRINAVVAAMLFTVMVAVAVTYLHSTPDLRQLGAWFGYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a709.pep	DIAKLISRGGLESMFFTQTIVILGMSLGGLLFALGAIPSLDAVRSFLTNAAGRXTFSVAM					
m709	DVVKLISRGGLESMFFTQTIVILGMSLGGLLFALGVIPSLLEARTFLTNAAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
a709.pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF					
m709	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
a709.pep	IXHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKKX					
m709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKKX					
	430	440	450	460		

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq

1	ATGGAAACCC	ACGAAAAAAT	CCGCCTGATG	CGCGAATTGA	ATAAATGGTC
51	CCAGGAGGAT	ATGGCGGAAA	AGCTGGCGAT	GTCCGCAGGC	GGGTATGCCA
101	AAATCGAACG	GGGCGAAACG	CAGTTAAATA	TCCCGCGTTT	GGAGCAGTTG
151	GCTCAGATTT	TCAAAATCGA	TATGTGGGAC	TTGCTCAAAT	CGGGCGGTGG
201	TGGGATGGTG	TTTCAGATTA	ATGAAGGTGA	TAGTGGTGGC	GATATTGCGT
251	TGTATGCGTC	GGGTGATGTT	TCGATGAAAA	TAGAATTTTT	AAAAATGGAG

m710.pep

```
1  METHEKIRLM RELNKSQED MAEKLAWSAG GYAKIERGET QLNIPRLQL
51  AQIFKIDMWD LLKSGGGGMV FQINEGDSGG DIALYASGV SMKIEFLKME
101 LKHCKEMLEQ KDKEIELLRK LTETV*
```

```
a710.seq
  1  ATGGAACCC  ACGAAAAAAT  CCGCTGATG  CGGAATTGA  ATAAATGGTC
51  CCAGGAGGAT  ATGGCGGAA  AGCTGGCGAT  GTCCGCAGCG  GGGTATGCCA
101 AAATCGAAGC  AGCGAAACG  CAGTTGAAT  TCCCGCGTTT  GGAGCAGTTT
151 CGCGAGATTT  TCAAATTGA  TAGTGGGAC  TTGCTCAAT  CGGCGCGCGG
201 CGGGATGGTG  TTGCAGATTA  ACGATGTGGA  TACCAACAGC  GGGGAATTTG
251 CAATCTATAC  CACTCAGGAT  GCATCNGGTA  AAGCTGGATT  TGTAAATG
301 GAATTAACG  ACTGTAAGA  AATGTTGGA  CACAAAGACA  AAGAAATCGA
351 GCTGCTCCGC  AAGCTGACCG  AAACCGTTTA  A
```

a710.pep

1	METHEKIRLM	RELNKSQED	MAEKLAMSAG	GYAKIERGET	QLNIPRLEQL
51	AQIFKIDMWD	LLKSGGGGMV	LQINDVDNTS	GEFAIYTAQD	ASGKAGFVKM
101	ELKHCKEMLE	HKDKETIELR	KLTETV*		

[illegible]

```

a710.pep      KLTETVX
               |||||
m710          KLTETVX
               120

```

1147

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
1  ATGCCCCGCGC CTGATTGTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAATAT TGATGCACGA CCTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACTGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTGCGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCTATAAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCCTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATT TAAAACCAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCCTATAAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWYDAVGD
151 SRTSPAHSAL DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYDYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFSTS FKQLEKEFYE VKQRLDIDGK
301 PKPEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
1  ATGCCCCGCGC CTGATTGTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAATAT TGATGCACGA CCTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACTGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTGCGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCTATAAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCCTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATT TAAAACCAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
```


1148

```

901 CCGGATAAAG AGCAGAAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

a711.pep

```

1 MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVYTIARMTD
51 LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFDYNAGRM
251 NYRPDLKYD RALAHQFAKA EMGGADFCTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

a711/m711 99.8% identity in 431 aa overlap

a711.pep	10	20	30	40	50	60
	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
m711	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
	10	20	30	40	50	60
a711.pep	70	80	90	100	110	120
	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
	70	80	90	100	110	120
a711.pep	130	140	150	160	170	180
	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
m711	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
	130	140	150	160	170	180
a711.pep	190	200	210	220	230	240
	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
	190	200	210	220	230	240
a711.pep	250	260	270	280	290	300
	RGFDYNAGRMNYRPDLKYDRALAHQFAKAEMGGADFCTSFKQLEKEFYEYVKQRLDIDGK					
m711	RGFDYNAGRMNYRPDLKYDRALAHQFAKAEMGGADFCTSFKQLEKEFYEYVKQRLDIDGK					
	250	260	270	280	290	300
a711.pep	310	320	330	340	350	360
	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
m711	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
	310	320	330	340	350	360
a711.pep	370	380	390	400	410	420
	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
m711	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
	370	380	390	400	410	420

1149

a711.pep

AKFMAKKKVLKX

|||||

m711

AKFMAKKKVLKX

430

1150

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```
m712.seq
1  ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTTTGCCGC
101 AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201 TTTGTTCCGA CAAGGCTCGC TGGCGCATTG ATGGTGCGC CAAGCATTGT
251 CCAACAACCC TTATTTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301 GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTCCCGGCA CGGCCACCGC
351 GCCGGGCGTG GTGGAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451 ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
501 TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551 CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
601 GCGGGTGCCA AAAATGCGGA CATTGCCACG GCCTTGTTCA AAGTGGCGGG
651 CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751 GCGTGTATCG GCGTATTGGG TATGAGTGCG GCCTTGAGCA CGGCCACCAC
801 CGCTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851 GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GCGGTTGTTG
901 GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
951 GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGCGA CTAATCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTAAAGAGC GAGATTTTGG ACGTGTGTAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GCGCGTGC GCAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCCGCCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GGCGCATTGA
1401 TTTGATTTTG TAA
```

This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>:

```
m712.pep
1  MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPKVL MVAFMLTAGI
51  QPALEPVQLF SDAEAADLFG QGSLAHLNVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNAIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAYL
301 AFEEDPAKPL NTLEIKGLAV TPDAQWPLFA ECNNALYNGL TPLTVVNNRV
351 QIMRAVSTYT KSANNTDDPA LLDITTTIRTL DYVRRSVKER IALRFPRDKL
401 SDRLLPKVKS EILDVLKLD QAEIENAEA NKGKLVVARA QNDPNRVNAI
451 IPADVNLH VFAGRIDLIL *
```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```

m713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCCTTTG GGCAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGTTTTT CCGAGGTTAC
651 TTTTGTGGCG CAATCGCACG GCCGCGAGCG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCCGCATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAAAGGC GGCAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```

m713.pep
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MVLDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGAD YSSPPVATLC WSRTDSRCNI
201 ERMIDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLLKVVYKD PTMTLHRPKT
251 VVVSDADNLA ALQQAQKQL ADWRLEGFTL TITVGGHKTR DGVLWQFGLR
301 VHVIDDEHGI DAVFFLMGRR FMLSMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGRK KGVSHKGGKG GKQQAETAVF E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```

a713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGTTTTT CTGAGGTTAC
651 TTTTGTGGCG CAATCGCACG GCCGCGAGCG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGCATGGA TGGACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG

```

1152

1101 CAAAAAAGGC GGCAAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

a713.pep

```
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDV VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGVD YSSPPVATLC WSRTDSRRNI
201 ERMDIEWDTD NRFSEVTFLL QSHGRSGDSA KHDWKVYKD PTMTLHRPKT
251 VVSDADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWQPGQR
301 VHVIDDEHGI DAVFFLMGRR FMSRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGGKG GKKQAETAVF E*
```

a713/m713 98.4% identity in 381 aa overlap

	10	20	30	40	50	60
a713.pep	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDVIGRLGPEAAIPDLSGESCE					
m713	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDVIGRLGPEAAIPDLSGESCE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a713.pep	VVIDGQIVMTGIIGSQRHGKSKGGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAKKL					
m713	VVIDGQIVMTGIIGSQRHGKSKGSRRLSLSGRDLAGFLVDCSAPQLNVKGMTVLDAKKL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a713.pep	AAPWPQIKAVVLKVENNPALDKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLVVGVD					
m713	AAPWPQIKAVVLKAENNPALGKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLVVGAD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a713.pep	YSSPPVATLCWSRTDSRRNIERMDIEWDTDNRFSEVTFLLAQSHGRSGDSAKHDLKVYKD					
m713	YSSPPVATLCWSRTDSRCNIERMDIEWDTDNRFSEVTFLLAQSHGRSGDSAKHDLKVYKD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a713.pep	PTMTLHRPKTVVSDADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWQPGQR					
m713	PTMTLHRPKTVVSDADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWQPGLR					
	250	260	270	280	290	300
	310	320	330	340	350	360
a713.pep	VHVIDDEHGI DAVFFLMGRRFMSRMDGTQ TELRLKEDGI WTPDAYPKKA EAARKRKGR					
m713	VHVIDDEHGI DAVFFLMGRRFMSRMDGTQ TELRLKEDGI WTPDAYPKKA EAARKRKGR					
	310	320	330	340	350	360
	370	380				
a713.pep	KGVS HKGKGGK GKKQAETAVFEX					
m713	KGVS HKGKGGK GKKQAETAVFEX					
	370	380				

1153

g714.seq not found yet

g714.pap not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```

m714.seq
1   ATGAGCTATC AAGACATCTT GCGGGGCTTG TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCAGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201 CGGTACGGGC AAAAACCGCC AGCACCCTGT GTTGCCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATCCGCGGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGCTA A

```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```

m714.pap
1   MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  RSAGQMLADW ERVLGLDGTG KNRQHRVLAV MAKLNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```

a714.seq
1   ATGAGCTATC AAGACATCTT GCGGGGCTTG TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCAGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201 CGGTACGGGC AAAAACCGCC AGCGCCGTGT GTTGCCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATCCGCGGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGATA A

```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```

a714.pap
1   MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  SSAGQMLADW ERVLGLDGTG KNRQRRVLAV MAKLNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pap	MSYQDILRGLLPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
	10	20	30	40	50	60
a714.pap	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAVNR					
	70	80	90	100	110	120
a714.pap	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAVNR					
	70	80	90	100	110	120
a714.pap	AGDRLAPQEI MWVWHVNVRG GNNRITRFRA GISAAGDRLT DYSDAVIESL FNRLKPAHTA					
m714	AGDRLAPQEI MWVWHVNVRG GNNRITRFRA GISAAGDRLT DYSDAVIESL FNRLKPAHTA					

1154

m714 AGDRLAPQEIMVWHVNVVRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
 130 140 150 160 170 180

a714.pep IRFTYRX
 |||||
 m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq
 1 ATGATTGATG TCAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTCCGCTA CGCAGGCCGT
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFEGGM
 101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGSLIP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq
 1 ATGATTGATG TCAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTCCGCTA CGCAGGCCGT
 151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFEGGM
 101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGSLIP*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq
 1 ATGAACAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
 51 GCGCGCCGCG GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
 201 TAAAGCAGGC GAAGGCAAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
 251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
 301 GAAGGCAAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA

1155

101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

m716.seq
 1 ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
 201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
 301 TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

m716.pep
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHNSAHG SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
 101 SK*

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHNSAHGSCGASKSAEGSCGA-----				
g716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGGASKSAEGSCGASKSAEG				
	10	20	30	40	50
	60	70	80	90	100
m716.pep	----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX				
	:				
g716	SCGAAASKAGEGKCGEGKCGATVKAHKHTKASKAKAKSAEGKCGEGKCGSKX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

a716.seq
 1 ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
 201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
 301 TCTAAATAA

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

a716.pep
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHNSAHG SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
 101 SK*

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHNSAHGSCGASKSAEGSCGAAGSKAG					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHNSAHGSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

g717.seq
 1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC


```

51  GGGTTTtagcc  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCCCTG  CGGCCGCTGC
251  TGTTTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCGCCGCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATTC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  GCGGAACACC  TCCGTCCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCTT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCCGTCCCG
601  CCGCGCCGCT  TTTGCGCCGC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTGTGCTCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTCG
751  ATGGGTATT  CGTTCGGCGG  GCGGGCATT  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTCCGTGC  AATCGAAGAA  AACGCCACGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCCCTC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCTCC  TCCTGCTGCC
951  GGAAACTAC  GCCGCCGTCC  GGTTTACCGT  CGTATCGTGT  ATGCTGccgc
1001  cgctGTTTT  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGACG  CGCGGCGCGG
1151  CGGTGCGCTG  TGCCGCCTCA  TTCTGGTGT  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATATGCA
1251  CACATTGTT  TGCCTgCCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  CCCcctgtt  gccggcgtAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AAATTGACAC  AAAGTGTTC  ATTATTGAA
1401  AAAACAAGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

g717.pep

```

1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCIGLDQA YVREYYAAAD KDTLFKTLFL PPLLFSAAIA ALLLSRPSLP
101  SEILFSLDDA AAGIGLVLEF LSFLPIRFL LVLRMGRAL AFSSAQLVPK
151  LAILLLLPLT VGLLHFPANT SVLTAVYALA NLAAAAFLF QNRCRLKAVR
201  RAPFSPAVLH RGLRYGIPLA LSSLAYWGLA SADRLFLKRY AGLEQLGVYS
251  MGISFGGAAL LLOSIFSTVW TPYIFRAIEE NATPARLSAT AESAALLAS
301  ALCLTGIFSP LASLLLPENY AAVRFTVWSC MLPLIFYTLT EISGIGLNVV
351  RKTRPIALAT LGALANLLL LGLAVPSSGT RGAAVACAAS FWLFFVFKTE
401  SSCRLWQPLK RLPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAAAYLAG
451  CILRHRKNLH KLFHYLKKQG FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

m717.seq

```

1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGGTTTtagcc  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCccccCGG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGCGGG  GCTGACGGTG
151  TCGGTGTTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACCT  TGTTCAAAAC  CCTGTTCCCTG  CGGCCGCTGC
251  TGCTGCCGCG  CGCGATAGCC  GCCCTGCTGC  TTTCGCCGCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCACT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  AGCGAACACC  GCGCTCCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCTT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCCGTCCCG
601  CACGCAACCG  TTTGCGCCGC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTCCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTCG
751  ATGGGTATTT  CGTTCGGCGG  GCGGCATT  TTGTTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGCGC  AATCGAAGAA  AACGCCCCGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCCCTC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCTCTCC  TCCTGCTGCC
951  GGAAACTAC  GCCGCCGTCC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTTTT  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCCGATCGC  GCTCGCCACC  TTGGGCGCGC  TGGCGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGCGCG  CGCGGCGCGG
1151  CGGTGCGCTG  TGCCGCCTCA  TTCTGGTGT  TTTTGTGCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATCTGCA
1251  CACATTGTT  TGCCTGACCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  TCCCTGTGTT  GCCGGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AGATTGACAC  AAAGTGTTC  ATTATTGAA
1401  AAAACAAGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

m717.pep
 1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
 51 SVLCLGLDQA YVREYYATAD KDTLFTLFL PLLSAAAI AALLSRPSLP
 101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLMEGRAL AFSSAQLVPK
 151 LAIIILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
 201 HAPFSPAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
 251 MGISFGGAAL LFQSIESTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
 301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
 351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
 401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAAYLAG
 451 CILRHRKDLH KLFHYLKKQG FPL*

m717/g717 96.4% identity in 473 aa overlap

m717.pep	10	20	30	40	50	60
	MDTKEILGYAAGSIGSAVLA	VIILPLLSWYFPADDIGRIV	LMQTAAGLTVSVLCLGLDQA			
g717	MDTKEILGYAAGSIGSAVLA	VIILPLLSWYFPADDIGRIV	LMQTAAGLTVSVLCLGLDQA			
	10	20	30	40	50	60
m717.pep	70	80	90	100	110	120
	YVREYYATADKDTLFTLFL	PLLSAAAI AALLSRPSLP	SEILFSLDDA AAGIGLVLE			
g717	YVREYYAADKDTLFTLFL	PLLSAAAI AALLSRPSLP	SEILFSLDDA AAGIGLVLE			
	70	80	90	100	110	120
m717.pep	130	140	150	160	170	180
	LSFLPIRFLLLVLRMEGRAL	AFSSAQLVPKLAIIILLPLTV	GLLHFPANTAVLTAVYALA			
g717	LSFLPIRFLLLVLRMEGRAL	AFSSAQLVPKLAIIILLPLTV	GLLHFPANTSVLTAVYALA			
	130	140	150	160	170	180
m717.pep	190	200	210	220	230	240
	NLAAAFLLFQNRCLKAVRHAP	FSPAVLH RGLRYGIPIAL	SSIAWGLASADRLFLKKY			
g717	NLAAAFLLFQNRCLKAVRRAP	FSPAVLH RGLRYGIPIAL	SSIAWGLASADRLFLKKY			
	190	200	210	220	230	240
m717.pep	250	260	270	280	290	300
	AGLEQLGVYSMGISFGGAALL	QSIESTVWTPYIFRAIEEN	NAPPARLSATAESAAALLAS			
g717	AGLEQLGVYSMGISFGGAALL	QSIESTVWTPYIFRAIEEN	NAPPARLSATAESAAALLAS			
	250	260	270	280	290	300
m717.pep	310	320	330	340	350	360
	ALCLTGIFSP LASLLLPENY	AAVRFIVVSC MLPPLFCTLA	EISGIGLNVVRKTRPIALAT			
g717	ALCLTGIFSP LASLLLPENY	AAVRFIVVSC MLPPLFCTLA	EISGIGLNVVRKTRPIALAT			
	310	320	330	340	350	360
m717.pep	370	380	390	400	410	420
	LGALANLLL LGLAVPSGG	ARGA AVACAASFWLFFAFKTE	SSCRLWQPLKRLPLYLHTLF			
g717	LGALANLLL LGLAVPSGG	TRGA AVACAASFWLFFAFKTE	SSCRLWQPLKRLPLYMHTLF			
	370	380	390	400	410	420
m717.pep	430	440	450	460	470	
	CLTSSAAYTCFGTPANYPLF	AGVWAAAYLAGCILRHRKDLH	KLFHYLKKQG FPLX			
g717	CLTSSAAYTCFGTPANYPLF	AGVWAAAYLAGCILRHRKDLH	KLFHYLKKQG FPLX			
	430	440	450	460	470	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

a717.seq
 1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
 51 GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
 101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGGG GCTGACGGTG
 151 TCGGTGTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
 201 CGCCGCCGAC AAGACACTT TGTTCAAAAC CCTGTTCTCG CCGCCGCTGC

1158

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251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTTGCT CGACGATGCC GCCGCCGGCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTCG
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGTCCAAG
451 CTCGCCATCC TGCTGCTGCT GCCCGTGACG GTCGGGCTGC TGCACTTTCC
501 GGCGAACACC GCCGTCCTGA CCGCGCTTTA CGCGCTGGCA AACCTTGCCG
551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGCTGAA GGCCGTCCGG
601 CGCGCACCGT TTTTCATCCG CGTCCTGCAT CGCGGCCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTTGTTTCT GAAAAAATAT GCCGGCCTAG AACAGCTCGG CGTTTATTCG
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTTCCGCGC AATCGAAGCA AACGCCCGCG
851 CCGCCCGCCT CTCGGCAACG GCAGAAATCCG CCGCCGCCCT GCTTGCCTCC
901 GCCCTCTGCC TGACCGGCAT TTTCTCGCCC CTCGCCTCCC TCCTGCTGCC
951 GGAAACTAC GCCGCCGTCC GGTTTATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTG CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCTGCTGCTG CTGGGGCTTG CCGTACCGTC CGGCGGCGCG CGCGGCGCGG
1151 CGGTTGCCTG TGCCGCCTCA TTTTGCTGT TTTTGTGTTT CAAGACCGAA
1201 AGCTCTGCC GCCTGTGGCA GCCGCTCAA CGCCTGCCG TTTATATGCA
1251 CACATTGTTT TGCCTGGCCT CCTCGGCGGC CTACACCTGC TTCGGCATC
1301 CGGCAACTA CCCCCTGTTT GCCGGCGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCCTGC GCCACCGGAA AGATTGTCAC AAAGTGTTC ATTATTGAA
1401 AAAACAAGGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

```

a717.pep
1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51 SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PPLLSAAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLF LSFLLPIRFL LVLMEGRAL AFSSAQLVSK
151 LAILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPSSAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPPLFCTLV EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFVFKTE
401 SSCRWQPLK RLPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLGA
451 CILRHRKDLH KLFHYLKKQG FPL*

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a717/m717 97.9% identity in 473 aa overlap

```

a717.pep      10      20      30      40      50      60
MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
|||||
m717          10      20      30      40      50      60
MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA

a717.pep      70      80      90      100     110     120
YVREYYAAADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLF
|||||:|||||
m717          70      80      90      100     110     120
YVREYYATADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLF

a717.pep     130     140     150     160     170     180
LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA
|||||
m717         130     140     150     160     170     180
LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA

a717.pep     190     200     210     220     230     240
NLAAAFLLFQNRCLKAVRRAPSSAVLHRLRYGIPIALSIAWGLASADRLFLKKY
|||||:|||||
m717         190     200     210     220     230     240
NLAAAFLLFQNRCLKAVRRAPSSAVLHRLRYGIPIALSIAWGLASADRLFLKKY

a717.pep     250     260     270     280     290     300
AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEANAPPARLSATAESAAALLAS

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|||||
m717      AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIENAPPARLSATAESAAALLAS
           250      260      270      280      290      300

           310      320      330      340      350      360
a717.pep  ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
|||||
m717      ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
           310      320      330      340      350      360

           370      380      390      400      410      420
a717.pep  LGALAAANLLLLGLAVPSGGARGA AVACASFVWFFVFKTESSCRLWQPLKRLPLYMHTLF
|||||
m717      LGALAAANLLLLGLAVPSGGARGA AVACASFVWFFAFKTESSCRLWQPLKRLPLYLHTLF
           370      380      390      400      410      420

           430      440      450      460      470
a717.pep  CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKLFHYLKKQGFPLX
||:|||||
m717      CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLFHYLKKQGFPLX
           430      440      450      460      470

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g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCGA AGCGTGTGG CCGCTGGGCT GGGTCGTTCA TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTTGG
251 AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTCGAGAT GGCCGACTGG
451 TGCGAAAAAT CGGCGGCGCG GCTGATTTTG GGGCAAACGC TGACCAGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCGCGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTTGA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCGAAAC TGGTGGATGT CGGCGTACAA
751 ATCCCCGAAA GCTGGGTGCG CGACAAACTG GTCATTCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGGTTGAGCC
951 CGATTTCAAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1   SDGLYVPRNF IHRPQSWFKW DKDNGLLLR RENPEGEALW PLGWVVHTQK
51  SRSVQQARNG LFRILSWLYM FKHYAVHDFA EFLEYGMPI RIGKYGAGAT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLQMAW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRDLLV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKFEEDTRE PKDIAVFADA IPKLVDVGVO
251 IPESWVRDKL VIPDVQEGEA VLVRQVPDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

a718.seq

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1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GGCGGAAATC GGTCAACAAC CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 CGGGCGCGCG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGCGCG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCC ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

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This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

a718.pep

```

1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHELFADI EERDS DIAAN MGTRKRALLT LNWRVAPERN
101 ATPEEKLSD QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFS DGL
151 YLPRNFIHRP QSWFKWDKDN GLLLR TRENP EGEALWPLGW VVHTQKRSV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLLRAVAEI GHNAAGIMPE GMEIELHNA NGMTSAGNPF LQMA DWCEKS
301 AARLILQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGFPLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

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a718/m718 98.4% identity in 380 aa overlap

	120	130	140	150	160	170
a718.pep	DSLPTLEDLIMDLMDAVGHGFSALEVEWVFS DGLYLPRNFIHRPQSWFKWDKDNGLLLRT					
m718	SDGLYVERNFIHRPQSWFKWDKDNGLLLRT					
				10	20	30
	180	190	200	210	220	230
a718.pep	RENPEGEALWPLGWVVHTQKRSRVQQARNGLFRTL SWLYMFKHYAVHDFAEFLELYGMPI					
m718	RENPEGEALWPLGWVVHTQKRSRVQQARNGLFRTL SWLYMFKHYAVHDFAEFLELYGMPI					
	40	50	60	70	80	90
	240	250	260	270	280	290
a718.pep	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPF LQMA DW					
m718	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQMA DW					

1161

	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQ					
m718	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEVRDRLVSDAKQVAQTITSQIIGPFLQ					
	160	170	180	190	200	210
a718.pep	360	370	380	390	400	410
	INYPHADPNRPVKFEFDTREPKDIAVFADAIPKLVGVQIPESWVRDKLVIPDVQEGEA					
m718	INYPHADPNRPVKFEFDTREPKDIAVFADAIPKLVGVQIPESWVRDKLVIPDVQEGEA					
	220	230	240	250	260	270
a718.pep	420	430	440	450	460	470
	VLVRQVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	VLVRQVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
	280	290	300	310	320	330
a718.pep	480	490	500	510	520	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	340	350	360	370	380	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATGCGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGGCGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAA ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCCGGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGATG GACGCGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAATCCG GAAGCGGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCAAAAATC CGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTCCGCAACG CTTTCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGGGAATC GGTCAACACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCGA CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAA CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGTGTGCG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQKEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDS DIAAN MGTRKRALLT LNWVRVAPPRN
101 ATPPEEKLSQ QAYEMMDSLP TLEDLIMDLN DAVGHGFSAL EWEVVFSDGL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRLRAVEI GHNAAGIMPE GMEIELHNAA NGTTATSNPF LQADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

```

351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
 401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
 451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
 501 DNAKLRTYMQ QALFISDILG QDHARA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq

1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
 51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
 101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
 151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
 201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
 251 GCAACGCGCG GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCCGGAAAT
 301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
 351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
 401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
 451 TACCTACCCC GAAACTTTAT CCACGCCCG CAAAGCTGGT TCAATGGGA
 501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CAAAATCCG GAAGGCGAAG
 551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAAATC GCGCAGCGTC
 601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCCTGGC TGTATATGTT
 651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGGAG CTGTACGGCA
 701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
 751 AACACCTGCG TTCGAGCGGT GCGGGAATC GGTCAACAAC CGGCAGGCAT
 801 CATGCCAGAA GGTATGGAAT TCGAGCTGCA CAACGCGGCA AACGCGATGA
 851 CTTCCGCCGG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
 901 GCGCGCGCGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
 951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCCGGATT
 1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
 1051 ATCGGACCGT TCCTGCAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
 1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
 1151 CCGACGCTAT CCCGAAACTG GTGGATGTGC GCGTACAAAT CCCCAGAAAGC
 1201 TGCGGTGCGC ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
 1251 GTTGGTGGCG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
 1301 CTTTATCCCG CCACACCGTA CCATCTAAGG CTACGGGCGA GCATCAGGAA
 1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
 1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
 1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
 1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
 1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep

1 MEPIMAKKNK KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
 51 LFEDAESGDI RAQHELFDADI EERDSIDIAAN MGTRKRALLT LNWRVAPPRN
 101 ATPEEEEKLS QAYEMMDSLP TLEDLIMDLN DAVGHGFSAL EVEWVFSDDL
 151 YLPRNFIHRP QSWFKWDKDN GLLRLTREN PEGEALWPLGW VVHTQKRSRV
 201 QOARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
 251 NTLRLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMDWCEKS
 301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
 351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
 401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
 451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
 501 DNAKLRTYMQ QALFISDILG QDHARA*

a718/m718-1 99.0% identity in 526 aa overlap

	10	20	30	40	50	60
a718.pep	MEPIMAKKNKTKTIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALEFEDAESGDI					
m718-1	MEPIMAKKNKTKTIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALEFEDAESGDI					
	10	20	30	40	50	60
a718.pep	RAQHELFDADIEERDSIDIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSQAYEMMDSLP					
m718-1	RAQHELFDADIEERDSIDIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSQAYEMMDSLP					
	70	80	90	100	110	120
a718.pep	RAQHELFDADIEERDSIDIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSQAYEMMDSLP					
m718-1	RAQHELFDADIEERDSIDIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSQAYEMMDSLP					
	70	80	90	100	110	120
a718.pep	TLEDLIMDLMDAVGHGFSALEVEWVFSGLYLPNFIHRPQSWFKWDKDNGLLLRTREN					
m718-1	TLEDLIMDLMDAVGHGFSALEVEWVFSGLYLPNFIHRPQSWFKWDKDNGLLLRTREN					
	130	140	150	160	170	180
a718.pep	TLEDLIMDLMDAVGHGFSALEVEWVFSGLYLPNFIHRPQSWFKWDKDNGLLLRTREN					
m718-1	TLEDLIMDLMDAVGHGFSALEVEWVFSGLYLPNFIHRPQSWFKWDKDNGLLLRTREN					
	130	140	150	160	170	180

a718.pep	190	200	210	220	230	240
	EGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMP	IRIGK				
m718-1	190	200	210	220	230	240
	EGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMP	IRIGK				
a718.pep	250	260	270	280	290	300
	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQ	MADWCEKS				
m718-1	250	260	270	280	290	300
	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQ	MADWCEKS				
a718.pep	310	320	330	340	350	360
	AARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQII	GPFLQINYP				
m718-1	310	320	330	340	350	360
	AARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQII	GPFLQINYP				
a718.pep	370	380	390	400	410	420
	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDVGVPQIPESWVRDKLVI	PDVQEGEAVLVR				
m718-1	370	380	390	400	410	420
	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDVGVPQIPESWVRDKLVI	PDVQEGEAVLVR				
a718.pep	430	440	450	460	470	480
	QVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLN	PMVRQAVAAL				
m718-1	430	440	450	460	470	480
	QVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLN	PMVRQAVAAL				
a718.pep	490	500	510	520		
	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQD	HARAX				
m718-1	490	500	510	520		
	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQD	HARAX				

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

```

1  ATGGCAAACG GGAACATGAA ACTGTCGTTG GTGTTAACCG CCCGAGATGA
51  CGGAGCGAGA CGGCTACTGG CTGATACTCA ACGACAATTA GATCGTACCG
101 CGAAATCGCG GCGCAACTT GAACGGCAA GCCATACTTA TGCCTTGACC
151 GGCATCCGCT CAGAAAAACA GATTCAACGC GAAATCATGC TGACACAGGC
201 TGCCTTTAAC CGTTTGCGGC GCAGCGGCAA GGCATCACAA AATGATTTGG
251 CACGGGCGGC GGTGCTACG CGTAACCGAA TTCGCGAGCT GAACGCGGAA
301 CTGAAACAGG GCACGGGATT TGCGGACAAG ATGGGAAAAA TCGGAAGATT
351 CGGTGCAGCT GCGGTGGCTG GTGGCGCGGC AGCGTATACG GTGCTTAAGC
401 CTGCTATGGA CAACAGAAAG CAGCTTGATG AGAACATCAA CCGCGTGTCC
451 AGACAGGCAT TTATTGAGGA TAACAGTAAA TCGGCAGCGT GGATTGCAAC
501 TGAAGGTGCG CAACAGATCA AGGATTGGC ACTTGAACCT GTCGAGAAAA
551 ATGGCGGGAC CCACGATAAG GCTTTGGATT TAATCAGCGG CATGATGACC
601 ACCGGTCTGA ATTTGCCCCA AACCAGAAT GAAGCGCAGG CGGCATATGC
651 TTTTGAACCT GCCTCAGAAG GCAGTGGCGA GGATACGGCA AAACGTATTA
701 AAACCTGAA AGATGGCGGC ATGAGCGGTA AAGACCTGCA ACTCGGGCTT
751 GAGCACGTCT TGCAATCGGG TTTAGACGGC ACTTTCGAGG TCGCGGATAT
801 GGTTCGGGAG CTGCCGAGCC TGCTCTCTGC CGCGCAACAG GCAGGGATGA
851 ATGGTGTCGG CGGTTTGGAC TACCTGCTCT CACTCTTACA ATCTGCGCGC
901 AATAAATCGG GCAGTCCTGC CGAAGCGGCG ACTAATGTGC AAAATCTTTT
951 GAGTAAAACT CTGTCGCCTG ACACGATAGG TCGTCTGAAG AAGATGGCAA
1001 ATCCGAATGA CCCGAAGAAA GGTGTCGATT GGATAGGCTC GGTGTGCAA
1051 GGCAAGCAAA ACGGCGAAAA CGCAGTGCAG GTGTTGTCCC GTCTTGCCGA
1101 TGCCATGCTA GTAAAGGATA AGCAATACCA AGATTATAAG AAACGCGCGG
1151 CTGCAGGCGA TAAGACGGCG GCGGAGCAGG CAAATATGCT TAAGGGCGCG
1201 CTTTGGCGC AACTGCTGCC TGATTGTCAG GCAAAACAAG GTTTGCTGGC
1251 TGCAACGGAT ATGACGCAAA TCCGTGAATA TATGGCTTCG TTGGCTGGCG

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1164

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1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGAGG CGGCGTGGCA GCAGGTGCCA CAGCGGCAGG CGGTAAGTTG
1651 CTGTCATGGG GAAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAAG GGTTCGCGTG GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAAA CAACGGTATC CGATTGGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTCACAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GCGCAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAGTG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CCGTATCAAG TGGCCATGTT
2151 CGGCCGTGGA GCGGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

```

m719.pep
  1 MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL ERQSHTYALT
 51 GIRSEKQIQR EIMLTQAAFN RLARSGKASQ NDLARAAVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLPAMDNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAYAFAL ASEGSGEDTA KLIKTLKDDG MSGKDLQLGL
251 EHVLSQGLDG TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLQSAA
301 NKSGSPAEEA TNVONLLSKT LSPDTIGRLK KMANPNPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKOGLLAATD MTQIREYMAS LAGVTLDNKG IAKNNEARML
451 SAAAQQEQQE SLAMLRRESLT GTLVDMETSF KKLAAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNNPALVKR AGLLGMLLYS ESLGDGTLPK GLRGTKTTPE
601 MINRLKNNGI RFEPAPKREQ ARGVVPQYLA APSAQPTDKM LSPLFSTQTA
651 AYQAAIQOOT AAYQAALAOD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVS RYQVAMFGRG AGQ*

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a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

```

m720.seq
  1 ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCCG
 51 CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTGTGCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGCAGG TGCAGATTAA TCGGGTGTTC TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGGCGTGC
251 TGGTGCACCC TGTTTGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTCCTT GAAAACGCCT
401 TTTTGGTCGA GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTTGTTGA TCGGGTGTTC GCGGTGGATG CGGGCGTATC
501 ACCTTTATGG GGCAGCGCGC TGGGCATTTC GAGTGCGGCA TCGGGTACGT
551 TTGGCGCGGT GCGCCGTTTG TTTGATTGTT ACAAAATTGC CTTTCCCGAT
601 CGGGGCGGAT ACAGTGCAGC GCGGTTTAAA AACGGCTCGG CCAAGCTGTT
651 TGCGGATATA TCGGTCATGG TAGATACTGG CATACGCCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGGTT GGTCCGCCGC ACAGCGGTTT
751 GACGGGGCTG CCGCTGTTGC CGACCGCGCC GCGCTATCC CTGATAATT
801 GCTGACCGGC CGCTTTTCAG ACGGCCTGCA AAACCGCCTG AACCGGTTAA

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1165

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851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CGGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTCGGTGGC AACGGCATT ATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTGTA TTGAGGTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGGCGG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
1151 TCATCAACCA AAAGCCGCGG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTAC GCGGATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
1 MSGWHTLLQD ASYKGVGFDI EVVDESNKA LAEHARPFVQ GIDLEDMGMT
51 GRQVQINAVF WKGKYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AEAQEIFVF ENAFLVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
251 DGAAAVADRA AAIPDNLLTG RFSDDLQNLRL NRLTAKQVQP VAQAVRLLST
301 SLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGGLTANAVY TEAYQTAE SL RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPHIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
1 GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCGGT
51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GGCGAAGAGA TGACCGCGCC CGATTTGATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
201 ACGGGCGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGGCA
301 GGCCGTCTGA ATGCGTTGGT TGCGGCGGTC ATCAACCAA AGCCGCGGCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGCG GCTCAATCCC
451 CATATCCACC ACCCCGCGTT TATCAAGCGC GGCACTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
1 GLQNLRLNRLT AKQVQPVQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51 EVNRAMRRRM QAEIAALRAV QTAAAESGGL TANAVYTEAY QTAESLRAAA
101 GRLNALVAAV INQKPPLIVR QAPIDGTIHQ IAHEFYGDIA RAAELVRLNP
151 HHHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

          250      260      270      280      290      300
m720.pep  SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNLRLNRLTAKQVQPVQAVRLLSTSSLL
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a720      GLQNLRLNRLTAKQVQPVQAVRLLSTSSLL
          10      20      30

          310      320      330      340      350      360
m720.pep  SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAAESGGLTANAVYTEAY
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a720      SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAAESGGLTANAVYTEAY
          40      50      60      70      80      90

          370      380      390      400      410      420
m720.pep  QTAESLRAAAAGRLNALVAAVINQKPPLIVRQAPIDGTIHQIAHEFYGDIAARAAELVRLNP
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a720      QTAESLRAAAAGRLNALVAAVINQKPPLIVRQAPIDGTIHQIAHEFYGDIAARAAELVRLNP
          100      110      120      130      140      150

          430      440
m720.pep  HHHHPAFIKRGTLVNSYAKX

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1166

a720 |||||
 HIHHPAFIKRGTLVNSYAKX
 160 170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAAGTCT GCCATATGGC GAATTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGCG GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCGCGCTC CGTGGGAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTCCGCG AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTTGAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTCGC TGCACCTGGC GGCTCGCAAA CGGGCGGCAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCG
1001 CAAAAATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC
1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>:

m721.pep
1 MSKNAQKLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPWYLTTEE
51 NGHDVALLAN SSRNQLVVDY EHQTLYKEKN GQPAPAAAGWM RWLEFTPKGM
101 FAEVWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON FMKELLQQLF DLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAKGVLPQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAAGTCT GCCATATGGC GAATTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGCG GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCGCGCTC CGTGGGAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTCCGCG AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCG
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTTGAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTCGC TGCACCTGGC GGCTCGCAAA CGGGCGGTAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCG
1001 CAAAAATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

```

a721.pep
  1 MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
 51 NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQOLF GLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLT KYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

```

a721/m721 99.2% identity in 353 aa overlap

	10	20	30	40	50	60
a721.pep	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
m721	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a721.pep	SSRNQLVVDYEHXTLYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
m721	SSRNQLVVDYEHQTLTYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a721.pep	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQOLF					
m721	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQOLF					
	130	140	150	160	170	180
	190	200	210	220	230	240
a721.pep	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a721.pep	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLVKQPGGLAFLTGFI					
m721	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLVKQPGGLAFLTGFI					
	250	260	270	280	290	300
	310	320	330	340	350	
a721.pep	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAAKMLGMSGEEFVKIKESGKX					
m721	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAAKMLGMSGEEFVKIKESGKX					
	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

```

m722.seq
  1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
 51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCTT GATACCGCG ACCGCGAGTA
201 TTGGAGCGG CATGCCTCCA TCGCGGGCTT GAGCCGCCG AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGACCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGCGGCA AATACCGCA ATCGCCGACG

```

1168

```

401 AGCCGGGCGC GCGCCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCCGCCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTG GAAATCATCC
551 GCGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAACGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

```

m722.pep
1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VDGGAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

```

a722.seq
1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCGC ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TCGCGGCTT GCGCCGCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGBA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGCGC GCGCCCAAT GTGCGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCGCGCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTG GAAATCATCC
551 GCGGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAACGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

```

a722.pep
1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```
m723.seq
1  ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCAGC CCCGAACACC TTATTTTAC CGTTTACAAA CACAATACCG
101 TCTTCGCCCG CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201 GGTTCGGGAT TTCGTGCGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTCG GCAGTGGCGT
351 CCACCAGCGC GGTTTGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CGGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTA CTGACC GCCTTGCCTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTCGCGCCA GCCGCCGTCA AACAGCAGGC CGCCGCGCCA AAATCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCCTT TTGTGCTCT TCGGCTTTT CCAAGGCTGT GGTGAGCATT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTTCGGCG GTTTCGGTT
851 TGTTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep
1  MRPKPRFRS VIACISVIT PEHLIFTVYK HNTVFARGHF FAAIHAQLH
51  FAFGHSTQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHOR GLCDLAVNQP LVVAVGELQD FQLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARETSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RVCCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGA AVSA VSGLLLVFAM MTPCFRRRRI
301 RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
1  -----+-----+-----+-----+-----+ 60
TACTCAAATCATTTAACGCTTTTTTTGCCGTGTTTGACGATTTTATAGCCGCTTTGG
a  M S L S K L A K K T A Q T A K N I G E T -

CTGCGCGCGGCCTTTCCGGGAAAAATCACGCTGGTGGTGTCTCCGAGCCGATACAGCGC
61 -----+-----+-----+-----+-----+ 120
GACGCGCGCCGGAAGCCCTTTTGTAGTGCACACACAGCAGGCTCGGCTATGTCGCG
a  L R A A F R G K I T L V V S S E P I Q R -

GTGCAGTTGAGCGGCTTGCCGACGAAACCCTGCAAGACCTGAACATTTGCAGGAATAC
121 -----+-----+-----+-----+-----+ 180
CACGTCAAATCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
a  V Q L S G L A D E T L Q D L E H L Q E Y -

GGCTTTGCCAGCCATCCGCCCCACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181 -----+-----+-----+-----+-----+ 240
CCGAAACGGTCGGTAGGCGGGCTGCCGTCGCTTCGCCATCACTATGGCGACCGCCGTTA
a  G F A S H P P D G S E A V V I P L G G N -
```

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241  -----+-----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACACTAACACACGTCGGTCGTGCCGTCGATGGCGTAGTTTTTGAATTC
a    T S H G V I V C S Q H G S Y R I K N L K -

      CCGGCGGAGACGGCGATTTTTAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301  -----+-----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATTAGTACTCCACGTTTTTAGCACTAATTCGTTCCGTTT
a    P G E T A I F N H E G A K I V I K Q G K -

      ATCATTGAGGCCGATTGCGACGTGTACCGGGTTAACTGCAACAATACGAGGTTAATGCG
361  -----+-----+-----+-----+-----+-----+ 420
      TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a    I I E A D C D V Y R V N C K Q Y E V N A -

      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAGTGCAGTGTGACGGCGCAA
421  -----+-----+-----+-----+-----+-----+ 480
      CGGTGCCTACGGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACTGCGCGGTT
a    A T D A K F N A P L V E T S A V L T A Q -

      GGCCAAATCAACGGCAACGGCGGCATGGCCGTGAGGGCGGCGACGGAGCCACCTTTAGC
481  -----+-----+-----+-----+-----+-----+ 540
      CCGGTTTAGTTGCCGTTGCCGCGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAATCG
a    G Q I N G N G G M A V E G G D G A T F S -

      GGCGATGTTAACCAAACGGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
541  -----+-----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGGCCGCCGTCGAATTGTGGCTGCCGCTGCACCACCGCCGTTA
a    G D V N Q T G G S F N T D G D V V A G N -

      ATATCGTTGCGCCAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGGCGGAA
601  -----+-----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCGTGGGCGTATGGCTGTCGTAGCCGCGTTTTTGAATGGCCGCTT
a    I S L R Q H P H T D S I G G K T L P A E -

      CCGGCATAG
661  ----- 669
      GGCCGTATC
a    P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglIII EcoRI HindIII KpnI NdeI NheI PstI SacI
Sali SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

```

m724.pep
1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEQ GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTGDVAVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

```

a724.seq
1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAATCAGC CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTG GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGCGAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCGGCGGAGA CGGCGATTTT TAATCATGAG GGTGCAAAAA TCGTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGATCCGG GTTAACGTGA
401 AACAAATACG GGTTAATGCG GCCACGGATG CCAAATTTAA CGCTCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```

1171

```

501 CGGCATGGCC GTCGAGGGCG GCGACGGAGC CACCTTTAGC GGCGATGTTA
551 ACCAAACGGG CGGCAGCTTT AACACCGACG GCGACGTGGT GGCCGGCAAT
601 ATATCGTTGC GCCAGCACCC GCATACCGAC AGCATCGGCG GCAAAACCTT
651 ACCGGCGGAA CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

```

a724.pep
1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

a724/m724 100.0% identity in 222 aa overlap

```

              10      20      30      40      50      60
a724.pep      MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY
              |||||
m724           MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY
              10      20      30      40      50      60

              70      80      90     100     110     120
a724.pep      GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQK
              |||||
m724           GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQK
              70      80      90     100     110     120

              130     140     150     160     170     180
a724.pep      IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS
              |||||
m724           IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS
              130     140     150     160     170     180

              190     200     210     220
a724.pep      GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX
              |||||
m724           GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX
              190     200     210     220

```

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

```

m725.seq
1  ATGGTGC GCA CGGTTAAAAG CTACAACGGC GAGGCCGACG ATTTGGCGGG
51  GCAAATCCAT ACGCTGCCTG CGGTTTGGGT AACGTATGGC GGCAGCAAAG
101 TTGAGCCTGC CAGCACCGGC GCGGTATGCG GACGTATCA GGATACCGCC
151 GAATTTGTGG TGATGGTGGC GGCCCGCAAT CTGCGCAACG AGCAGGCGCA
201 GCGGCAAGGC GGATCGACA GCCGCGAAAT CGGCAGCAAC GATTTAATCC
251 GCGCTGTTGC CCGCTGCTT GACGGCCAGC GGCTCGGTTT TGCCGATAGC
301 CGCGGCTTGG TGCCCAAAGC GGTGCGCGCG ATTGCCAATC ATGTGCTGGT
351 GCAAAACGCC GCAGTAAGCA TATATGCGGT TGAGTATGCC ATCCGCTTTA
401 ACACCTGCGG GTTGGAATAT GACCGCTACC CCGAACGCAC CGACAATCCC
451 GACGACCCCA ACCATATCTT TACCAAGTAT CAGGGTACAT TGAGCGAGCC
501 GTGGCCTGAT TTCGAGGGGT TGGACGGCAA AATTTACGAC CCGCAATCCG
551 CCGATGAAT ACCTGTAAAC CTAACCCTTA AGGATAAGCA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

```

m725.pep
1  MVRTVKS YNG EADDLAQI H TLPVWVTY G GSKVEPAST G GVCGRYQDTA
51  EFVVMVA ARN LRNEQAQR QG GIDSREIGS N DLIRAVRRL L DGQRLGFADS
101 RGLVPKA VRA IANHVLVQ NA AVSIYAVE YA IRENTCGLE N DRYPERTDNP
151 DDPNHIF TKY QGTLSEP WPD FEGLDGKI YD PQSADEIPV N LTLKDKQ*

```


a725.seq not found yet

a725.pep not found yet

g726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

```
m726.seq
  1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
 51  CCCC GAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101  CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151  GTTTTAACCC CGCCGCGCCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
201  ATGGAAAATC AGCAAAGCCG CCGCCGCCGC CCGTTTCGCC AAACAAAAAA
251  CCGCCTTGGC ATTCGCGCTC GCGGAAAAGG CGGACGAACT CAAAAACAGC
301  CTCTTGCGCG GCTATCCCCA AGTGGAAATC GACAGCTTTT ACAGGCAGGA
351  AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401  TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451  AAAGTTATCG AAAAATCCGC CCGCCTGGCT GTTGCCGCCG GCGCGATTAT
501  CGGAAAGCGT CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551  CCGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601  GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

```
m726.pep
  1  MTIYFKNGFY DDTLGGIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
 51  VLTPPRPSDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
101  LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVIE
151  KVIEKSARLA VAAGAIIGKR QQLEDKLNTI ETAPGLDALE KEIEEWTLNI
201  G*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

```
a726.seq
  1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCAGCAT
 51  CCCC GAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101  CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151  GTTTTAACCC CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
201  ATGGGAAATC GCGGAAGCCG CTGCGCGCCG CCGTTTCGCC GAACAAAAAA
251  CCGCCACGGC ATTCGCGCTC GCGGCAAAGG CGGACGAACT CAAAAACAGC
301  CTCTTGCGCG GCTATCCCCA AGTGGAAATC GACAGCTTTT ACAGGCAGGA
351  AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401  TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451  AAAGTTGTCTG AAAAATCCGC CCGCCTGGCC GTTGCCGCCG GCGCGATTAT
501  CGGAAAGCGG CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551  CAGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601  GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

```
a726.pep
  1  MTIYFKNGFY DDTLGSIEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
 51  VLTPPRPSEY HEWDGKKWEI GEAAAAARFA EQKTATAFRL AAKADELKNS
101  LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVIE
151  KVIEKSARLA VAAGAIIGKR QQLEDKLNTI ETAPGLDALE KEIEEWTLNI
201  G*
```

a726/m726 95.5% identity in 201 aa overlap

```

              10      20      30      40      50      60
a726.pep      MTIYFKNGFYDDLGSIEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPPRPSEY
              |||
m726           MTIYFKNGFYDDLGGIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPPRPSDY
              10      20      30      40      50      60
```

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```

              70      80      90      100      110      120
a726.pep    HEWDGKKWEIGEA AAAARFAEQKTATAFR LAAKADELKNSLLAGYPQVEIDSFYRQEKEA
            |||||:|:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726        HEWDGKKWKISKAAAAARFAKQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep    LARQADNNAPTMLAQIAAARGVELDVLIEKVVEKSARLAVAAGAIIGKRQQLEDKLNIT
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726        LARQADNNAPTMLAQIAAARGVELDVLIEKVVEKSARLAVAAGAIIGKRQQLEDKLNIT
              130      140      150      160      170      180

              190      200
a726.pep    ETAPGLDALEKEIEEWTNIGX
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726        ETAPGLDALEKEIEEWTNIGX
              190      200

g727.seq    not found yet

g727.pep    not found yet

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1  ATGAATCTCG TGAAACTGCT GCGGAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTTGC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAC TATGCGCGCG AACTGGAAC
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTCTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIPFPFD SRNPNTGFRL FSPQIPPNET QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1  ATGAATCTCG TGAAACTGCT GCGGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAC TACGCCCGCG AACTGGAACA
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCTGAA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DFGHHGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep    MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

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```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN
           10      20      30      40      50      60
           70      80      90      100     110     119
a727.pep  YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m727      YARELELARA EAKKYEVKAHAVGMALAKKQAEVSRLKTE--RDLCKIPFPD SRNPNTGTF
           70      80      90      100     110
           120     130     140
a727.pep  IDGFGHHGLQLYKRALGYGNX
m727      RLFSQPIPPNTQIPPX
           120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

```

g728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTGCTTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGG ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG GGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTT
901 ATTGCACAAT CTTGACGCGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGATG GCGGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGGAAGATT TGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

```

g728.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQ AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMQT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

```

m728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAAT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTGCTTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

```

```

501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GAAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG AGGGATGAAG CGGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACG AAATCTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GGCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGGAATAAT TGGAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

```

m728.pep
  1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
 51 AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHLGICYQM AQVYLAKYRD VANDEQKVD FRKESNRIAS DSRNSVIFYQN
251 MRELMPRGMK ANSLVVGIDA DGLPQKVYWS FDNGKKRQSF EYYLKNLNF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

m728.pep	10	20	30	40	50	60
	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA					
g728	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPEPNPNAFVAKLARLFRNA					
	10	20	30	40	50	60
m728.pep	70	80	90	100	110	120
	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	130	140	150	160	170	180
	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSNVYGGTVHGENYETTGEYRVV					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	190	200	210	220	230	240
	WQPDGSVFDAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVD FRKESNRIAS					
g728	WQPDGSVFDAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVD FREESNRIAS					
	190	200	210	220	230	240
m728.pep	250	260	270	280	290	300
	DSRNSVIFYQNMRELMPRGMKANSLVVGIDADGLPQKVYWSFDNGKKRQSFEYYLKNLNF					
g728	DSRDYVIFYQNMRELMPRGMKANSLVVGIDADGLPQKVYWSFDNGKKRQSFEYYLKNLNF					
	250	260	270	280	290	300
m728.pep	310	320	330	340	350	360
	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					

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```

g728      IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
           310      320      330      340      350      360

           370
m728.pep  YAEAAARRSGRRDL SHX
           |||||
g728      YAEAAARRSGRRGL SHX
           370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

```

a728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCGAAACTT
151 GCCCGCTGT TCCGAAATGC CGACAGGGCG GTTGTTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA
301 GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGAAGAGGT
351 TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTTT
401 CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGGCGC GGGAAATCG GGAAGATGT TTATGAGCAT
601 TGCCTCGGGT GTTATCAGAT GGCCAGGTA TATTTGGCGA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCGCGGAA GAGAGTAACC
701 GGATTGCGTC GGAATCGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
751 TTGATGCCCC GAGGGATGAA GGCAACAGT CTTGTGGTCG GCTATGATGC
801 GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTGACAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
951 CTATCATGCG CAACAGACGT GGTATTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTGAA CTGGAAGAT
1051 TTGAAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

```

a728.pep
1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSLSQSRPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGCVQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

a728 / m728 96.3% identity in 377 aa overlap

```

           10      20      30      40      50
a728.pep  MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA
           |||||
m728      MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
           10      20      30      40      50      60

           60      70      80      90      100     110
a728.pep  DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLLALAVRLSRLKEKAKWFHVTEQEHGEEV
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728      DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLLALAIRLSRLKEKAKWFHVTEQEHGKEV
           70      80      90      100     110     120

           120     130     140     150     160     170
a728.pep  WLDYYIGEGGLVAVSLSQSRPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
           ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728      WLDYHIGEGGLVAVSLSQSRPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
           130     140     150     160     170     180

```

1177

	180	190	200	210	220	230
a728.pep	WQPDGSVFDAASGRGKIGEDVYEHCLGQYMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGSVFDAAGRGKIGEDVYEHCLGQYMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVIFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFYEYLLKNGNLF					
m728	DSRNSVIFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFYEYLLKNGNLF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDEKEVSR					
m728	IAQSSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAAARRSGGRRDLSHX					
m728	YAEAAAARRSGGRRDLSHX					
		370				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

```

1  ATGAATACTA CATTGAAAAC TACCTTGACC TCTGTTGCAG CAGCCTTTGC
51  ATTGTCTGCC TGCACCATGA TTCCTCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCGGAAAC CTTCCAAAAC GACACATCGG TTTCTTCCAT CCGCGCGGTT
151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACAGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATCG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGGCTCGCGC CAAGGCAGCT TGAGCGGCgg
351 caaTGTCAGC AGCAGCTACA ATGTCGGACT GGGTGcGGca tCTTACGAAC
401 TCGATCTGTT CgGGCGCGTG CGCagcaacA GcgaagcAGC ACTGcaggGC
451 tATTTTGCCA GCGTTGCCAA CcgCGATGCG GCACATTTGa ttCtGATTGC
501 CACCGTTGCC AAAGCCTATT TCAAcgaGcG TTATGCCGAA AAAGcgaTgT
551 CTTTGGGCGCa gcGTGTCTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTGCGGT ACAAGGCAGG CGTGATTTCG GCGTTCGCCC TCGCCAGCA
651 GGAAGCCTTG ATTGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCa
701 gcCGCGAACA GCGCGCAAT GCCTTGCGAA CCTTGATTAA ccGTCCGATA
751 CCCGAaagCC TGCCCGCCGG TTTGCCGTTG GACAagcAGT TTTTGTGTA
801 AAAACTGCCT GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGACA
851 TCCGCGCCGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 gcgCGCGCCg ccTTTTTCCC GTCCATCCGC CTGACCGGAA GCGTCGGTAC
951 GGGTTCGTGC GAATTGGGCG GGCTGTTCAA AAGCGGCACG GCGGTTGGG
1001 CGTTCGCTCC GTCTATTACC CTGCCGATTT TTACTTGGGG AACGAACAAG
1051 GCGAACCTTG ATGTGGCAAA ACTGCGCCAA CAGGCACAAA TTGTGCTTA
1101 TGAATCCGCC GTCCAATCCG CCTTCAAGA CGTGGCAAAC GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG CTTGGTCGGA CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGATTGTC TCGATGCGGA ACGCATCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CGCTCgacGG CGGATTGAAA CGGGATACCC AAACCGGCAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

```

1  MNTTLKTLT SVAAAFALSA CTMIPQYEQP KVEVAETFQN DTSVSSIRAV
51  DLGWHDYFAD PRLQKLIDIA LERNLSLRTA VLNSEIYRQK YMIERNLLP
101 TLAANANGSR QGSLSGGNVS SSYNVGLGAA SYELDLFGRV RSNSEALQG
151 YFASVANRDA AHLILIATVA KAYFNERYAE KAMSLAQRLV KTREETYKLS

```

```

201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINRPI
251 PEDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGTVGTGSA ELGGLFKSGT GVWAFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QQIVAYESA VQSAFQDVAN ALAAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSQA LDLLDAERIS YSAEGAALSA QLTRAENLAD
451 LYKALDGGGLK RDTQTKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2465>:

```

m729.seq
  1 ATGGATACTA CATTGAAAAC CACCTTGACT TCTGTTGCAG CAGCCTTTGC
 51 ATTGTCTGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAACG GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGCGCCGTC
151 GATTTAGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACCGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
351 CAATGTAAAG AGCAGCTACA AAGTCGGACT GGGTGCGGCA TCTTACGAAC
401 TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTGCGCA GCACCGCCAA CCGCGATGCG GCACATTTGA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTACGCCGAA GAAGCGATGT
551 CTTTGCGCGA ACGTGTTTT AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTACGTT ACAAGGCAGG CGTGATTTCG GCGTCGCCC TACGTACGCA
651 GGAAGCCCTG ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA
701 GCCGCGAACA GCGCGCGCAAT GCCTTGGCAA CCTTGATTAA CCAACCGATA
751 CCCGAAGACC TGCCTGCCGG TTTGCCGCTG GACAAGCAGT TTTTGTGTA
801 AAAACTGCCG GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 GCACGCGCCG CCTTTTCCG ATCCATCCGC CTGACCGGAA CCGTCGGTAC
951 GGGTTCGACC GAATTGGGTG GGTGTTCAA AAGCGGCACG GGCCTTTGGT
1001 CGTTCGCGCC GTCTATTACC CTGCCGATT TTACCTGGGG TACGAACAAG
1051 GCGAACCTTG ATGTAGCCAA GCTGCGCCAA CAGGTACAAA TCGTTGCCTA
1101 TGAATCCGCC GTCCAATCCG CATTTCAGA CGTGGCAAAC GCATTGGCGG
1151 CCGCGAGACA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG CTTGGTCCGC CTGCGTTACA AGCACGGCGT
1251 ATCCGGCGCG CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATGCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2466; ORF 729>:

```

m729.pep
  1 MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
 51 DLGWHDFYAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANDSR QGSLSGGNVS SSYKVLGAA SYELDLFGRV RSSSEAALQG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PEDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGTVGTGSA ELGGLFKSGT GVWSFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QQIVAYESA VQSAFQDVAN ALAAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSQA LDLLDAERSS YAAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 729 shows 95.7% identity over a 467 aa overlap with a predicted ORF (ORF729.a) from *N. gonorrhoeae*:

m729 / g729 95.7% identity in 467 aa overlap

```

          10      20      30      40      50      60
m729.pep  MDTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDFYAD
          |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g729      MNNTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFQNDTSVSSIRAVDLGWHDFYAD
          10      20      30      40      50      60

```

1179

	70	80	90	100	110	120
m729.pep	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANDSRQGSLSGGNVS					
g729	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANGSRQGSLSGGNVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m729.pep	SSYKVLGAASYELDLFGRVRSSEAAALQGYFASTANRDAHLSLIATVAKAYFNERYAE					
g729	SSYNVGLGAASYELDLFGRVRSNSEAALQGYFASVANRDAHLILIATVAKAYFNERYAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m729.pep	EAMSLAQRVLKTREETYKLSELRYKAGVISAVALRQOEALIESAKADYAHAAARSREQARN					
g729	KAMSLAQRVLKTREETYKLSELRYKAGVISAVALRQOEALIESAKADYAHAAARSREQARN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m729.pep	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
g729	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m729.pep	ARAAFFPSIRLTGTVGTGSAELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLRQ					
g729	ARAAFFPSIRLTGTVGTGSELGGLFKSGTGVWAFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
m729.pep	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA					
g729	QAQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA					
	370	380	390	400	410	420
	430	440	450	460		
m729.pep	LDLLDAERSSYAAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	LDLLDAERISYSAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQTKX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

```

1  ATGGATACTA CATTGAAAAC CACCTTGACT TCTGTTGCAG CAGCCTTCGC
51  ATTATCCGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGTGC GGTC
151 GATTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACCGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
351 CAATGTAAGC AGCAGCTACA AAGTCGGACT GGGTGC GGCA TCTTACGAAC
401 TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTCGCCA GCACCGCCAA CCGCGATGCG GCACATTTGA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTATGCCGAA GAAGCGATGT
551 CTTTGGCGCA ACGTGT TTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTACGTT ACAAGGCAGG CGTGATTTCG GCCGTCGCCC TACGTCAGCA
651 GGAAGCCCTA ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA
701 GCCGCGAACA GCGCGCAAT GCCTTGCGAA CCCTGATTAA CCAACCGATA
751 CCCGACGACC TGCCCGCCCG TTTGCCGTTG GACAAGCAGT TTTTGTGTTGA
801 GAAGCTGCCG GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 GCACGCGCCG CCTTTTCC ATCCATCCCG CTGACCGGAA GCGTCGATAC
951 GCATTCTGCC GAATTGGGCG GGCTGTTCAA AAGCGGCACC GCGGTTGGT
1001 TGTTCCGACC TTCCATTACC CTGCCGATT TTACCTGGGG TACGAACAAG

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1180

```
1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTTCAAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

```
a729.pep
  1  MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
 51  DLGWHDYFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNNLLP
101  TLAANANDSR QGSLSGGNVS SSKVGLGAA SYELDLFGRV RSSSEALQOG
151  YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
201  ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251  PDDLPAGLPL DKOFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301  ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351  ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401  ASKEALRLVG LRYKHGVSGA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451  LYKALGGGLK RDTQTDK*

a729 / m729    98.1% identity in 467 aa overlap

      10      20      30      40      50      60
a729.pep  MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDYFAD
          |||
m729      MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDYFAD
      10      20      30      40      50      60

      70      80      90     100     110     120
a729.pep  PRLQKLIDIAL ERNTSLRTA VLNSEIYRKQ YMIERNNLLP TLAANANDSR QGSLSGGNVS
          |||
m729      PRLQKLIDIAL ERNTSLRTA VLNSEIYRKQ YMIERNNLLP TLAANANDSR QGSLSGGNVS
      70      80      90     100     110     120

      130     140     150     160     170     180
a729.pep  SSKVGLGAAS YELDLFGRV RSSSEALQOG YFASTANRDA AHLSLIATVA KAYFNERYAE
          |||
m729      SSKVGLGAAS YELDLFGRV RSSSEALQOG YFASTANRDA AHLSLIATVA KAYFNERYAE
      130     140     150     160     170     180

      190     200     210     220     230     240
a729.pep  EAMSLAQRVL KTREETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN
          |||
m729      EAMSLAQRVL KTREETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN
      190     200     210     220     230     240

      250     260     270     280     290     300
a729.pep  ALATLINQPI PDDLPAGLPL DKOFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
          |||
m729      ALATLINQPI PDDLPAGLPL DKOFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
      250     260     270     280     290     300

      310     320     330     340     350     360
a729.pep  ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK ANLDVAKLRQ
          |||
m729      ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK ANLDVAKLRQ
      310     320     330     340     350     360

      370     380     390     400     410     420
a729.pep  QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR ASKEALRLVG LRYKHGVSGA
          |||
m729      QVQIVAYEAA VQSAFQDVAN ALAAREQLDK AYDALSKQSR ASKEALRLVG LRYKHGVSGA
      370     380     390     400     410     420
```

1181

	430	440	450	460
a729.pep	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
	:			
m729	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
	430	440	450	460

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

g730.seq

```

1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GGC GGT CGCA  CTCATACAGC  CCGCCCTCGC  GCGCGACTTG  GCGCAAGACC
101 CGTTCATTAC  CGATAACACC  CAACGGCAGC  ACTACGAACC  CGGCGGCAAA
151 TACCACCTCT  TCGGcgaCCC  GCGCGGCAGC  GTTTCGACCC  GCACCGGCAA
201 AATCAACGTC  ATCCAAGACT  ATACCACCA  GATGGGCAAC  CTGCTCATCC
251 AACAGGCGGC  AATCCAAGGC  AATCTTGGTT  ACACCGTCCG  CTTTCCGGA
301 CACGGACACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 AAGCGAAGAA  AAAGGCAACG  TTGACGACGG  CTTTACCGTG  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCCGCCG  ATGCCTACGA  CGGCCCGAAG
451 GCGGGCAATT  ACCCAAACC  TACGGGCGCA  CGAGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCCGCA  GTATCAAAC  CAATCCGACC  GACACCGGCA
551 GCATCCGGCA  ACGCATATTC  GACAACTACA  ACAACCTCGG  CAGCAATTTC
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TGTCAACGGC  GTCGCCGCCG
701 AGCGGCTCAA  CCCCTTTATC  AGCGGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCGA  TCGCGAACAT
801 CGCCCCCTTA  CCCGCCGAGG  GCAAATTCGC  CGCCATCGGC  GGCTTGGGCA
851 GCGCGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTGTA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCCGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GCGGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  TGGGGATTTT  TCTAAATCCT  ACACCTGCTC  CTTCCACGGC
1051 AGCACCTTGG  TCAAACGGC  AGACGGCTAC  AAAGCCATTG  CCCATATTCA
1101 AGCCGGAGAC  CGCGTCTTT  CCAAGGACGA  GGCAAGCGGA  GAAACGGGAT
1151 ACAAACCCGT  TACCGCCCGA  TACGGCAATC  CGTATCAAGA  AACCCTTAC
1201 ATTGAAGTTT  CAGACGGCAT  CCGCAACAGC  CAAACCCTGA  TTTCCACCG
1251 CATCCACCG  TTTTATTCGG  ACGGCAATG  GATTAAGGCG  GAAGATTAA
1301 AAGCGGGAAG  CCGGCTGTTA  TCCGAAAGCG  GCAAAACCCA  AACCCTCGC
1351 AACATCGTTG  TCAAACCAA  ACCGCTCAA  GCCTACAATC  TGACCGTTGC
1401 CGATTGGCAT  ACCTACTTCG  TCAAGGTA  TCAGGCGGAA  ACGGAAGGG
1451 TTTGGTTCA  TAATGATTGT  CCGCCTAAAC  CAAAACCAAC  CAATCATGCC
1501 CAACAAAGAA  AAGAAGAAGC  TAAAAACGAT  TCTCATCGAA  GTGTGGGAGA
1551 TTCCAATCGT  GTCGTTGCGG  AAGGAAAGCA  ATATTAGAT  TCCGACACAG
1601 GAAACCATGT  TTATGTAAAA  GGAGATAAAG  TGGTTATTCT  AACTCCTGAT
1651 GGAAGACAGG  TAACTCAATT  TAAGAACTCG  AAAGCCAATA  CGTCAAAAAG
1701 GGTAAAAAAT  GGGAAATGGA  CACCAAAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

g730.pep

```

1  VKPLRLTNL  LAACAVAAVA  LIQPALAADL  AQDPFITDNT  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGKINV  IQDYTHQMG  LLIQQAIIQG  NLGYTVRFSG
101 HGHEEHAPFD  NHAADSASEE  KGNVDDGFTV  YRLNWEGHEH  HPADAYDGPK
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIF  DNYNNLGSNF
201 SDRADEANRK  MFEHNAKLDR  WGNMSEFVNG  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAAIG  GLGSAAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVKNLTKAAK  PGKAAVSGDF  SKSYTCSFHG
351 STLVKTAGDY  KAIAHIQAGD  RVLKDEASG  ETGYKPV TAR  YGNPYQETVY
401 IEVSDGIGNS  QTLISNRIHP  FYS DGKWIKA  EDLKAGSRL  SESGKTQTVR
451 NIVVKPKPLK  AYNLTVADWH  TYFVKGNQAE  TEGVWVHND  PKPKPTNHA
501 QQRKEEAKND  SHRSVGDSNR  VVREGKQYLD  SDTGNHVYVK  GDKVVILTPD
551 GRQVTQFKNS  KANTSKRVKN  GKWTPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

m730.seq

```

1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GCGGCGCGCA  CTCATACAGC  CCGCCCTCGC  GCGCGACTTG  GCGCAAGACC

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1182

```

101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTTCCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTTCCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCGCGG ATGCCTACGA CGGCCCGAAG
451 GCGGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCGCA GTATCAAAC CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTC
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCGCGG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TCGCAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTGA CCGGTGGATA
901 CAGGAAAATC CCAATGCCGC CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAA GGCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATCTT ATAAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATTAGAAG AAAAAGTAT GGTTCATCAA
1151 AATTTATTAA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAAA GAACAATTTT AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAAA TTAAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAAAACG TGCAGAATTT TGGTTTAAAT ACGGTGTTC TACACAAGTT
1351 AAGTCATATA TTGAATCAAA AGGCGGCATT GTTAAACAG GTTAGGAGA
1401 TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
1 VKPLRLRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51 YHLFGDPRGS VSDRTGKINV IQDYTHQMG NLLIQQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIS DNYSNLGSNF
201 SDRADENRKM FEHNAKLDR WGNMSEFING VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAAETV EAVFNVAAAA KVAKLAKAAK PGKAAVSGDF ADSYKKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPNFNLQKN RKQIKATIEA ANQQGKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

```

g730 / m730 93.0% identity in 344 aa overlap

```

g730.pep      10      20      30      40      50      60
VKPLRLRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730          10      20      30      40      50      60
VKPLRLRLTNLLAACAVAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS

g730.pep      70      80      90      100     110     120
VSDRTGKINVIQDYTHQMGNLLIQQAIIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730          70      80      90      100     110     120
VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE

g730.pep     130     140     150     160     170     180
KGNVDDGFTVYRLNWEGHEHHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730         130     140     150     160     170     180
KGNVDEGFTVYRLNWEGHEHHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT

g730.pep     190     200     210     220     230     240
DTRSIRQRIFDNYNNLGSNFSRDEANRKMFEHNAKLDRWGNMSEFVNGVAAGALNPFI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730         190     200     210     220     230     240
DTRSIRQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNMSEFINGVAAGALNPFI

```

1183

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAAKPGKAAVSGDFSYSYTCSEFHGSTLVKTADGY					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAGKPGKAAVSGDFADSYKKKIALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVNTARYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRKTDGSSKFINGREIDAVTNDALIAQKRTISAIKPKNFNLQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1  GTGAAACCGC  TCGAAGACT  CATCAAGCTC  CTTGCCGCT  GTGCCGTAGC
51  GCGCGCCGCA  CTCATACAGC  CCGCCCTCGC  GCGCGACTTG  GCGCAAGACC
101 CGTTCATTAC  CGATAACGCC  CAACGCGCAGC  ACTACGAACC  CGGAGGCAAA
151 TACCACCTCT  TCGGCGACCC  GCGCGGCAGC  GTCTCCGACC  GCACCGGTCA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCG  GATGGGCAAC  CTGCTCATCC
251 AGCAGGCAAA  CATCAACGGC  ACAATCGGCT  ACCACACCCG  CTTTCCGGA
301 CACGATACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 GAGCGAAGAA  AAAGGCAACG  TTGACGAAGG  CTTTACCGTA  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCGCGCG  ATGCCCTACG  CGGCCCGAAG
451 GCGCGCAATT  ACCCCAAACC  TACGGGTGCA  CGCGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCAGCGA  GCATCAAAT  CAATCCGACC  GACACCGCA
551 GCATCCGGCA  ACGCATATCC  GACAATTACA  GCAACCTCGG  CAGCAATTC
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTTCGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TATCAACGGC  GTCGCCCGCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCAA  TCGGCAACAT
801 CGCCCCCTTG  CCCGCCGAGG  GCAAATTCGC  CGTCATCGGC  GGCTTGGGCA
851 GCGTGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTGTA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCCG  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCCGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GGCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  CGGGGATTTT  TCTGCTGCAT  ACAATACAAG  AACAACAGAA
1051 AAAGTTACTA  CAGAAACAGA  GGGGTTAAAT  AGAATCAGAC  AGAACCAGAA
1101 AAATAGTAAT  ATACATGAGA  AAAATTATGG  AAGAGATAAT  CCTAATCATA
1151 TTAATGTTTT  ATCTGGAAAT  TCTATACAAC  ATATACTGTA  TGGAGATGAA
1201 GCAGGAGGTG  GGCATCTTTT  TCCTGGCAAA  CCTGGTAAGA  CAACATTCCC
1251 CCAACATTGG  TCAGCCAGTA  AAATAACTCA  TGAAATTAGT  GATATCGTTA
1301 CATCCCCAAA  AACGCAATGG  TATGCACAGA  CTGGAACAGG  CGGCAATAT
1351 ATTGCTAAAG  GAAGACCAGC  TAGGTGGGTA  TCATATGAAA  CGAGAGATGG
1401 AATTCGTATC  AGAACAGTTT  ATGAACCTGC  AACAGGAAAA  GTGGTAACGT
1451 CATTCCCCGA  TAGAACCTCT  AATCCCAAAT  ATAACCCTGT  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1  VKPLRLRIKL  LAACAVAAAA  LIQPALAADL  AQDPFITDNA  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGQINV  IQDYTHRMGN  LLIQQANING  TIGYHTRFSG
101 HGVEEHAPFD  NHAADSASEE  KGNVDEGFTV  YRLNWEHGH  HPADAYDGP
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRI  DNYSNLGSNF
201 SDRADEANRK  MFEHNAKLDR  WGNSEFFING  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAVIG  GLGSVAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVNLTAAK  PGKAAVSGDF  SAAYNTRTTR
351 KVTETETGLN  RIRQNQKNSN  IHEKNYGRDN  PNHINVLSGN  SIQHILYGDE
401 AGGGHLFPGK  PGKTTFPQHW  SASKITHEIS  DIVTSPKTQW  YAQTGTGGKY
451 IAKGRPARVW  SYETRDGIRI  RTVYEPATGK  VVTAFPDRTS  NPKYNPVK*

```

a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730.pep	VKPLRRLIKLLAACAVAAAALIQPALAADLAQDFFITDNAQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRRLTNLLAACAVAAAALIQPALAADLAQDFFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
	190	200	210	220	230	240
a730.pep	DTRSIRQIRISDNYSNLGNSFSDRADEANRKMFEHNAKLDRWGNSMEFINGVAAGALNPFI					
m730	DTRSIRQIRISDNYSNLGNSFSDRADEANRKMFEHNAKLDRWGNSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a730.pep	SAGEALGIGDILYGTTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a730.pep	QENPNAAETVEALVNVLPFAKVKNLTKAAPGKAASVSGDFAAYNTRTRKVTETETGLN					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAPGKAASVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	
	370	380	390	400	410	420
a730.pep	RIRQNQKNSNIHEKNYGRDNPNNHINVLGNSIQHILYGDEAGGGHLFPKGKPTTFPQHW					
m730	QLYQNAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIIDKPKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

```

g731.seq
1  gattttcgag cgttttcatG CGAGAACGGT TTGTCTGTGC GCGTCCGCAA
51  TTTGGACGGC GGCAAAATCG CGTTGCGGCT GGACGGCAGG CGTGCCGTCC
101 TCTCTTCCGA CGTTGCCGCA TCCGGCGAAC GCTATACCGC CGAACACGGT
151 TTGTTTCGAA ACGGAACCGA GTGGCACCAG AAAGGCGGCG AAGCCTTTT
201 CGGCTTTACC GATGCCTACG GCAATTCGGT CGAAACTTCC TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2476; ORF 731.ng>:

```

g731.pep
1  DFRAFSCENG LSVVRNLDG GKIALRLDGR RAVLSSDVAA SGERYTAENG
51  LFGNGTEWHQ KGGEAFFGFT DAYGNSVETS CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

```

m731.seq
1  ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTTGT CTTTGCGGCG
51  CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGCGGG CATATGCCGC
101 CCGTTCAAAA CCAAGCCGGC ACGGACGATT TTCGGGCGTT TTCCTGCGAG
151 AACGGTTTGT CTGTGCGCGT CCGCCATTG GACAGCGGCA AAGTCGCGTT
201 GCGGCTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG

```

1185

251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
 301 CACCAGAAAG GCGGCCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

m731.pep
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSC
 51 NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

g731/m731 95.2% identity in 84 aa overlap

g731.pep				10	20	30
				DFRAFSCENGLSVRVRNLDGGKIALRLDGR		
m731	LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCENGLSVRVRHLDGKVALRLDGR					
	20	30	40	50	60	70
g731.pep		40	50	60	70	80
		RAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX				
m731		RAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX				
	80	90	100	110	120	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

a731.seq
 1 ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTGT CTTGGCGGC
 51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CCGACGAGGG CATATGCCGC
 101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCCTGCGAG
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTG GACGGCGGCA GAATCGCGTT
 201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGG AACCGAGTGG
 301 CATCAGAAAG GCGGCCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

a731.pep
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSC
 51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

a731/m731 94.4% identity in 126 aa overlap

a731.pep		10	20	30	40	50	60
		MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTADFRAFSCENGLSVHVRRL					
m731		MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCENGLSVRVRHL					
		10	20	30	40	50	60
a731.pep		70	80	90	100	110	120
		DGGRIALRLDGRRAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE					
m731		DSGKVALRLDGRRAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE					
		70	80	90	100	110	120
a731.pep	TSCRARX						
m731	TSCRARX						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

g732.seq
 1 ATGTCGAAAC CTGTTTTTAA GAAATCGCA CTTTATACTT TGGGTGCAAT
 51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTGCC GCCGagaagg
 101 ACGGgcgGGA TAACGAagtc CTGCCGTGTC AATCCATCCG TACGATGGCG

```

151 GAGGTTTACG GTCAGATTAA GGCAAACTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGAGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGTTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTGCGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCGTTCCCGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCCTGCCG AGTTGAAAAC GATTCCGATG ACGgtatTTGG TcaaTTCCGG
951 TTCggttCC GCGTCGGAGA TTGtcgCCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTCAGGC ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GGCGGACCTG
1201 GTCGACACAC TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAAC
1251 CcttgCGTA CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGTG CTTCAAGGCG GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

g732.pep

```

1 MSKPVEFKKIA LYTLGAISGV AVSLAVQGFA AEKDGRDNEV LPVQSIRTMA
51 EVYGGQIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGFEFGLGME IGQEDGFVKV VSPIEDTPAE RAEVKSDFI VKIDNVSTRG
151 MTSVEAVKMA RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSAE FLPSEAVVVS TKGRDGKDDM VLKAVPEDYV YGMGGDPLAG
301 IPAELKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFQKGSVQT
351 LIPLNSGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNNKDKDK K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

m732.seq

```

1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGCGGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTGCGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CCATTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCCGCTTCC GCGTCGGAGA TTGTCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA

```

```

1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GGCGGATTTG
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGTG CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACCAAGT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGCTTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732.pep

```

1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EVYGGIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLGA
301 IPAEKLTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLNSGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKADKPA VKEGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKDK KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

	10	20	30	40	50	60
m732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGGIKANY					
g732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGGIKANY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m732.pep	VSPIDTPAERAGVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
g732	VSPIDTPAERAEVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m732.pep	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKNKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKNKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEDYVYGMGGDSLGA					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDPLAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m732.pep	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLNSGSAV					
g732	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLNSGSAV					
	310	320	330	340	350	360

a732.seq

1	ATGTCGAAAC	CTGTTTTTAA	GAAAATCGCA	CTTTATACTT	TGGGTGCAAT
51	CAGCGGCGTG	GCCGTCAGTC	TGGCGTGCA	GGGTTTTGCC	GCCGAGAAGG
101	ACAGGCGGGA	TAACGAAGTC	CTGCCGCTGC	AATCCATCCG	CACAATGGCG
151	GAGGTTTACG	GTCAAATCAA	GGCAAACTAC	TATCAGGACA	AACCCGATGC
201	CGATTGTGTT	GAAGGTGCGA	TGAAGGTGAT	GGTGGCCGGT	TTGGATCCGC
251	ATTCCGAATA	TATGGATAAA	AAAGGTTATG	CCGAGATAAA	GGAGTCCACC
301	AGCGGCGAAT	TTGGCGGCTT	GGGGATGGAA	ATCGGCGAGG	AAGACGGATT
351	TGTCAAAGTG	GTTTCGCGCA	TTGAGGACAC	GCCTCGGGAA	CGGGCGGGGG
401	TGAAAAGCGG	CGATTTCATT	TGAAAAATCG	ATAATGTTTC	GACACGCGGC
451	ATGACCGTCA	GCGAAGCGTG	GAGAAAAATG	CGGGGCAAGC	CGGGTACGAA
501	GATTACTTTG	ACGCTGTCGC	GCAAAAATGC	CGACAAGCCG	ATAGTCGTCA
551	ACCTGACCCG	TGCCATTATT	AAAGTGAAAA	CGCTCCGCCA	TCACCTGATC
601	GAACCCGATT	ACGGCTATAT	CCGCGTGTCT	CAGTTCCAAG	AGCGGACGGT
651	CAAAGCGCTC	AATACCGCCG	CAAAAGAGCT	GGTAAAGGAA	AATAAAGGAA
701	AAACCGTCAA	GGGGTGTGGT	TTGAGTTTGC	GCGACGACCC	CGGCGGGCTT
751	TTGACTGGCG	CGGTGCGCGT	GTCGGCGGCA	TTTCTGCCGT	CTGAAGCAGT
801	CGTCGTCAGC	ACCAAGGGAC	GCGACGGCAA	AGACCGCATG	GTACTIONGAA
851	CCGTTCCTGA	AGATTATGTG	TACGGGATGG	GCGGCGATTG	GTTGGCGGGC
901	ATTCTTGCCG	AGTTGAAAAA	CATACCGATG	ACGGTATTGG	TCAATTCCGG
951	TTGCGGTTCG	GCGTCGAGAA	TTGTCTCAGG	TGCATTTCAG	GATCATAAAC
1001	GCGCGGTCAT	CGTCGGTACG	CAGAGCTTCG	GCAAAGGTTT	GGTTCAGACT
1051	TTGATTCTCT	TGTCCAACGG	CAGCGCGGTC	AAGCTGACAA	CGGCACTGTA
1101	TTATACGCCG	AACGACCGTT	CTATTACAGG	GCAGGGGATT	GTTCCCGATG
1151	TGCAAGTAAA	AGATAAGGAA	CGCATTTTTT	AAAGCCGCGA	GGCGGATTGT
1201	GTCGGACACA	TCGGCAATCC	TTTGGCGCGC	GAGGATTGTA	ACAGTGAACC
1251	CCTTGCCGTG	CCGCTTGAAA	AAGATGCGGA	TAAGCCCGCT	GTAAGAGAAA
1301	AAGGTAAAAA	GAAAAAGGAC	GAGGATTTGT	CTTCAAGGCG	GATTCCCAAC
1351	CCTGCCAAAG	ACGACCAAGT	GCGGAAAGCT	TTGGGATTTG	TCAAGTCGCC
1401	CGAGCAGTGG	GAGAAGTCTT	TGGGGCTGGC	TGGGAAAAAG	CCGTTTTCAA
1451	ATAAAGATAA	GAAAGATAAA	AAAGATAAGA	AGTAG	

a732.pep

1	MSKPVFKKIA	LYTLGAISGV	AVSLAVQGFA	AEKDRRDNEV	LPVQSIRTMA
51	EVYQGQIKANY	YQDKPADLDF	EGAMKGMVAG	LDPHSEYMDK	KGYAEIKEST
101	SGEFGGLGME	IGQEDGFKVK	VSPIEDPAE	RAGVKSQGDFI	VKIDNVSTRG
151	MTVSEAVKMK	RQKPGTKITL	TLSRKNADPK	IVVNLTRAI	KVKSVRHHLI
201	EPDYGYYRVS	QFQERTVESV	NTAAKELVKE	NKGKPLKGLD	LDRDDPGGL
251	LTGAVGVSA	FLPSEAVVVS	TKGRDGKDRM	VLKAVPEDYV	YGMGSDSLAG
301	IPAEILTPMS	TVLVNSGSAS	ASEIVAGALQ	DHKRAVIVGT	QSFQKGSVQT
351	LILPSNGSAV	KLTTALYYTP	NDRSITQAQGI	VPDVEVKDK	RIFESREADL
401	VGHIGNPLGG	EDVNSETLAV	PLEKDADKPA	VKEKGKKKKD	EDLSSRRIPN
451	PAKDDQLRKA	LDLVKSPQEW	QKSLGLAAKK	PVSNKDKKKD	KDKK*

1189

a732/m732 99.6% identity in 494 aa overlap

	10	20	30	40	50	60
a732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPQSIRTMAEVYGOIKANY					
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPQSIRTMAEVYGOIKANY					
	10	20	30	40	50	60
a732.pep	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
a732.pep	130	140	150	160	170	180
	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLRKNADKP					
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLRKNADKP					
	130	140	150	160	170	180
a732.pep	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
m732	IVVNLTRAIKVKSVRHHLLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
a732.pep	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAG					
m732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAG					
	250	260	270	280	290	300
a732.pep	310	320	330	340	350	360
	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
m732	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
	310	320	330	340	350	360
a732.pep	370	380	390	400	410	420
	KLTTALYYTPNDRSIAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
m732	KLTTALYYTPNDRSIAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
a732.pep	430	440	450	460	470	480
	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAALK					
m732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAALK					
	430	440	450	460	470	480
a732.pep	490					
	PVSNDKKDKKKKKX					
m732	PVSNDKKDKKKKKX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51  GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTTATCC CGATACCGTC TATGAAGGTT TGAAAAACGa cgACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCC CGGGTGCGCA CGCCCATTTG GGA CTGCTGC

```

1190

251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep

1 MMNPKTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDTDS
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGACTGCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep

1 MMNPKTLSRL SLCAAVLALT ACGNGQKSL YYYGGYPDTV YEGLKNDTDS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

	10	20	30	40	50	60
m733.pep	MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDTDSL	LGKQTEKMEK				
g733	MMNPKTLGRLSLCAAVLALTACAGGGHKNLYYYGGYPDTVYEGLKNDTDSL	LGKQTEKMEK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m733.pep	YFVEAGNKKMNAAPGAHAHLGLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG					
g733	YFAEAANKMNAAPGAHAHLGLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG					
	70	80	90	100	110	120
m733.pep	GKRX					
g733						
	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGACTGCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

1191

```

1  MMNPKTL SRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
51  LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

a733/m733 100.0% identity in 123 aa overlap

```

              10      20      30      40      50      60
a733.pep      MMNPKTL SRL SLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK
              |||||
m733          MMNPKTL SRL SLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK
              10      20      30      40      50      60

              70      80      90      100     110     120
a733.pep      YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEERKLFPEESGVFMDFLMKTGKG
              |||||
m733          YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEERKLFPEESGVFMDFLMKTGKG
              70      80      90      100     110     120

a733.pep      GKRX
              ||||
m733          GKRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

```

g734.seq
1  ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGGATGCAAA CGATGTTTTG CAGGTAAAA CCACAAAAGA AGATTCCGCG
151 AAAAGCGAAG CGTTTGCCGA GTTGAAGCC TTTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAACAGTG TATTGCACGT CATCTTCTTA TTACGGCGGG
451 GCTGTTGCTT CCTTAATCCA ACACCTGAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

```

g734.pep
1  MMKKILAVSA LCLMTAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
51  KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
101 MRVENAVVIT SPRFTSVHGV ALNQCIKKYG AQGQCGLTV YCTSSSYGG
151 AVRSLIQHLK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

```

m734.seq (partial)
1  TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCGG TCGTGTGCTG
51  GAACAATACC TGTGTGCGCG TGGCATAACC GAAAGCCTTG GGCGCGCTGC
101 GTGTGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTAC GAGCGTTCAT
151 CAGGTCGCAC TCAACCAGTG CATCAAAAAA TACGGCGTAC AGGGACAATG
201 CGGCTTGGA ACAGTGTATT GCACATCTTC TTCTTATTAC GGCGGAACGT
251 TCGGCTCTTT GATTCAAAAT CTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

```

m734.pep (partial)
1  SGIAEPTGCR SVVSLNNT CVALAYPKAL GALRVDNAV VITS PRFTSVH
51  QVALNQCIKK YGVQGCGLT TVYCTSSSY GGTVRS LIQN LK*

```

m734/g734 92.4% identity in 92 aa overlap

```

              10      20      30
m734.pep      SGIAEPTGCRSVVSLNNTCVALAYPKAL
              :|||
g734          VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEPTGCRSVVSLNNTCVSLAYPKAL

```

		40	50	60	70	80	90
m734.pep		GALRVDNAV	VITSPRFTSVH	QVALNQCIKKYGV	QGCGLET	VYCTSSSY	YGTVRSLIQN
g734		GAMRVENAV	VITSPRFTSVH	QVALNQCIKKYGA	QGCGLET	VYCTSSSY	YGGAVRSLIQH
		100	110	120	130	140	150
m734.pep	LKX						
g734	LKX						
	160						

```
a734.seq
1  ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGACTGCGGC
51  GGCACGGGCT GCCGATACCT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGAATGCAAA CGATGTTTTC CAGGTTAAAA CCACAAAAGA AGATTCCGAC
151 AAAAGCGAAG CGTTTGCCGA GTTGAAGACT TTCTGCAAAG GTCAGGACAC
201 CATTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCGCG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TTATCAGGTC GCACTCAACC AGTGCATCAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATTGCACGT CTTCTCTTA TTACGGGGGA
451 ACTGTGCGCT CTTTGATTCA AAATCTCAAA TAA
```

a734.pep

1	<u>MMKKILAVSA</u>	<u>LCLMTAAARA</u>	ADTYGYLAVV	QNPQNANDVL	QVKTTKEDST
51	KSEAFAELEA	FCKGQDTLAG	IAEDEPTGCR	SVVSLNNTCV	ALAYPKALGA
101	MRVENAVVIT	SPRFTSVYQV	ALNQCICKYG	AQGQCGLETV	YCTSSSYGG
151	TVRSLIIONLK	*			

```

      10      20      30      40      50      60
a734.pep  MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA
          |||||
g734      MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA
          |||||

      70      80      90      100     110     120
a734.pep  FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVALAYPKALGAMRVENAVVITSPRFTSVYQV
          |||||
g734      FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV
          |||||

      70      80      90      100     110     120
a734.pep  ALNQCICKYGAQGQCGLETVYCTSSSYGGTVRSLIQNLKX
          |||||
g734      ALNQCICKYGAQGQCGLETVYCTSSSYGGAVRSLIQHLKX
          |||||

      130     140     150     160
a734.pep  ALNQCICKYGAQGQCGLETVYCTSSSYGGTVRSLIQNLKX
          |||||
g734      ALNQCICKYGAQGQCGLETVYCTSSSYGGAVRSLIQHLKX
          |||||

      130     140     150     160

```

```
m735.seq
1  ATGAATCTCG  TGAAACTGCT  GGCGAATAAC  TGGCAACCGA  TTGCCATTAT
51  CCGGCTTGTC  GGCACGGGCT  TGGCTGTGTC  GCACCATCAA  GGCTACAAGT
101 CGGCATTGTC  GAAGCAGCAG  GCGGTATCG  ACAAGATGGA  GCGCGACAAG
151 GCGCAAGCCC  TGCTGTTGTC  GGCTCAAAC  TATGCGCGCG  AACTGGAACT
201 GGCACGCGCG  GAAGCTAAAA  AATATGAAT  CAAGGCGCAC  GCTGTCGGCA
251 TTGCTTTGCG  GAAAAACAG  CCGGAAGTCA  GCCGTCTGAA  AACGGAAAAA
301 AAAAAGGAAA  TCGAAAAATG  CCTTACTCAA  GACCGTAAAA  ATGCAAGCGG
```

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351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQO AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNASGGCI DFGSHGLQL YNRALGYGN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GCGCGGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGCTGTA AACGGAAT
301 AAAAAGGAAA TCGAAAATGT CCTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQO AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DFGHHGLQL YKRALGYGN*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQOAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQOAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a735.pep	YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
	130	140				
a735.pep	DGFHHGLQLYKRALGYGNX					
m735	DFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCCGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGCG
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTTCG TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGCAGCAACT GGGTCCCGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCC CGCGTTTTTG GCGGGGCGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTC AACGTCGCGG GCATTTTCGG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGAACAAAC ATTACGATAC ATTACGATGT AATCAACGGT

601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

g736.pep

1 MNFIRSVGAK TLGLIQSFGS ITLFLNLA KSGTAFARPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTQLEAM NVMAVNPVAR VVAPRFWAGV
 151 FSPMLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPMQNN ITIHVDVING
 201 LIKSAAFGVA VTIAVHQGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

m736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
 51 CTTCGGCAGT ATCAGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
 101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
 151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTTCG TCGGTATGGT
 201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATCAAA TCCGCCGATA
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGC CGCAACT GGGTCCCGTG
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
 401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCG CGCGTTTTTG GCGGGGCGTG
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
 501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
 551 GGCCGCAGAT GCAGAACAAAC ATTACGATAC ATTACGATGT AATCAACGGT
 601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

m736.pep

1 MNFIRSVGAK TLGLIQSLGS ITLFLNLA KSGTAFVRPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMAVNPVAR VVAPRFWAGV
 151 FSPMLLASIF NVAGIFGAYL VGVTWLGLDS GIFWSQMNN ITIHVDVING
 201 LIKSAAFGVA VTIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

m736/g736

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	: : : :					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNLA KSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	: : : :					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m736.pep	MKTTEQLEAMNVMAVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
	: : :					
g736	MKTTGQLEAMNVMAVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					
g736	GIFWPMQNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCIPITSEGILRASTRTVVSS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

a736.seq

```

1  ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51  TCTCGGCAGT ATCAGCTGT TTCTGCTGAA TATTCTGGCG AAATCCGGTA
101 CGGCTTTCGT CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGTGATTGT TGCCGTTTCA GGGCTGTTTG TCGGCATGGT
201 CTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCGCTGT TGC CGCAACT GGGTCCGGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGAACAGCT CGAAGCGATG AACGTGATGG
401 CGGTAAACCC CGTCGCCCGA GTGTTGCGC CGCGCTTTTG GCGGGCGTG
451 TTTTCCATGC CGCTTTTGGC TTCGATTTTC AACGTGGCGG GTATTTTCGG
501 CGCGTATTG GTCGGTGTAA CCTGGCTGGG CTTGGACAGC GGTATTTTCT
551 GGTGCAAAAT GCAGAACAC ATCAGGATAC ATTACGATGT AATCAACGGT
601 CTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCGTCC CGACCTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

a736.pep

```

1  MNFIRSVGAK TLGLIQSLGS ITLFLNILA KSGTAFVRPR LSVRQVYFAG
51  VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMVNPVAR VVAPRFWAGV
151 FSPMLLASIF NVAGIFGAYL VGVTLWGLDS GIFWSQMNN ITIHVDVING
201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNVMVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
m736	MKTTEQLEAMNVMVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					

1196

```

m736      GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS
           190      200      210      220      230      240

           250      259
a736.pep  ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

```

g737.seq
1  atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51 CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

```

g737.pep
1  MNIKHLLLTA AATALLGISA PALAHHDGHC DDDHGHAHQ HGKQDKIISR
51  AQAEKAARAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

```

m737.seq
1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51 CATTTCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

```

m737.pep
1  MNIKHLLLTS AATALLSISA PALAHHDGHC DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

```

m737/g737
           10      20      30      40      50      60
m737.pep  MNIKHLLLTS AATALLSISAPALAHHDGHD DDDHGHAHQ HNKQDKIISR AQAEKAALAR
           |||||:|||||:|||||:|||||:|||||:|||||
g737       MNIKHLLLTAAATALLGISAPALAHHDGHD DDDHGHAHQ HGKQDKIISR AQAEKAARAR
           10      20      30      40      50      60

           70      80      90      100     109
m737.pep  VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           |||||:|||||:|||||:|||||:|||||:|||||
g737       VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

1197

```

a737.seq
1  ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51  CATTTCGGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCGGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

```

a737.pep
1  MNFKRLLLLTA AATALMGISA PALAHHDHGHG DDDHGHAHQ HSKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLLTA	AATALMGISA	PALAHHDHGHG	DDDHGHAHQH	SKQDKIISR	AQAEKAALAR
m737	MNIKHLTSA	ATALLSIS	APALAHHDHGHG	DDDHGHAHQH	SKQDKIISR	AQAEKAALAR
	10	20	30	40	50	60
	70	80	90	100	109	
a737.pep	VGGKITDIDL	EHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
m737	VGGKITDIDL	EHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

```

g738.seq
1  ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCGC CCAAACCTGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCGCGC
151 GCGGCCGCGC TGATTGTCTC GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTTATCC CGGAATGAAC
301 GACATCGCCT CTTGGGTTT CATCTTGCTC GCCGTGACG CGTGGGCCTG
351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCATcgtT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
451 CAGTTTGCCG GCTGGGAAAA CACCCCCCTG CTTCAAAACA TCATCGTTCA
501 CAGAGGGCAA GCGGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTGCCTCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTGCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACTTGCC GCGCCAAAGC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CGGCTGGAAC AGTTTTGCCC AACAAACCTT CCTGATCAAT GCCGAACAGC
1001 ACACCATACA CGACAACCTC CTCAGCACCT TGTTACCCCA TTCCACAAC
1051 ATCATCCTCC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
1151 CCCCCGCATC ACTTTTCTCT CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTTCTCG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCGC CATATTGCGA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
1401 CCCC GCCGCT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAAC
1451 TGCGCTATAT TTCCGCAAAC AGCCGATGCT TGTCCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAG CACTAAAATA CCGCCCTTAC TCCGCCACCT

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1198

1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
 1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
 1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
 1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAAACA
 1801 AAACCTGCA AATGA

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pep

1 MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
 51 AAGLIVLLFL TAGKKLFDVK IPAISFLLEA MAAFWWLQAR LMNLIYPGMN
 101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
 151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
 201 KIPAAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPEW YFRSDKSNRR
 251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
 301 EWNKALAAAFQ SAPIFGHWGN SFAQOTFLIN AEQHTIHDNF LSTLFTSHSN
 351 IILQLLAEMG ISGTLVAAT LLTGIAGLLK RSLTPASLEL LCALAVSMCH
 401 SMLEYPLWYV YFLIPFGLML FLSPAASDGI IAFKKAANLG ILTASAAIFA
 451 GLLHLDWTYT RLVNSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF
 501 SLVNFALPEY PETQTWAEAA TLKALKYRPY SATYRIALYL MRQKVAEAK
 551 QWMRTQSY YPYLMPRYADE IRKLPVWAPL LPELLKDCCKA FFAAPGHPET
 601 KPCK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

1 ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCGG CCAAAGTCCC
 51 GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
 101 TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
 151 GCAGCCGGCC TGATTGTCCT GTTGTTCTCT ACGGCAGGAA AAAAACTGTT
 201 TGATGTCAA ATCCCGGCCA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
 251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
 301 GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTCAGCG CGTGGGCGTG
 351 CCGGAGCTTG GTCGCACTC TCGGACAAGA ACGCATCGTG ACCCTGTTTG
 401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
 451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAAACA TCATCGTTTA
 501 CAGCGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
 551 ACTACCTCAT GTGGGGCATA CTCGCCGCGG CTAACCTCAA CGGACAACGA
 601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
 651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
 701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAATC CAACAGGCGG
 751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCGAAT
 801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAACTG
 851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCAAATC
 901 GAATGGAATA AAGCCCTTGC CGCCTTCAG TCCGCCCGCA TATTCGGGCA
 951 CGGCTGGAAC AGTTTTGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
 1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTACCCCA TTCCACAAC
 1051 ATCGTCTCC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
 1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
 1151 CCCCCGCATC GCTTTTCTTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
 1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTTCA TCCCTTTCGG
 1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
 1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTCGCA
 1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
 1401 CCCCGCCACT GACGACAGTG CCAAACCCCT CAACCGGAAA ATCAACGAGT
 1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
 1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
 1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCCAC TCCGCCACCT
 1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
 1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCgTACCTGA TGCCCCGATA
 1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GCGCGCGCTG CTACCCGAAC
 1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
 1801 AAACCTGCA AATGA

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pep

1 MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

```

51  AAGLIVLLFL TAGKKLFQDVK IPAISFLLFA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHFGQERIV TFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR
201 KIPAALGVIC LIMQTAVLGL VNSRTILTYI AAIALILPEW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN TILEFTTGIR YETAVERVAN GGFTDLPRQI
301 EWNKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNIYDNL LSNLFTHSHN
351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RLVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVKVAEK
551 QWMRATQSY YPYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

m738/g738

m738.pep	10	20	30	40	50	60
	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
g738	10	20	30	40	50	60
	MSAETTVSGARPAAKLPIYILPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL					
m738.pep	70	80	90	100	110	120
	TAGKKLFDVKIPAISFLLFMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
g738	70	80	90	100	110	120
	TAGKKLFDVKIPAISFLLFMAAFWWLQARLMNLIYPGMNDIASWVFILLAVSAWACKSL					
m738.pep	130	140	150	160	170	180
	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
g738	130	140	150	160	170	180
	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGQRN					
m738.pep	190	200	210	220	230	240
	NLGHYLMWGILAAAYLNGQRKIPAALGVICLIMQTAVLGLVNSRTILTYIAAIALILPEW					
g738	190	200	210	220	230	240
	NLGHYLMWGILASAYLNGQRKIPAALGAICLIMQTAVLGLVNSRTILTYIAAIALILPEW					
m738.pep	250	260	270	280	290	300
	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNTILEFTTGIRYETAVERVANGGFTDLPRQI					
g738	250	260	270	280	290	300
	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNAILEFTTGIRYETAVERVANGGFTDLPRQS					
m738.pep	310	320	330	340	350	360
	EWNKALAAFQSAPIFGHGWN SFAQQTFLINAEQHNIYDNL LSNLFTHSHNIVLQLLAEMG					
g738	310	320	330	340	350	360
	EWNKALAAFQSAPIFGHGWN SFAQQTFLINAEQHTIHDNFLSTLFTSHNIIQLLAEMG					
m738.pep	370	380	390	400	410	420
	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
g738	370	380	390	400	410	420
	ISGTLLVAATLLTGIAGLLKRSLTPASLFLCALAVSMCHSMLEYPLWYVYFLIPFGLML					
m738.pep	430	440	450	460	470	480
	FLSPAESDGI AFKKAANLGILTASAAIFAGLLHLDWYTYRLVNAFSPATDDSAKTLNRK					
g738	FLSPAESDGI AFKKAANLGILTASAAIFAGLLHLDWYTYRLVNSFSPAADDSAKTLNRK					

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEETLKSLKYRPHSATYRIALYL					
g738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEETLKALKYRYPYSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQGVKVAEAKQWMRATQSYYPYLMPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQGVKVAEAKQWMRATQSYYPYLMPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPET					
	550	560	570	580	590	600
m738.pep	KPCKX					
g738	KPCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

```

a738.seq
1  ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCGCGCG CCAAACCTGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
151 GCAGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTACTC GCCGTCAGCG CGTGGGCCTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAAACA TCATTGTTTA
501 CAGCGGGCAA GCGGTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCGG CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTTCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GCGGGTTTCA CAGACCTGCC GCGCCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCCGA TATTGGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCACAAAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTTCTCG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTTCGA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GCGCCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCGG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

```

a738.pep
1  MPAETTVSGA HPAAKLPYI LPCFLWIGIV PFTFALRLQP SPDFYHDAAA
51  AAGLIVLFLF TAGKKLFDVK IPPISFLLEF MAEFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYGOERIV TLFWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR

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1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
 251 TILGIAAAVF LTALFQFSMN TILFTTGIR YETAVERVAN GGFTDLPRQI
 301 EWRKALAAEQ SAPIFGHGWN SFAQQTFLIN AEQHNHNDNL LSNLFTHSHN
 351 IVLQLLAEMG ISGTLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
 401 SMLEYPLWYV YFLIPFGLML FLSPAESDG IAFKKAANLG ILTASAAIFA
 451 GLLHLDWYTYT RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
 501 SLVNFALEPY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVKVAEK
 551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
 601 KPCK*

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAHPAAKLPYILPCFLWIGIVPFTFALRLQSPDFYHDAAGLIVLLFL					
m738	MPAETTVSGAHPAAKLPYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
	70	80	90	100	110	120
a738.pep	TAGKKLFDVKIPPIISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
m738	TAGKKLFDVKIPAIISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a738.pep	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
m738	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a738.pep	NLGHYLMWGIILAAAYLNGQRKIPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
m738	NLGHYLMWGIILAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
	250	260	270	280	290	300
a738.pep	YFRSDKSNRRRTILGIAAAVF LTALFQFSMN TILFTTGIR YETAVERVAN GGFTDLPRQI					
m738	YFRSDKSNRRRTILGIAAAVF LTALFQFSMN TILFTTGIR YETAVERVAN GGFTDLPRQI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a738.pep	EWRKALAAEQSAPIFGHGWN SFAQQTFLINAEQHNHNDNL LSNLFTHSHNIVLQLLAEMG					
m738	EWNKALAAEQSAPIFGHGWN SFAQQTFLINAEQHNIDNLLSNLFTHSHNIVLQLLAEMG					
	310	320	330	340	350	360
	370	380	390	400	410	420
a738.pep	ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
m738	ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
	430	440	450	460	470	480
a738.pep	FLSPAESDGIAFKKAANLGILTASAAIFAGLLHLDWYTYTRMVNAFSPATDDSAKTLNRK					
m738	FLSPAESDGIAFKKAANLGILTASAAIFAGLLHLDWYTYTRLVNAFSPATDDSAKTLNRK					
	430	440	450	460	470	480
	490	500	510	520	530	540
a738.pep	INELRYISANSPMLSFYADFSLVNFALEPY PETQTWAEATLKSLEYRPHSATYRIALYL					
m738	INELRYISANSPMLSFYADFSLVNFALEPY PETQTWAEATLKSLEYRPHSATYRIALYL					
	490	500	510	520	530	540

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	550	560	570	580	590	600
a738.pep	MRQ GK VAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDKAFAAAPGHPEA					
m738	MRQ GK VAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDKAFAAAPGHPEA					
	550	560	570	580	590	600
a738.pep	K P C K X					
m738	K P C K X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG AAAAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCGAACCGGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCTG TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACA
551 CGCCGGCCAA ACCCATAAA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739.pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVG QDAAQPEHHH AASSEPAQPD GTESGSGLP
101 SPAAPKKNRV KPRPSDARA ADLTGTGTQ AENTLKETPV LPTNAPHPEP
151 RKETPEKQAO PKETPKKET PKENHTKPD PKNTPAKPHK EILDNLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG AAAAAACCCT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCGAACCGGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CGCCCAAAGA
501 AAACCATACC AAACCGGACA CCCGAAAAA CAGCCGCCC AAACCCATA
551 AAGAAATTCT CGACAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739.pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQADTAQT DRQDDAGTQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAO PKETPKENHT KPDTPKNTPP KPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

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	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTE PQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSAAPKKNRVKPPADTAQT					
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSLPSAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD					
g739	ADSLTGTGTAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKTPKENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPKHKEILDKLF					
g739	PKNTPAKPKHKEILDNLF					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1   ATGGCAAAAA AACC GAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATCAAC CCGAACGGCG ACAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAACAA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAGAAA CACCCGAAAA ACAGGCACAG CCCAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGCCTAA ACCCCATAA GAAATCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1   MAKKPNKPFRLTPKLLIRAVLLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSLP
101 SPAAPKKNRV KPQPADTAQT DRQPDAGAQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPD PNTPPKPKH EILDNLF*

```

a739/m739 93.9% identity in 197 aa overlap

	10	20	30	40	50	60
a739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAIGIVSTFNPNGDKTLQTE PQHTDSPRET					
m739	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
a739.pep	EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDSESGSLPSAAPKKNRVKPPADTAQT					
m739	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSAAPKKNRVKPPADTAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a739.pep	DRQPDAGAQ AENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
m739	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD					
	130	140	150	160	170	

1204

```

              190
a739.pep      PKNTPPKPKHKEILDNLFX
              |||||
m739          PKNTPPKPKHKEILDKLF
              180   190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gccCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gGTTTGATT
201 GAAACgtcaa ACCATGTTTC TGTTTATTCC GATTGTTTTC CTGATTGTGT
251 ATTTGTTCCA CTATTTCCGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFEETIKHH LKQGFDLKRQ TMLFPIIVL LVVYLFHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCCTT
51 GGCgACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAa
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK
51 FVLFDITIKHH LKQEFDLKRQ TMLFPIIIL LIVYLFHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

              10      20      30      40      50      60
m740.pep      MSRNLLVRWLA VCLIPLATL AVFAANPPED KLOHLINGIILACEATFLFKFVLFDITIKHH
              |||||
g740          MSRNLLVRWLA VCLIPLATL AVFAANPPED KPOHLINGIILACEATFLFKFVLFETIKHH
              10      20      30      40      50      60

              70      80      90
m740.pep      LKQEFDLKRQ TMLLFIPIILLIVYLFHYFGAFX
              ||| |||||:|||||:|:|||||
g740          LKQGFDLKRQ TMLFPIIVLVVYLFHYFGAFX
              70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT
51 GGCgACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFDITIKHH LKQEFDLKRQ TMLLFIPIIL LIVYLFHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

              10      20      30      40      50      60

```

1205

```

a740.pep  MSRNLLVRWLVLVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
|||||||:|||||||  |||||||  |||||||  |||||||  |||||||  |||||||
m740      MSRNLLVRWLAVCLIPLATLAVFAANPPEDKLOHLINGIILACEATFLFKFVLFDTIKHH
              10      20      30      40      50      60

              70      80      90
a740.pep  LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
|||||||  |||||||  |||||||  |||||||  |||||||  |||||||
m740      LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1  GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTC
51  TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTG GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAACAGGA TCACCTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCAG CGATTGGGCG GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAACTG ACCTATACCA TAGATTTTCG CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCCTCCGCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1  VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPQNGTLTL SAQGAETFK AGGKDNSLNT GKLNNDKISR
101 FDFVQKIEVD GQTITLASGE FQIYQDHSV VVALRIEKIN NPDKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 GHGKIEHLKT PEQVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGEKV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1  GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201 GGCGGCACAA GGTGCGGAAA AACTTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGGCAGCT CATTAACCTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTTCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GGCGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGCGGGA
551 AACTGACCTA CACCATAGAT TTCGCGGCCA AGCAGGGAAA CGGCAAAATC
601 GAACATTGGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGAT GGAAGAGGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1  VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHKDKGL
51  QSLTLDQSVR KNEKLKLAAQ GAEKTYGNDD SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFTQ EQIQDSEHSG KMVAKRQFRI

```

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151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYYTID FAAKQGNNGKI
 201 EHLKSPELNV DLAAADIKPD GKRHAIVSGS VLYNQAEKGS YSLGIFGGKA
 251 QEVAGSAEVK TVNGIRHIGL AAKQ*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCLSLTT---	ALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQ			
g741	VNRTTFCCLSLTAGPDSRLQRRGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLEA				
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRKNEKLKLAQAQGAEKTY---	GNGDSLNTGKLKNDKVSRLFIRQIEVDGQLITLESGE			
g741	SIPQNGTLTSAQGAEKTFKAGGKDNSLNTGKLKNDKISRFDVQKIEVDGQTITLASGE				
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHSALTAFQTEQIQDSEHSGKMKVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGT				
g741	FQIYKQDHSAVVALRIEKINNFDKIDSLINQRSFLVSDLGGEHTAFNQLPDG-KAEYHGK				
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGGKLTYYTIDFAAKQGNNGKIEHLKSPELNVDLAAADIKPDGKRHAIVSGSVLYN				
g741	AFSSDDADGKLTYYTIDFAAKQGHGKIEHLKTPEQNVELASAELKADEKSHAVILGDTRYG				
	180	190	200	210	220
	240	250	260	270	
m741.pep	QAEKGSYSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAQKQX				
g741	GEEKGTYRLALFGDRAQEIAGSATVKIGEKVHEIGIADKQX				
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq

1	GTGAACCGAA	CTGCCTTCTG	CTGCCTTCT	TTGACCGCGG	CCCTGATTCT
51	GACCGCCTGC	AGCAGCGGAG	GCGGCGGTGT	CGCCGCCGAC	ATCGGCGCGG
101	TGCTTGCCGA	TGCACTAACC	GCACCGCTCG	ACCATAAAGA	CAAAAGTTTG
151	CAGTCTTTGA	CGCTGGATCA	GTCCGTCAAG	AAAAACGAGA	AACTGAAGCT
201	GGCGGCACAA	GGTGCGGAAA	AAACTTATGG	AAACGGCGAC	AGCCTCAATA
251	CGGGCAAATT	GAAGAACGAC	AAGGTCAGCC	GCTTCGACTT	TATCCGTCAA
301	ATCGAAGTGG	ACGGGCAGCT	CATTACCTTG	GAGAGCGGAG	AGTTCCAAGT
351	GTACAAACAA	AGCCATTCCG	CCTTAACCGC	CCTTCAGACC	GAGCAAGTAC
401	AAGATTCGGA	GCATTCAGGG	AAGATGGTTG	CGAAACGCCA	GTTCAAGATC
451	GGCGATATAG	CGGGTGAACA	TACATCTTTT	GACAAGCTTC	CCGAAGGCGG
501	CAGGGCGACA	TATCGCGGGA	CGGCATTCCG	TTCAGACGAT	GCCAGTGGAA
551	AACTGACCTA	CACCATAGAT	TTCGCCGCCA	AGCAGGGACA	CGGCAAAATC
601	GAACATTTGA	AATCGCCAGA	ACTCAATGTT	GACCTGGCCG	CCTCCGATAT
651	CAAGCCGGAT	AAAAAACGCC	ATGCCGTCAT	CAGCGGTTCC	GTCCCTTTAC
701	ACCAAGCCGA	GAAAGGCAGT	TACTCTCTAG	GCATCTTTGG	CGGGCAAGCC
751	CAGGAAGTTG	CCGGCAGCGC	AGAAGTGGAA	ACCGCAAACG	GCATACGCCA
801	TATCGGTCTT	CGCCCAAGC	AGTAA		

This corresponds to the amino acid sequence <SEQ ID 2538; ORF 741.a>:

a741.pep

1	VNRTAFCCLS	LTAALILTAC	SSGGGGVAAD	IGAVLADALT	APLDHKDKSL
51	QSLTLDQSVR	KNEKLKLAQ	GAEKTYNGD	SLNTGKLKND	KVSRLFDFIRQ
101	IEVDGQLITL	ESGEFQYKQ	SHSALTALQT	EQVQDSEHSG	KMKVAKRQFRI
151	GDIAGEHTSF	DKLPEGGRAT	YRGTAFGSDD	ASGKLTYYTID	FAAKQGHGKI
201	EHLKSPELNV	DLAASDIKPD	KKRHAIVSGS	VLYNQAEKGS	YSLGIFGGQA
251	QEVAGSAEVE	TANGIRHIGL	AAKQ*		

a741/m741 95.6% identity in 274 aa overlap

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCLSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
m741	VNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLLAAQGAEKTYGNGDSLNTGKLNKDKVSRFDIFRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKLLAAQGAEKTYGNGDSLNTGKLNKDKVSRFDIFRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPPEGGRATYRGTAFGSDD					
m741	SHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPPEGGRATYRGTAFGSDD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYYTIDFAAQQGHGKIEHLKSPELNVDLAASDIKPKKRHAVISGSVLYNQAEKGS					
m741	AGGKLTYYTIDFAAQQNGKIEHLKSPELNVDLAADIKPDGKRHAVISGSVLYNQAEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAAKQX					
m741	YSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAAKQX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

m742.seq

1	ATGGTTTACG	GCATTGCCGA	AGCCGATGCG	GGCGACAGCA	GTGTGCTTAC
51	TTTGGGCGGC	ATGTATCAGA	AGAGTAGGGA	GGTTCCTGAT	TTTTCGGGCA
101	TTATTTTGCC	CTGTGAAAT	CAGAAACTG	CCCCGTTTCA	TTCAACGCCT
151	GCCTGCAACC	GGCCTTTGCA	ACTGCCGCGC	AACACTTATT	TGGGGGAGGA
201	TTGGTCGCGG	TTAAGTGCCG	ACAAATACAA	CCTTTTCTCA	GGATTCAAAC
251	ATGTGTTTGA	CAACGGTTGG	CAGCTCAATG	CCGAAGTGTC	TTATACCAAG
301	AATGAATCCG	ATGCCAAGGT	GGGGCAGTTT	TTTCTGAAAA	ACGAATATGC
351	GGCGGGTTTG	TCGGGTGAGG	ATGCCGTAGG	CTTTTGTACT	GAAAAAACCG
401	AAGTCATCCC	GTTTCGAGCCG	AAAGATAAGG	CATTGGAGAA	ACTGAAAGCA
451	TATCGTGATG	AAACCGCCAA	GGAATACCGG	GAGCGCAAAG	ACGATTTTGT
501	TAAAAACCGT	TTTGATAATA	CTGCTTTCGA	ACAGTATCGC	AGCCGCCCGTG
551	CCGCAGAACG	CAAAGCCGGT	TTTGACAAGT	GTATGAGTGA	CCCTTTCGCG
601	CTGGACTTTA	TCTGTCAAGG	TTCTTGGGGG	GATCCGGGCG	TTGATGCCGA
651	CAAGGCGGAA	TTTGTGCGATA	AAGCCCTTGC	GAAGGAGGGC	ATCTTTAATA
701	ATGCGGCACA	ACGTTTTCCTA	AACAGCCTGT	ATGACTCTTC	CTTTAATCGG
751	AAGGCTACCG	CCAACCGACG	ATACAGTTAT	ATGCCGTTGC	GGCATAACAA
801	AGACGACCGC	CAATGGGGAA	TAAACTTGA	CCTGACCGGC	ACATATGGGC
851	TGTTCCGGCG	GGAGCATGAT	TTCTTTGTGC	GCTATGCCTA	CGGTGATGAA
901	AAGATACGTT	CGGAATATCT	AGAAATCTAC	GAACGCCGCT	ACAGAGTACG
951	TCCGAATACG	GGGGCAACGC	ACGGCGTGTA	TGCGGGAAGT	TGTCAGGAGG
1001	AGCCGGACGG	CGATTGTGCG	TCTCCTTTGG	TCAGGGGGCA	TAAAGAACCC
1051	GATTGGCAGG	CGTACGATGA	AAAAGGCAAC	CGTACCGTTT	ATGCCGAAGA
1101	ATGCAGGAAC	GCCAAGAAAA	TAAAAACCGA	GCCCAAGCTC	GATGCCGAAG
1151	GCAAGCAGGT	GTATTACTAT	GACGAATACA	GCGGCAGCCG	GACACCGGTA
1201	TATGTCGATG	TATATGAGCT	GGACGAAAAA	GGCAACAAGA	TTCAGGAGAC
1251	CAATCCCAGC	GGCAGCGCTG	CCTTTACCGG	TTTTTCCGGT	ACGGTGCCCG
1301	TTTGGAAGAC	CGTCAAAGTG	GCAGACGACC	ATGTTCTTGC	GCTGTATAAC
1351	TACGCCAAAT	ACCTCAACAC	CAACAAAACC	CATTGCTGTA	CTGCCAGCAC
1401	GCGTTTCAAC	GTAACCGGCC	GACTGCACCT	TTTGGGCGGG	CTGCACTACA

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1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCTG ATTTTCGGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTCCA GTGCAGACCC GTACAACCTC AGCAATTCA
2051 CACCCGTGCA CATATTCGGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGCGCG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACCTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

m742.pep

```

1 MVYGIAEADA GDSSVLTGG MYQKSREVPD FSGIILPCEN QKTAPFSSTP
51 ACNRLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNGW QLNAEVSYTK
101 NESDAKVGQF FLKNEYAAGL SGEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDKCMSDFPA
201 LDFICQGSWG DPGVDADKAE FVDKALAKEG IFNNAQRFP NSLYDSSFNR
251 KATANRRYSY MPLRHTKDDR QWGIKDLTG TYGLFGREHD FFGVYAYGDE
301 KIRSEYLEIY ERRYVRPNT GATHGVYAGS CQEEPDGDL SFLVRGHKEP
351 DWQAYDEKGN RTVYAEERN AKKIKTEPKL DAEGKQVYYY DEYSRSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKTVKV ADDHVPALYN
451 YAKYLNTNKT HSLTASTRFN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IRADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQDNDVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGKVVS RGAEFELSGE LNEDWKVFAG
651 YTYNKSRYKN AAEVNAERLA KNSSADPYNF SNFTPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

a742.seq

```

1 ATGGTTTACG GCATTGCCGA AGCCGATGCG GGCACAGCA GTGTGCTTAC
51 TTTGGGCGCG ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTTCGGGCA
101 TTATTTTGTC CTGTGAAAAT CAGAAACTG CCCCGTTCAG TTCAACGCCCT
151 CCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTGAGTGCTG ACAATAACAA CCTTTTCTCA GGTTCACAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCGAGTT TTTCTGAAAA ACGAACATGC
351 GCGGGGTTTG TCAGATGAGG ATGCGGTAGG CTTTTTGACC GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGACG AAACCGCCAA GGAATACCGT GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTCGA GCAGTACCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACGAGT GTATGAGTGC CCCTTTTGGC
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGTG TTGATGCCGA
651 CAAGTCGGAA TTTGTGATA AAGCCCTTGC GAAGGAAGGC ATCTTAATA
701 ATGCGGCACA ACGTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACCTTGA CCTGACCGGC ACATATGGGC
851 GTTTCGGGCG GGAGCATGAT TTCTTGTCTG GCTATGCCCTA CGGCGATGAA
901 AAGATACGTT CCGAATATCT GGAATCTAC GAACGCCGCC ACAGAGTACG
951 TCCGAATACA GGGGCAACGC ACGGCGTGTA TGCGGGAAGT TGTGAGGGG
1001 AGCCGGACCG TGATTGTCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAT GCCAAGAAAA TAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGACGCG GACGCCAGTA

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a742.ppt

1	MVYGIAEADA	GDSSVLTGG	MYQKSREVPD	FSGIILSCEN	QKTAPFSSPT
51	ACNRPLQLPR	NTLGEDWSR	LSADKYNFES	GFKHVFDNGW	QLNAEVSYTK
101	NESDAKVQGF	FLKNEHAAGL	SDEDAVNGFLT	EKNEVIPFEP	KDKALEKLKA
151	YRDETAKEYR	ERKDDFVKNR	FDNTAFEQYR	SRAEAERKAG	FDECMASFFA
201	LDFICQGSWG	DPGVDADKSE	FVDKALAKEG	IFNNAAQRF	NSLYDSSFNR
251	KATANRRYSY	MPLRHTKDDR	QWGIKLDLTD	TYGLFGREHD	FFVGAYGDE
301	KIRSEYLEIY	ERRHRVRPNT	GATHGVYAGS	CQGEPDGDL	SPLVRGHKEP
351	DWQAYDEKGN	RTVYAEERN	KKKIKTEPKL	DAEGKQVYY	DEYSGSRTPV
401	YVDVYELDEK	GNKIQETNPD	GTPAFTGFSG	TVPVWKTVKV	ADDHVPALYN
451	YAKYLNTAKT	HSLTAGTRFN	VTGRLHLLPG	LHYTRYETSQ	TKDMPVRYGQ
501	PASDFQNTSS	IKADQDHYTA	KMQGHKLLTPY	AGITYDLTPQ	QSIYGSYTKI
551	EKQDNDVDS	AKTVLPPLVG	TNIEYVGWKA	FLQGRNLASF	ALFYLEQKNR
601	TVVDFGVYVP	AGGKQGSFQT	VAKPIGVVS	RGAEFELSGE	LNEDKWFVAG
651	YTYNKSGYKN	AAEVNAERLA	KNTGADPYNF	SNETPVHIFR	FGTSFHIPNT
701	GLTVGGGVSA	QSGTSSLYNI	RQGGYGLIDG	FVRYELGKHA	KLSLIGTNLN
751	GRTYFENNYN	RTRGANNFYG	EPRTVSMKLD	WOF*	

	10	20	30	40	50	60
a742.pep	MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILSCENQKTAPFSSTPACNRPLQLPR					
m742	MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILPCENQKTAPFSSTPACNRPLQLPR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a742.pep	NTYLGEDWSRLSADKYNLFSGGFKHVF DNGWQLNAEVSYTKNESDAKVGQFFLKNEHAAGL					
m742	NTYLGEDWSRLSADKYNLFSGGFKHVF DNGWQLNAEVSYTKNESDAKVGQFFLKNEYAAGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a742.pep	SDEDAVGFLTEKNEVIPFEPKD KALEK LKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR					
m742	SGEDAVGFLTEKNEVIPFEPKD KALEK LKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR					
	130	140	150	160	170	180
	190	200	210	220	230	240
a742.pep	SRRAAERKAGFDECM SAPFALDFICQGSWGDPGV DADKSEFVDKALAKEGIFNNAQRFP					

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|||||:|||||:|||||
m742  SRRAAERKAGFDKCMSDPFALDFICQGSWGDPGVDADKAEFVDKALAKEGIFNNAQRFP
      190      200      210      220      230      240
      250      260      270      280      290      300
a742.ppep NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKLDTGTGYGLFGREHDFVGYAYGDE
      |||||:|||||:|||||
m742  NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKLDTGTGTGLFGREHDFVGYAYGDE
      250      260      270      280      290      300
      310      320      330      340      350      360
a742.ppep KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGE PDGDLSSPLVRGHKEPDWQAYDEKGN
      |||||:|||||:|||||
m742  KIRSEYLEIYERRYVRPNTGATHGVYAGSCQEEP DGDLSSPLVRGHKEPDWQAYDEKGN
      310      320      330      340      350      360
      370      380      390      400      410      420
a742.ppep RTVYAEECR NAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQTNP
      |||||:|||||:|||||
m742  RTVYAEECR NAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQTNP
      370      380      390      400      410      420
      430      440      450      460      470      480
a742.ppep GTPAFTGFSGTVPVWKTVKVADHDHPALYNYAKYLNTNKTSLTAGTRFNV TGRLLHLLGG
      |||||:|||||:|||||
m742  GTPAFTGFSGTVPVWKTVKVADHDHPALYNYAKYLNTNKTSLTAGTRFNV TGRLLHLLGG
      430      440      450      460      470      480
      490      500      510      520      530      540
a742.ppep LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLT PYAGITYDLTPQ
      |||||:|||||:|||||
m742  LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLT PYAGITYDLTPQ
      490      500      510      520      530      540
      550      560      570      580      590      600
a742.ppep QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAF LQGRNLASFALFYLEQKNR
      |||||:|||||:|||||
m742  QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAF LQGRNLASFALFYLEQKNR
      550      560      570      580      590      600
      610      620      630      640      650      660
a742.ppep TVVDFGYVPGAGGKQGSFQTVAKPIGKVSRGAEFELSGELNEDWKV FAGYTYNKSRYKN
      |||||:|||||:|||||
m742  TVVDFGYVPGAGGKQGSFQTVAKPIGKVSRGAEFELSGELNEDWKV FAGYTYNKSRYKN
      610      620      630      640      650      660
      670      680      690      700      710      720
a742.ppep AAEVNAERLAKNTGADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
      |||||:|||||:|||||
m742  AAEVNAERLAKNSADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
      670      680      690      700      710      720
      730      740      750      760      770      780
a742.ppep RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGE PRTVSMKLD
      |||||:|||||:|||||
m742  RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGE PRTVSMKLD
      730      740      750      760      770      780

a742.ppep WQFX
      |||
m742  WQFX

a742/ p25184
sp|P25184|PUPA_PSEPU      FERRIC-PSEUDOBACTIN      358      RECEPTOR      PRECURSOR
>gi|94923|pir||S15169
```

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ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi|45723 (X56605)
 pseudobactin uptake protein [*Pseudomonas putida*] Length = 819
 Score = 152 bits (381), Expect = 6e-36
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADHDV-PALYNYAKYLNTNKTSLTAGTRFNVTLRLHLLGGLHYTRYETSQTKDM 494
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y
 Sbjct: 511 QTPKPGDDEIIPGI----QYNISNRQSGYFVASRFNLTDLLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTYPAGITYDLTPQOSIYGSYTKIFKQQ 554
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q
 Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPO 609

Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRNLNASFALFYLEQKNRTVVDFGVYPGAGGK 614
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG
 Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGEFLEGRNLNANIALYMKRONLAESTNEVVPDSGGL 668

Query: 615 QGSFQTVAKPIGKVVSRGAEEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674
 S + + +G + ELSGE+ W VF GY++ ++
 Sbjct: 669 IAS-----RAVDGAETKGVDELSEVLPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +
 Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGWEKLTGCGGVNWNKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
 RY + + +L N+ + Y Y G+ YG PR ++ L + F
 Sbjct: 768 TSIMARYRINESLAATLNVNNIFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTT CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
 151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC
 351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
 401 TGACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGCGCAA AATCGACGTG
 451 TCTCCGAGTA CCGATTGGGC GGTATTATGAC CATATTGAAG TTGTACGGGG
 501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCATT
 551 TGATCCGTAA GTGA

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep
 1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPOQS VSVITRSLD DKAVHTLEEA
 101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
 151 SPSTD LAVYD HIEVVRGATG LTQSNSEPGG TVNLIRK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTT CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTG
 151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC

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351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGTATTATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```

a743.pep
1  MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
51  GKTEKTRSYT IDRMSTATGM RIAGKDPQS VSVITRSLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTD LAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR

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a743/m743 98.9% identity in 187 aa overlap

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              10      20      30      40      50      60
a743.pep  MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT
          |||
m743      MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT
              10      20      30      40      50      60

              70      80      90     100     110     120
a743.pep  IDRMSTATGMRIAGKDTQPQSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRD SGLQTRFL
          |||
m743      IDRMSTATGMRIAGKDTQPQSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRD SGLQTRFL
              70      80      90     100     110     120

              130     140     150     160     170     180
a743.pep  SRGFYIDQIGEDGITVNVAGRSGYTAKIDVSPSTD LAVYD HIEVVRGATGLTQSNSEPGG
          |||
m743      SRGFYIDQIGEDGMTVNVAGRSGYTAKIDVSPSTD LAVYD HIEVVRGATGLTQSNSEPGG
              130     140     150     160     170     180

a743.pep  TVNLIRKR
          |||
m743      TVNLIRKX

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g744.seq not found yet

g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

```

m744.seq
1  ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
51  CAGAAAGA GAAATAAAG ATTTATTTAA CCGAATATTT GTAAAGGAG
101 AATATTTGGA TGAATTATGT GAACCAATA TTTCGTTTTT AATCGGAGAA
151 AAGGGAACGT GAAAGACAGC ATATGCTGTT TATTTAACTA ATAACCTCTA
201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACGTGTTT AGATTTTACA
301 AGTATTTGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCAATATT TAATAAATTT AAGGCCTTAG
401 ATGAGGCTAT AAATGAATAT TATTATGGCG CTTTGTATCC GGAATTTGTA
451 CAAGCAATAA CTTTAATAGA AAATTCAAAA GAAGCTGCGG AAATGATTTT
501 TGGAAAATTT GTTAACTAG GTGAAGAGGA ATCCCAACAA ATAACCTTTA
551 CAGAAAGTAA ATTCCAAGCA AATTTAGGTT TTATTGAAAG AAAATTTAAA
601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTATTATGA
651 TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701 GTGTAAAGG TCTTGCTAAC GCCATATGGA TGTAAATAA TGATATCTTC
751 CCTTCCATTA AAGATAGTAA GGAAGGATG AGAGTTGTGT TATTGATTAG
801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAT ACCCAACTTC
851 AAGATAATTC AGTATTTTGA GACTGGAGGA CGGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTTGATCAT CTTTGTAGAA CCCAGCAAGA
951 AAAACAAGAT AGTTAGAAA AAGGCAACTC ATGGGATTAT TATTTCCCT
1001 GGAATGCTCC TAATTACAT GATGAGTATA AAAATTTAAC TTCATTATT
1051 AGCTTCCTAA GAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTTACTT
1201 GGTGAAATCA AAGATCATCT TTTGTTTTAT TATAGTCAAA GTGATTATCA
1251 AAATTCCTGT AAATTTTTTG AATTTTAAA CGGGAAGAT AGATTTAAAT

```

1213

```

1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGAAAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTTA AAGATAGAAA TTATGCAAAAT
1501 ATTTCTCCTA AAATAAAAAAC TGAAACTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGAACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

```

m744.pep
  1 MKPLKTFLEF FVDAANYRRR ENKDLFNRIK VKGEYLDELK EPNISFLIGE
  51 KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLKK ARHLTVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIFNKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEESQO ITFTESKFOA NLGFIERKFK
201 DALSQLKLD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVVLLIRPDI FDSLGLQONN TKLQDNSVFL DWRTDYKSYR
301 SSKIFGVFDH LLRTQQEKQD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKSKEDY VVAEDFDNTS FQREYSIYLL
401 GEIKDHLLEY YSQSDYQNFL KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVEIPKFMS TANEFLQFLF DLNVIAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTPEKKNK Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

```

m745.seq
  1 ATGTTTTGGC AACTGACCGT TGTTCAGTA ACCGCCGTCA TTGCACTGGG
  51 GACAATATTC ATCAATAAGA AAACCTCAAA GCAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTCGCCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGCGATTT ACTTACCGTA ATCAATCGGC ACGAGTTTGA TCGGTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTTG TTTAAACGGC TGCATTGCAC
351 CAACTTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGTT
451 GCATTATGGA AAGCAAACCC CCTAAGGCA TCTGATTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

```

m745.pep
  1 MFWQLTVVSV TAVIALGTIF INKKTSKQKA TLDVILNDYQ DAQFVEADNH
  51 ISPYIRGTAV DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPV MKIREEERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

```

g746.seq
  1 ATGTCGGAAA ACAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
  51 ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGTT CCGATCCTGC CGACAGCAAT
151 CCCGCACCGC AGGCCGGCGA AACC GGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCACAA ACCCTGCCT TGAATCCGC CGCCGAAAAAC GGGGAAACCG
251 CGCCGACAA ACCGCGAGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAACACGTA GCGCGCCCGC TGGTGCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGGTTTGGA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACC GAAGCA GGCAAAACAA
451 CGCGTGCCTG AAAAAGTGTC GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCGAAAAC TGCTGCCGAA AAAACCAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

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```

751 GCGCAAAAAA CCGACAAAGC GGACAAAACC AAAACCGCCG AGAAGGAAAA
801 ATCCGGCAAG GCGGGCAAAA AAGCCGCCAT TCAGGCAGGT TATGCCGAAA
851 AAGAACGCCG CTTGAGCCTC CAGCGCAAAA TGAAGCGCGC GGTATCGAT
901 TCGACCATCA CCGAAATCAT GACCGACAAC GGCAAGTTT ACCGCGTCAA
951 ATCAAGCAAC TATAAAAACG CAAGGGATGC CGAACGCGAT TTGAACAAAC
1001 TCGCGGTGCA CGGCATCGCC GGCCAGGTAA CGAATGAATA G

```

This corresponds to the amino acid sequence <SEQ ID 2552; ORF 746.ng>:

```

g746.pep
1  MSENKQNEVL TGYEQLKRRN RRRLVTASSL VAASCILLAA ALSSDPADSN
51  PAPQAGETGA TESQTANTAQ TPALKSAAEN GETAADKPQD LAGEDKPSAA
101 DSEISEPENV GAPLVLINDR LEDSNIKGLE ESEKLQQAET AKTEPKQAKQ
151 RAAEKVSATA DSTDTVAVEK PKRTAEPKPQ KAERTAEAKP KAKETKTAEK
201 VADKPKTAAE KTKPDTAKSD SAVKEAKKAD KAEGKKTAEK DRSDGKKHET
251 AQKTDKADKT KTAEEKESGK AGKKAIIQAG YAEKERALS L QRMKAAGID
301 STITEIMTDN GKVYRVKSSN YKNARDAERD LNKLRVHGIA GQVTNE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2553>:

```

m746.seq
1  ATGTCGGAAC ACAAACAAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
51  ACGGGCGCAAC CGCCGCGGCC TCGTAACGGC AAGTTGCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
151 GCCGGCGGAA CAAGCGGCGT AGAAAACAAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCTTG AAATCCGCGC CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCCGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGAGCGCCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGGC AACTGCCGAC
451 AGTACGGATA CGGTAGCGGT TGA AAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAA GCGCAAGAAA
551 CCAAAACCGC CGAAAAGTT GCCGACAAAC CGAAAACCTG CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAAG AAGCGAAAAA
651 AGCCGACAA GCTGAAAGCA AAAAAACAGC CGAAAAGAC CGTTCGGACG
701 CGAAAAAACA CGAAACGGCA CAAAAACCG ACAAAGCGGA CAAGACCAA
751 ACCGCCGAGA AGGAAAAATC CGGTAAAAAA GCCGCCATT AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGGCGGCGG
851 GTATCGATTG GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAAAT CAAGCAACTA TAAAAACGCA AGGGATGCCG AACGCGATT
951 GAACAAATTG CGCGTACAGG GTATCGCCGG TCAGGTAACG AATGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2554; ORF 746>:

```

m746.pep
1  MSENKQNEVL SGYEQLKRRN RRRLVTASCL VAASCILLAA ALSSGPAEQT
51  AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINERL EDSNIKGLEA SEKLQQAETA KTAPKQAKQR AAEKVPTAD
151 STDTVAVEKP KRTAETKPK AERTAKAKPK AKETKTAEKV ADRPKTAAEK
201 TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QKTDKADKTK
251 TAEKEKSGK AAIQAGYAEK ERALS LQRM KAAGIDSTIT EIMTDNGKVY
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

```

m746/g746      89.9% identity in 346 aa overlap

          10      20      30      40      50
m746.pep  MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQT----AGETSG
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g746       MSENKQNEVL TGYEQLKRRNRRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGETGA
          10      20      30      40      50      60

          60      70      80      90     100     109
m746.pep  VENKAAGAAQT PALKSAA-----DKPQDLAGEDKPSAADSEISEPENVGAPLVLINER
          : | | | | | | | | | | | | | | | | | | | | | | | | | | |
g746       TESQTANTAQT PALKSAAENGETAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDR
          70      80      90     100     110     120

```

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```

      110      120      130      140      150      160      169
m746.pep  LEDSNIKGLEASEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPQ
          |||||
g746      LEDSNIKGLEESEKLQQAETAKTEPKQAKQRAAEKVSATADSTDVAVEKPKRTAEPKPQ
          130      140      150      160      170      180

      170      180      190      200      210      220      229
m746.pep  KAERTAKAKPKAKETKTAEKVADKPKTAAEKT KPDTAKSDSAVKEAKKADKAESKKTAEK
          |||||:|||||
g746      KAERTAEAKPKAKETKTAEKVADKPKTAAEKT KPDTAKSDSAVKEAKKADKAEGKKTAEK
          190      200      210      220      230      240

      230      240      250      260      270      280
m746.pep  DRSDGKKHETAQKTDKADTKTAEKEKSGK---KAAIQAGYAEKERALS LQRKMKAAAGID
          |||||
g746      DRSDGKKHETAQKTDKADTKTAEKEKSGKAGKAAIQAGYAEKERALS LQRKMKAAAGID
          250      260      270      280      290      300

      290      300      310      320      330
m746.pep  STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          |||||
g746      STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          310      320      330      340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```

a746.seq
1  ATGTCCGAAA  ACAACAAAA  CGAAGTCCTG  AGCGGTTACG  AACAACTCAA
51  ACGGCGCAAC  CGCCGCCGCC  TCGTAACGGC  AAGTTGCCTG  GTTGCCGCCT
101 CCTGCATCCT  GCTGGCAGCC  GCCCTCAGTT  CCGGCCCTGC  CGAACAGACT
151 GCCGGCGAAA  CAAGCGGCGT  AGAAAAACAA  GCGGCAGGTG  CGGCACAAAC
201 CCCTGCTTGG  AAATCCGCCG  CCGACAAACC  GCAGGACTTG  GCAGGCGAAG
251 ACAAGCCTTC  TGCCGCCGAC  AGCGAAATCA  GCGAGCCTGA  AAACGTAGGC
301 GCGCCGCTGG  TGCTGATTAA  CGACCGCCTC  GAAGACAGCA  ACATCAAAGG
351 TTTGGAAGCA  TCCGAGAAAC  TGCAACAGCG  AGAAACCGCC  AAAACCGCAC
401 CGAAGCAGGC  AAAACAACGC  GCTGCCGAAA  AAGTGCCGGC  AACTGCCGAC
451 AGTACGGATA  CGGTAGCGGT  TGAAAAACCG  AAACGCACTG  CCGAAACAAA
501 ACCGCAAAAA  GCGGAACGCA  CTGCCAAAGC  CAAGCCCAAA  GCCAAAGAAA
551 CCAAAACCGC  CGAAAAAGTT  GCCGACAAAC  CGAAACTGCG  CGCCGAAAAA
601 ACCAAACCGG  ATACGGCAAA  ATCCGACAGC  GCGGTAAAG  AAGCGAAAAA
651 AGCCGACAAG  GCTGAAAGCA  AAAAAACAGC  CGAAAAAGAC  CGTTCGGACG
701 GCAAAAAACA  CGAAACGGCA  CAAAAAACCG  ACAAGCGGGA  CAAGACCAAA
751 ACCGCCGAGA  AGGAAAAATC  CGGTAAAAAA  GCCGCCATTC  AGGCAGGTTA
801 TGCCGAAAAA  GAACGCGCCT  TAAGCCTCCA  GCGCAAAATG  AAGGCGGCGG
851 GTATCGATTG  GACCATCACC  GAAATTATGA  CCGACAACGG  CAAAGTTTAC
901 CGCGTCAAA  CAAGCAACTA  TAAAAACGCA  AGGGATGCCG  AACGCGATTT
951 GAACAAATTG  CGCGTACACG  GTATCGCCGG  TCAGGTAACG  AATGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```

a746.pep
1  MSENKQNEVL  SGYEQLKRRN  RRRLVTASCL  VAASCILLAA  ALSSGPAEQT
51  AGETSGVENK  AAGAAQTPAL  KSAADKPQDL  AGEDKPSAAD  SEISEPENVG
101 APLVLINDRL  EDSNIKGLEA  SEKLQQAETA  KTAPKQAKQR  AAEKVPATAD
151 STDVAVEKEP  KRTAETKPQK  AERTAKAKPK  AKETKTAEV  ADKPKTAAEK
201 TKPDTAKSDS  AVKEAKKADK  AESKKTAEKD  RSDGKKHETA  QKTDKADTK
251 TAEKEKSGKK  AAIQAGYAEK  ERALS LQRKM  KAAGIDSTIT  EIMTDNGKVV
301 RVKSSNYKNA  RDAERDLNKL  RVHGIAGQVT  NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746: 99.7% identity in 332 aa overlap

```

      10      20      30      40      50      60
a746.pep  MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
          |||||
m746      MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
          10      20      30      40      50      60

```

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```

          70      80      90      100     110     120
a746.pep  AAGAAQT PALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA
          |||||||
m746      AAGAAQT PALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA
          70      80      90      100     110     120

          130     140     150     160     170     180
a746.pep  SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKQAERTAKAKPK
          |||||||
m746      SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKQAERTAKAKPK
          130     140     150     160     170     180

          190     200     210     220     230     240
a746.pep  AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
          |||||||
m746      AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
          190     200     210     220     230     240

          250     260     270     280     290     300
a746.pep  QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRKMKAAAGIDSTITEIMTDNGKVY
          |||||||
m746      QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRKMKAAAGIDSTITEIMTDNGKVY
          250     260     270     280     290     300

          310     320     330
a746.pep  RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          |||||||
m746      RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          310     320     330

```

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

```

m747.seq
1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGACG  GTGACAAAAC CAAATGGGC  CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2558; ORF 747>:

```

m747.pep
1   LTPWADAYAD LRGKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTIIKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

```

a747.seq
1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAACC
201 CCGTGAGATT GTTTTGACG  GCGACAAAAC CAAATGGGC  CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2560; ORF 747.a>:

```

a747.pep
1   LTPWADAYAD LRGKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

1217

Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

	10	20	30	40	50	60
a747.pep	LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGSVIGLNVGKQLTDSVGLFDPYYR					
m747	LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKGSVIGLNVGKQLTDSVGLFDPYYR					
	10	20	30	40	50	60
	70	80	90	100		
a747.pep	HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX					
m747	HKTIYKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX					
	70	80	90	100		

a747/m80195

gi|150271 (M80195) outer membrane protein [Neisseria meningitidis] Length = 272

Score = 59.3 bits (141), Expect = 6e-09

Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGSVIGLNVGKQLTDSVGLFDPYYR 60

+ PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+

Sbjct: 174 INPWSEVKFDLNSRYKLNTGVNLLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95

+T + E + GD + ++ EYG RV F

Sbjct: 234 QRTYKESGEFSVTTKSGDVSILTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

g748.seq

```
1 ATGAGTCAAA ACCAACCCGC ACAACCGACC AAACGCAATC TGTTCAAAAC
51 CGCCCTTGCC GTCGCGCGCA TCGGCGCAAT CGGAGGTTAT TTCGCGCGCA
101 AAAAAACAGG CGAAACCGCC GAACGCACCG CCGAAAGCCA AACTCGCCC
151 CAAGCCTATC CCTGTACGG CGAACATCAG GCAGGTATCG TTACGCCCGG
201 GCAGGCGTTT TCCATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACACTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGCGG GAGAATACCA AGACGGCGAC GACAAACTCC CGTCAGCCGG
351 CAGCGGCATT TTGGGTAAAG CTTCAACCC CGACGGATTG ACCGTTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAAACGGTTC ATTTGCAGGA AATGCGCGAC TTCCCAACG ATAAGCTGCA
501 AAAAAGCTGG TGGACGGCG ATTTGAGCCT GCAAACTGCG GCCTTCAACC
551 CCGAAACCTG CCAAACCGCC CTGCGCGACA TCATCAAAAC CACCGCCCAA
601 ACCGCCGTCA TCCGTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCCGAGAC GGCACGGGCA
701 ACCCCAAGTT TTCCGATCCC AAAACCGCCG ACGAGGTTTT ATGGACGGGC
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGCGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCGCTTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GGCGAAAATA CAGCGGGGCG
901 CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTTC CCAAAGACCC
951 CGAGGGTGAT ATCAGCCCA AAGACAGCCA TATGCGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCTCAAA AAACACTGCC TCTTCGCGCG CGCCTACAGC
1051 TATTCTCGCG GACCCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAATC TTGCCGACGG TTTCATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTCTTCG TCTTGCCCGG CGTGGGAAAA GCGGATTCT TGGGACAAGG
1251 GCTGCCGGGC GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

```
1 MSQNQAQPT KRNLFKTALA VGAIGAIGGY FGGKKQGETA ERTAESQHS
51 QAYPCYGEHQ AGIVTPROAF SIMCAFDVTA QSAKQLENLF RLTARIEFL
101 TQGGYQDGD DKLPASAGSI LGKAFNPDGL TVTVGVSSSL FDGRFGLKDK
151 KTVHLQEMRD FPNDKLQKSW CDGDLSQLIC AFTPETCQTA LRDIKHATA
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTWG
251 VAANSLDEPE WAKNGSYQAV RLIRRFVEFW DRTPLEQETD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHMRL ANPRDPEFLK KHCLFRFRAYS
351 YSRGPASSGQ LDVGLVFVCY QANLADGFIF VQNLNNGEPL EEYISPFGGG
```

401 YFFVLPGVGK GGFLGQGLPG V*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2563>:

m748.seq

```

1 ATGAGCAAAA AACAAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAC
51 CGCGATCGCA GCCGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
201 GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACGCTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGCGG CGCAATACCA AGACGGCGAC GACAAACTTC CGCCAGCCGG
351 CAGCGGCATT TTGGGCAAG CCTTCAACCC CGACGGGTG ACCGTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAACCGATT CATTGCAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA
501 AAAAAGCTGG TGCGACGGCG ATTTGAGCCT GCAAATCTGT GCCTTCACCC
551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAACCA CACCGTCCAA
601 ACCGCCGTTA TCCGTTGGAG TATCGACGGG TGGCAGCCCA AATCGGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTACGGGAC GGCACGGGCA
701 ACCCCAAAGT TTCCGATCCC AAAACTCGCG ACGAGGTTTT GTGGACGGGG
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCACTTTGT CGAGTTTTGG GACAGGACGC
851 CGTTTCAAGA GCAAACCGAC ATTTTCGGGC GCGCGAAATA CAGCGGTGCG
901 CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTTG CCAAAGACCC
951 CGAGGGTGAT ATCAGCCCCA AAGACAGCCA TATACGCTCG GCGAATCCGC
1001 GCGATCCCGA ATTCCTCAA AAACACCGCC TCTTCGCGCG CGCCTACAGC
1051 TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTCT GGCTGGTGT
1101 CGTCTGCTAT CAGGCAAACC TTGCGGACGG ATTCATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTTT CGGCGGCGGC
1201 TATTTCTTCG TCTTGCCCGG CGTGGAAAAA GCGGCGTTTT TGGGCAAGG
1251 GCTGCTGGGC GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2564; ORF 748>:

m748.pep

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1 MSKKQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKQGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPQQAF SIMCAFDVTA QSAKQLENLF RLTARIEFL
101 TQGGEYQDGD DKLPPAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KPIHLQEMRD FSNDKLQKSW CDGDLQLQIC AFTPETCQAA LRDIKHTVQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTWG
251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLQEOTD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHRL ANPRDPEFLK KHRLFRRAYS
351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VQNLNGEPL EEYISPFGGG
401 YFFVLPGVEK GGFLGQGLLG V*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

m748/g748 95.0% identity in 421 aa overlap

	10	20	30	40	50	60
m748.pep	MSKKQPAQPTTRTLFKTAIAAGAVGAIGGYLGKKQGETAERTAESQHSPQAYPCYGEHQ					
g748	MSQNPQAQPTKRNLFKTALAVGAIGAIGGYFGKKQGETAERTAESQHSPQAYPCYGEHQ					
	10	20	30	40	50	60
m748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGEYQDGD DKLPPAGSGI					
g748	AGIVTPRQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGEYQDGD DKLPSAGSGI					
	70	80	90	100	110	120
m748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGEYQDGD DKLPPAGSGI					
g748	AGIVTPRQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGEYQDGD DKLPSAGSGI					
	70	80	90	100	110	120
m748.pep	LGKAFNPDGLTVTVGVGSSLFDRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLQLQIC					
g748	LGKAFNPDGLTVTVGVGSSLFDRFGLKDKKTVHLQEMRDFPNDRKLQKSWCDGDLQLQIC					
	130	140	150	160	170	180
m748.pep	LGKAFNPDGLTVTVGVGSSLFDRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLQLQIC					
g748	LGKAFNPDGLTVTVGVGSSLFDRFGLKDKKTVHLQEMRDFPNDRKLQKSWCDGDLQLQIC					
	130	140	150	160	170	180
m748.pep	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
g748	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
	190	200	210	220	230	240

	190	200	210	220	230	240
g748	AFTPETCQTALRDIKHTAQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
m748.pep	250	260	270	280	290	300
g748	KTADEVLTWGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDFGRRKYSGA					
	250	260	270	280	290	300
m748.pep	310	320	330	340	350	360
g748	PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
	310	320	330	340	350	360
m748.pep	370	380	390	400	410	420
g748	LDVGLVFVCYQANLADGFIQVQNLLNGELEEYISPFGGGYFFVLPVGVGKGGFLGQGLLG					
	370	380	390	400	410	420
m748.pep	VX					
g748	VX					

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a748.seq
1  ATGAGCAAAA ACCAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51  CGCGATCGCA GCTGGAGCAG TCGGCGCAAT CGGAGGTTAT TCTCGCGCCA
101 AAAAACGGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACCTCGCC
151 CAAGCTCATC TCTGTTACGG CGAACATCAG CAGGCGATCG TTAACGCCGG
201 CGAGGCGTTT CCGATTATGT GCGCGTTGCA CGTAACGCGC CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTT CGCAGCGTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGGCG GTGAATACCA AGCTCGGACC GACAAACTTC CGCCAGCGCG
351 CAGCGGCATT TGGGCAAAAG ACCTTCAAGC CAGCGGGTTG ACCGTTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAACCGATTG ATTTGTCAGG AATCGCGCAC TTCTCCAAAG ATAAGCTGCA
501 AAAAACCTGG TCGCAGCGCG ATTTGAGCCT GCAATCTGTG GCCTTCAACC
551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAACA CACCGTCCAA
601 ACCCGCGTTA TCCGCTGGAG TATCAGCGGG TGGCAGCCTA AATCCGAACC
651 CGGCGCGATG GCGCGCGCA ACCTGTTGGG TCTCCGCGAC GGCACGGGCA
701 ACCCCAAAGT TTCGACCCCC AAAACTGCCG ACGAGGTTTT GTGACCGGGG
751 GTGGCGGCCA ACAGCTTCGA CGCAACCGAG TGGGCGAAAA ACGGCAGTAA
801 TCAGGCAGTG CGCCTTATCC GCGACTTTGT TGAGTTTGGG GACGAGCGCG
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GGCGCAAATA CAGCGGCGCG
901 CGGATGGAGC GCAA AAAAGA AGACGACCAA CTGAGTTTGG CCAAGAACCC
951 CGAGGGGAAT ACCACGCCCA AAGCAGACCA TATACGCTTG CCGAATCCGC
1001 GCGATCCCGA GTTCTTTAAA AAACACCGCC TCTTCCGCGC CGCCTACAGC
1051 TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATATCT GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAAAC TTGCCGACGG ATTACGTTTC GTGCAAAAGC
1151 TCCTCAACGG CGAACCAGTG GAAGAATACA TCAGCCCCCT CGGCGGCGCC
1201 TATTTCTTCG TCTTCCCGCG CGTGGAAAAA GGCAGCTTTT TGGGCGAAGG
1251 GCTGCTGGGG TGTATAAA

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a748.pap
1  MSKNQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKRGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPQQA F SIMCAFDVTA QSAQLENLF RDTLRQIEFL
101 TQGGEYQDGD DKLPAPAGSGI LGKAFNPDL TVTVGVGSSL PDGFRGLKDK
151 KPIHLQEMRD FSNDKLQKSW CDGDLSLQIC AFTPETCQAA LRDIKHTVQ
201 TAVIRWSIDG WQPKSEPM AARNLLGFRD GTGNPKVSDT KTADEVLTSG
251 VAANSLEDEP WAKNGSYQAV RLRIHFVEVF DRTLPEQSDT IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGN TTPKDSHRL ANPRDPEFLK KHRLFRAYS
351 YSRGLASSGQ LGLVGLFVCY QANLADGFIF VONLLNGEPL EEEYSPFGGG
401 YFFVLPGVEK DDVLPQGLLG V*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

	10	20	30	40	50	60
a748 .pep	MSKNQPAQPTTRRTLFKTAIAAGAVGAIGGYLGKKRGETAERTAESQHSFQAYPCYGEHQ					
m748	MSKKQPAQPTTRRTLFKTAIAAGAVGAIGGYLGKKQGETAERTAESQHSFQAYPCYGEHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
a748 .pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGEYQDGGDKLPPAGSGI					
m748	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGEYQDGGDKLPPAGSGI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a748 .pep	LGKAENPDGLT VTVGVGSSLF DGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGLSLQIC					
m748	LGKAENPDGLT VTVGVGSSLF DGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGLSLQIC					
	130	140	150	160	170	180
	190	200	210	220	230	240
a748 .pep	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
m748	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a748 .pep	KTADEVLTWGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDFGRRKYSGA					
m748	KTADEVLTWGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDFGRRKYSGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
a748 .pep	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
m748	PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
a748 .pep	LDVGLVFVCYQANLADGFI FVQNLLNGE PLEEYISPFGGGYFFVLP GVEKGGFLGQGLLG					
m748	LDVGLVFVCYQANLADGFI FVQNLLNGE PLEEYISPFGGGYFFVLP GVEKGGFLGQGLLG					
	370	380	390	400	410	420
a748 .pep	VX					
m748	VX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

g749.seq

```

1  ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTGGGTTT
51  GACCGCGTGC CAGCCGCCGG AGCGGAGAAA AGCCGCGCCG GCCCGTCCG
101 GTGAGACCCA ATCCGCCAAC GAAGCGGTT CGGTCGGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GAATCTGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AGGGCGTGAT GGTGGTGGAC GAACGCGAAA ATATCGCCCC GGGGCTTTCC
301 GACAAAATGA CCGTAaccct GCTGCCGGGC GAATACGAAA TGACCTGCGG
351 CCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAGCCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGCCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG CGGCGAAAAC
501 CAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGCCACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATCGGTGTG AAGACGACTT
651 CAAAGACGGT CGGAAAGATG CCGGGTTTAC CGGCTTCCAC CGTATCGAAC
701 ACGCCCTTTG GGTGGAAAAA GACGTATCCG GCGTGAAGGA AACC GCGGCC
751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATGGC

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801	GttccctCCG	GGCAAAGTGG	TGGCGGCGC	GTCCGAAC TG	ATTGAAGAAG
851	CGCGCGGCGAG	TAAATACAG	GGCGAAGAAG	ACCTgtacAG	CCACCCGGAT
901	TTGAGCGCACT	TCCAAGCTAA	TGCGGACGGA	TCTAAAAAAA	TCGTGCGATT
951	GTTCGCTGCTG	TGTATTGAGG	CCAAATCAAA	AGCCTTGTGT	GAAAAAACCG
1001	ATACCAACCT	CAACACGGTG	AACGAAATTA	TGGCGAAATA	CCGACACAAA
1051	GACGGTTTTG	AAACCTACGA	CAAGCTGAGC	GAAGCGCACC	GCAAAGCATT
1101	ACAGCGTCTCT	ATTAACGCGC	TGCGCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGGTT	GAAATAA			

g749.pap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

m749.seq

1	ATGAGAAAA	TCAATTGTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCGCGTGC	CAGCCGCGCG	AGGCGGAGAA	AGTGCGCGCG	GCAGCGTCCG
101	GTGAGCGCGCA	AACGCCCAAC	GAGGCGGGTT	CGGTGAGTAT	CGCCGCTCAAC
151	GACAATGCTT	CGCAACCGAT	GGAAGTGACC	GTGCCGAGCG	GACAGGTTGTT
201	GTTCAAATATT	AAAAACAACA	GCGGCGCGCA	GCTCGAATGG	GAAATCCTGA
251	AAGGCGGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATCTGCCCC	CGGACTTTCC
301	GATAAAATGA	CGGTACCCCT	GTTGCGGGGC	GAATACGAAA	TGACTTGGCG
351	TCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCGC	CACGAAGGCG	GATTTGGAAT	AGATGTCCCA	ACCGCTGCCC
451	GACTATAAAG	CCTACGTTCA	AGGCGAGGTT	AAAGAGCTTG	TGGCGAAAAA
501	CAAAACTTTT	ACCGAAGCCG	TCAAAGCAGG	CGCATTTGAA	AAGCGCAAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCACATTAC	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGCGTG	AAGACGACTT
651	CAAAGACCGC	GCGAAAGATG	CCGGATTTCAC	CGGCTTTTAC	CGTATCGAAT
701	ACGCCCTTGA	GGTGGAAAAA	GACGTGTCCG	GCGTGAAGGA	AATTGCAGCG
751	AAACTGTATG	CGCATGTGCA	AGCCCTGCAA	AAAGAAATCG	ACCGATTGGC
801	GTTTCTCTCG	GCGAAGGTGG	TGCGGCGGCG	TGCGCAACTG	ATTGAAGAAG
851	TGGCGGGCAG	TAAATCAGC	GCGGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGACT	TCCAAGGCCAA	TGTGGACGGA	TCTAAAAAAA	TCGTGCGATT
951	GTTCCGCTCG	CTGATCGAGG	CAAAAACAA	AGGCTTTGTT	GAAAAACCCG
1001	ATACCAACTT	CAACAGGTC	ACAGAAATT	TGCGGCAATA	CGGACTATAA
1051	GACGGTTTGT	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAGCGTT
1101	ACAGGCGCTCT	ATTACACGCG	TTGCGGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTT	GAATAAA			

m749.pap

1	MRKFNLTLAL	VMLALGLTAC	QPPEAEKAAP	AASGEAQTN	EGGSVSIAVN
51	DNACEPMELT	PVSQGVVFN	KNNSGRKLEW	EILKGVMVVD	EENRIAPGLS
101	KDMTVTLPLG	EYEMTCGLLT	NPRKGLVTD	SGFKDTANEA	DREKLSQPLA
151	DYKAYALGVE	KELVAKTKTF	TEAVKAGDIE	KAKSLFADTR	VHYERIEPIA
201	ELFSELDPEI	DAREDDFKDG	AKDAGDTFGH	RIEYALWVEK	DVDSGVKEIAA
251	KLMTDVEALQ	KEIDALAFPP	GKVVGGASEL	IEEVAGSKIS	DESGRYSDTH
301	LSDFQANVDG	SKKIVDLFR	LIEAKNNKAL	EKTDNTMFKV	NEILKAYRTK
351	GDFTYDKLG	EADRKALQAS	INALAEDLAL	LRGLIGLK*	

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

m749.pep MRKFNLTALSVMLALGLTACOPPEAEKAAPASGEAQTANEGGSVSIIVNDNACEPMELT
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 g749 MRKFNLTALSVMLALGLTACOPPEAEKAAPASGETQSANEGGSVGIIVNDNACEPMNLT
 10 20 30 40 50 60

1222

	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNSGRKLEWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
g749	VPSGQVVFNIKNNSGRKLEWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVADSGFKDTANEADLEKLPQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRVHYERIEPIAELEFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
g749	KAKSLFAATRVHYERIEPIAELEFSELDPVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
g749	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLS					
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

a749.seq

1	ATGAGAAAAAT	TCAATTTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCCGCTGC	CAGCCGCCGG	AGGCGGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAC	GAGGCGGGTT	CGGTCAGTAT	CGCCGTCAAC
151	GACAAATGCT	GCGAACCAGT	GGAAGTACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAATCCTGA
251	AAGGCGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATCGCCCC	CGGACTTTCC
301	GATAAAATGA	CCGTCACCCCT	GTTGCCGGGC	GAATACGAAA	TGACTTGCGG
351	TCITTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCCG	CAACGAAGCG	GATTGGGAAA	AACTGTCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTATGTTC	AGGCGAAGTC	AAAGAGCTGG	TGGCGAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGCGTG	AAGACGACTT
651	CAAAGACGGC	GCGAAAGATG	CCGGATTAC	CGGCTTCCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCCG	GCGTGAAGGA	AATTGCAGCG
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC
801	GTTTCCTCCG	GGCAAGGTGG	TCGGCGGCGC	GTCCGAAGTG	ATTGAAGAAG
851	TGGCGGGCAG	TAAATCAGC	GGCGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGACT	TCCAAGCCAA	TGTGGACGGA	TCGAAAAAAA	TCGTCGATTT
951	GTTCCGTCGG	TTGATCGAGA	CCAAAAACAA	AGCCTTGTG	GAATAAACCG
1001	ATACCAACTT	CAAACAGGTC	AACGAAATTC	TGGCGAAATA	CCGGACTAAA
1051	GACGGTTTGG	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAGCGTT
1101	ACAGGCCTCT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTT	GAATAAA			

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

a749.pep

1	MRKFNLTALS	VMLALGLTAC	QPPEAERAAP	AASGEAQTAN	EGGSVSIAVN
51	DNACEPMELT	VPSGQVVFNI	NNSGRKLEW	EILKGVVVDD	ERENIAPGLS
101	DKMTVTLLPG	EYEMTCGLLT	NPRGKLVVTD	SGFKDTANEA	DLEKLSQPLA
151	DYKAYVQGEV	KELVAKTKTF	TEAVKAGDIE	KAKSLFADTR	VHYERIEPIA
201	ELFSELDPIV	DAREDDFKDG	AKDAGFTGFH	RIEYALWVEK	DVSGVKEIAA
251	KLMTDVEALQ	KEIDALAFPP	GKVVGGASEL	IEEVAGSKIS	GEEDRYSHTD

1223

301 LSDFOANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
a749.pep	MRKFNL	TALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	AVNDNACEPMELT			
m749	MRKFNL	TALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	AVNDNACEPMELT			
	10	20	30	40	50	60
	70	80	90	100	110	120
a749.pep	VPSGQVVFN	IKNNSGRKLEWEILKGMVVD	ERENIAPGLSDKMTVTLLPGEYEMTCGLLT			
m749	VPSGQVVFN	IKNNSGRKLEWEILKGMVVD	ERENIAPGLSDKMTVTLLPGEYEMTCGLLT			
	70	80	90	100	110	120
	130	140	150	160	170	180
a749.pep	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTTEAVKAGDIE					
m749	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a749.pep	KAKSLFADTRVHYERIEPIAELFSELD	PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK				
m749	KAKSLFADTRVHYERIEPIAELFSELD	PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK				
	190	200	210	220	230	240
	250	260	270	280	290	300
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGA	SELIEEVAGSKISGEEDRYSH				
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGA	SELIEEVAGSKISGEEDRYSH				
	250	260	270	280	290	300
	310	320	330	340	350	360
a749.pep	LSDFOANVDGSKKIVDLFRPLIETKNKALLEKTD	TNFKQVNEILAKYRTK	DGFETYDKLG			
m749	LSDFOANVDGSKKIVDLFRPLIETKNKALLEKTD	TNFKQVNEILAKYRTK	DGFETYDKLG			
	310	320	330	340	350	360
	370	380	389			
a749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
m749	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq
 1 GTGAAACCGC GTTTTATTG GGCAGcctGC GCCGTCCTGC CGGCCGCCCTG
 51 TTCGCCCGAA CTGCGCCGCG AAAAACTGT ATccgCCGCA TCCCAAGCCG
 101 CATCCACACC TGTCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC
 151 GTTGTGCCGA AGAATCCCGA ACgcgtcgcc gtgtAcgaCt ggGCGGCGTt
 201 ggaTACGCTG ACCGAGCCGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG
 251 TGCGCGTGGA CTATTGCGAG CCTGCATTG ACAAGGCGGC AACGGTGGGG
 301 ACGCTGTTG AGCCCGATTG CGAATCCCTG CACCGCCACA ATCCGCAGTT
 351 TGTCATTACC GCGGGGCCGG GTGCGGAAGC GTATGAACAG TTGGCGAAAA
 401 ACGCGACCAC CATAGATTG ACGGTGGACA ACGGCAATAT CCGCACCAGC
 451 GCGGAGAAGC AGATGGAGAC CCTGTCGCGG ATTTTCGTA AGGAAGCGCG
 501 CGTGGCGGAA TTGAATGCGC AGATTGACGC GCTGTTCGCC CAAAAGCGCG
 551 AAGCCGCCAA AGGCAAGGA CGCGGGCTGG TGCTGTCGGT TACAGGCAAC
 601 AAGGTGTCCG CCTTCGGCAC GCAATCGCGG TTGGCAAGTT GGATACACGG
 651 CGACATCGGC CTGCCGCCCG TGGACGAATC TTTACGCAAC GAAGGGCACG
 701 GGCAGCCCGT TTCCTTCGAA TACATCAAAG AGAAAAACCC CGGCTGGATT
 751 TTCATCATCG ACCGCACCGC CGCCATCGGG CAGGAAGGGC CGGCTGCCGT

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801 GGAAGTGTG GATAACGCGC TGGTATGCGG CACGAACGCT TGGAAGCGCA
 851 AGCAAAATCAT CGTCATGCCT GCCGCGAACT ACATTGTGCG GGGCGGCGCG
 901 CGGCAGTTGA TACAGGCGGC GGAACAGTTG AAGGCGGCGT TTGAAAAGGC
 951 AGAACCCGTT GCGGCGCAGT AG

This corresponds to the amino acid sequence <SEQ ID 2574; ORF 750.ng>:

g750.pep

1 VKPRFYWAAC AVLPAACSPE PAAEKTVSAA SQAASTPVAT LTVPTARGDA
 51 VVFKNPERVA VYDWAALDTL TEPGVNVGAT TAPVRVDYLQ PAFDKAATVG
 101 TLFEPCESL HRHNPQFVIT GGPGAAYEQ LAKNATTIDL TVDNGNIRTS
 151 GEKQMETLSR IFGKEARVAE LNAQIDALFA QKREAAKGKG RGLVLSVTGN
 201 KVSFAFTQSR LASWIHGDIQ LPPVDESIRN EGHGQPVSE YIKEKNPGWI
 251 FIIDRTAAIG QEGFAAVEVL DNALVCGTNA WKRKQIIVMP AANYIVAGGA
 301 RQLIQAAEQL KAAFEKAEPV AAQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2575>:

m750.seq

1 GTGAAACCGC GTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCGCCTG
 51 TTCGCCGGA CTTGCCGCGG AAAAACTGT ATCCGCGCGA TCCGCATCTG
 101 CCGCCACGCT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
 151 AATCCCGAAC GCGTCGCGGT GTACGACTGG GCGGCGTGG ATACGCTGAC
 201 CGAATTGGGC GTGAATGTGG GCGCAACCAC CGCGCCGCTG CGCGTGGATT
 251 ATTTGACGCC TGCAATTTGAC AAGGCGGCAA CGGTGGGGAC GCTGTTGAG
 301 CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
 351 CGGGCCGGGC GCGGAAGCGT ATGAACAGTT AGCGAAAAAC GCGACCACCA
 401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
 451 ATGGAGACCT TGGCGCGGAT TTTCGGCAAG GAAGCGCGCG CGGCGGAATT
 501 GAAGGCGCAG ATTGACGCGC TGTTCCGCCA AACGCGCGAA GCCGCCAAG
 551 GCAAAGGACG CGGGCTGGTG CTGTCGGTTA CGGGCAACAA GGTGTCGCC
 601 TTCGGCACGC AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
 651 ACCGCCTGTA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
 701 CCTTCGAATA CATCAAGAG AAAAAACCCG ATTGGATTTT CATCATCGAC
 751 CGTACCGCCG CCATCGGGCA GGAAGGGCCG GCGCTGTCTG AAGTATTGGA
 801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAAATCATCG
 851 TCATGCTGCG CGGGAAGTAC ATTGTCGCGG GCGGCGCGCG GCAGTTGATT
 901 CAGGCGGCGG AGCAGTTGAA GCGGCGGTTT AAAAAGGCAG AACCCGTTGC
 951 GCGGGGAAAA AAGTAG

This corresponds to the amino acid sequence <SEQ ID 2576; ORF 750>:

m750.pep

1 VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
 51 NPERVAVDW AALDTLTELQ VNVGATTAPV RVDYLQPAFD KAATVGTLFE
 101 PDYEALHRYN PQLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
 151 METLARIFGK EARAELKAO IDALFAQTR EAKGKGRGLV LSVTGNKQSA
 201 FGTQSRSLASW IHGDIQLFPV DESLRNEGHG QPVSEFYIKE KNPWFIFID
 251 RTAAIGQEGP AAVEVLDNAL VRGTNAWKRK QIIVMPAANY IVAGGARQLI
 301 QAEEQLKAFF KKAEPVAAGK K*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

m750/g750 93.8% identity in 322 aa overlap

	10	20	30	40	50
m750.pep	VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASA-----ATLTVPPTARGDAVVPKNPERVA				
g750	VKPRFYWAACAVLPAACSPEPAAEKTVSAAASQAASTPVATLTVPPTARGDAVVPKNPERVA				
	10	20	30	40	50
	60	70	80	90	100
m750.pep	VYDWAALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLPDYALHRYNPNQVIT				
g750	VYDWAALDTLTEPGNVGATTAPVRVDYLQPAFDKAATVGTLPDCELSLHRHNPQFVIT				
	70	80	90	100	110
	120	130	140	150	160
m750.pep	GGPGAAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFA				

1225

g750	GGPGAEAYEQ	LAKNATTID	LTVDNGN	IRTSSE	GKOMET	LSRIFG	KEARVA	ELNAQ	IDALFA
	130	140	150	160	170	180			
m750.pep	180	190	200	210	220	230			
	QTREAAK	GKGRGL	VLSVTG	NKVS	AFGTQ	SRLAS	WIGHD	IGLPP	VDESLR
g750	QKREAAK	GKGRGL	VLSVTG	NKVS	AFGTQ	SRLAS	WIGHD	IGLPP	VDESLR
	190	200	210	220	230	240			
m750.pep	240	250	260	270	280	290			
	YIKEKNP	DWIFI	IDRTAA	IGQEG	PAAEV	LDNAL	VRGTN	AWKRK	QIIVM
g750	YIKEKNP	DWIFI	IDRTAA	IGQEG	PAAEV	LDNAL	VRGTN	AWKRK	QIIVM
	250	260	270	280	290	300			
m750.pep	300	310	320						
	RQLIQAA	EQLKAA	FKKAE	PVAAG	KKX				
g750	RQLIQAA	EQLKAA	FEKAE	PVAAG	QX				
	310	320							

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2577>:

```

a750.seq
1      GTGAACCCGC  GTTTTTATTG  GGCAGCCTGC  GCCGTCCTGC  TGACCCGCTG
51     TTGCGCCGAA  CCTGCCGCGC  AAAAAACTGT  ATCCGCGCA  TCCGCACTCG
101    CGGCCACACT  GACCGTCGCG  ACCGCGGGCG  GCGATGCCGT  TGTGCCGAAG
151    AATCCCGAAC  GCGTCGCGGT  GTACGACTGG  GCGGCGCTTG  ATACCGCTGAC
201    CGAATTGGGT  TGAATTGTGG  GCGCAACCAC  GCGCGCGGTG  CGCGTGGATT
251    ATTTGCAGCC  TGCATTTGAC  AAGCGGGCAA  CGGTGGGGAC  GCTGTTCCGAG
301    CCCGATTACG  AAGCCCTGCA  CCGCTACAAT  CCTCAGCTTG  TCATTATCCG
351    CGGGCCGGGG  CGGGAAGCGT  ATGAACAGTT  GGGCAAAAA  GCACACCACA
401    TAGATCTGAC  GGTGGACAAC  GGCAATATCT  GCACCAGCGG  CGAAAAGCAG
451    ATGGAGACCT  TTGCGCGGAT  TTTTCGGCA  GAAGCGCGCG  CGGGCGGAAT
501    GAAGGCGCAG  ATTGACGCGC  TGTTCGCCCA  AACGCGCGGA  GCGGCCAAAG
551    GCAAAGGACG  CGGGCTGGTG  CTGTGCGTTA  CGGGCAACAA  GGTGTCGCCC
601    TTCGCCACGC  AGTCGCGGTT  GGCACAAGTG  ATACACGGCG  ACATCGGCCCT
651    ACCGCTGTGA  GACGAATCTT  TAGCAAGTGA  GGGCGACGGG  CAGCCTGTTT
701    CCTTCGAATA  CATCAAAGAG  AAAAACCCCG  ATTGGATTTT  CATCATCGAC
751    CGTACCGCGC  CCATCGGGCA  GGAAGGGCGG  GCGGCTGTGC  AAGTATTGGA
801    TAACGCGCTG  GTACGCGGCA  CGAACGCTTG  GAAGCGCAAG  CAATATCTGC
851    TCATGCGCTG  CGCGAATCAT  ATTGTCGCGG  GCGGCTCGCG  GCAGTTGATT
901    CAGGCGCGCG  AGCAGTTGAA  GGAGGCGGTT  GAAAAGGCAG  AACCCTGTGC
951    GCGGGGGAAA  GAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2578; ORF 750.a>:

a750.pap					
1	VKPRFYWAAC	AVLLTACSPE	PAAEKTVSAA	SASAATLTVP	TARGDAVVPK
51	NPERVAVIDW	AALDTLTTEL	VNVGATTAPV	RV DY LQPAFD	KAATVGLTFE
101	PDYEALHRYN	PQLVITGGPG	AEAYEQLAKN	ATTIDLTVDN	GNIRTSGEKQ
151	METLARIFGK	ERAAELKQAK	IDALFAQTRE	AAKGKGRGLV	LSVTGNKVSA
201	FGTQSLASW	IHGADILFPV	DESLRNHGSH	QPVSFYEIKE	KNPDWFTIID
251	RTAAIIQGGP	AAEVDLNLAL	VRGTNAWKRK	QIIVMPAANY	I VAGGSRQLI
301	QAAEQLEKAF	EKAEPVAAKG	E*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

a750/m750 98.8% identity in 321 aa overlap

	10	20	30	40	50	60
a750.pep	VKPRFYWAACAVLLTACSPEPAAEKT	VSAASASAATLT	VPTARGDAV	VV	PKNPERVA	VYDW
m750	VKPRFYWAACAVLLTACSPEPAAEKT	VSAASASAATLT	VPTARGDAV	VV	PKNPERVA	VYDW
	10	20	30	40	50	60
	70	80	90	100	110	120
a750.pep	AALDTLTELGVNVGATTAPVRVDY	LQPAFDKAA	TGTLFEPDY	EALHRYNP	Q	LVTGGPG
m750	AALDTLTELGVNVGATTAPVRVDY	LQPAFDKAA	TGTLFEPDY	EALHRYNP	Q	LVTGGPG

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	70	80	90	100	110	120
	130	140	150	160	170	180
a750.pep	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARI FGKEARAAELKAQIDALFAQTRE					
m750	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARI FGKEARAAELKAQIDALFAQTRE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a750.pep	AAKGKGRGLVLSVTGNKVSFAFGTQSRSLASWIHGDIGLPPVDES LRNEGHGQPVSFEYIKE					
m750	AAKGKGRGLVLSVTGNKVSFAFGTQSRSLASWIHGDIGLPPVDES LRNEGHGQPVSFEYIKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a750.pep	KNPDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWKRRQIIIVMPAANYIVAGGS RQLI					
m750	KNPDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWKRRQIIIVMPAANYIVAGGS RQLI					
	250	260	270	280	290	300
	310	320				
a750.pep	QAAEQLKEAFKAEPVAAGKEX					
m750	QAAEQLKAAFKKAEPVAAGKKX					
	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

m751.seq..

```
1  ATGGCTTGGA GTATGTTTGC CACAACCCAA GCCGATAGAG CGGTAAGGTC
51  TGCAACTGCA CCTAAAGAAA TGTGGTTCCA TAAGAAGATA ATAGATGAAA
101 AAACAGGTAA AGTATCCTTT GATACCAGAC AAATTTGGTC ATTGAATGAT
151 TTAAGCAAGG AAGAACTGGC AAGCATTCAA GACACAAATG GCAAAGTTAT
201 TACTGTGTCT AATCCTGGTA TTTTCAATAA TCGAGAAGAT TCATTAAGCA
251 ACGCAGCAAA ACAAAATCGT AATAGTACAA ACGGTAGTGG TGTATTGCA
301 GTCATGAATC CTCCAACAGG GAAATATAAA TCTGATTCTA ATAACAAAAT
351 AAAAGATTTT TTATGGCTCG GTTCAAGTCT TGTTCCTGAA CTGATGTATG
401 TCGGTTACGA CCAATTAAAT AATAAAGTGT TCCAAGGCTA TTTACCCAAA
451 ACCAATTTCAG AAAAACTGAA TCAAGATATT TATCGAGAGG TTCAAAAAAT
501 GGGTAACGGC TGGTCGGTTG ATACCAGTAA TCACAGTCGT GGGGGAATTA
551 CAGCAAGCGT TTCCTTAAAA GATTGGGTAA ACAATCAAAA ACAAAATGGC
601 ATTGCCCCAA TCAGAAAAGC ACGTTTCTAT GGTACAGCCA CAAATGTGCA
651 GAATGATTAC GCCGATGTTT TACAGAAAAA CGGCTATACC TATACGGGTG
701 CAGACGGCAA AACTTATAAC AGCGGATCCT ACTCAATCGT GCATGATAAA
751 GATTTTGTGG GGAACAAATG GATACCTTTC TTGCTAGGAA CCAATGACAC
801 CACACAAGGT ACATGTAAGG GGTGTGCTA TTCGCATAGC AGTTATTTTG
851 CGGAGGTGCC AAAAGCAGGT ACAAAGAAT TTGATGACTA TGTAAAAATA
901 TGGGGTGAAG TTGAATATGA CGCTCAAGGT AAGCCAATTA ACAAACTTAA
951 ACCCATACTG GTAGAACCAA ACAAAACAAA AGATAATGAA AAATATGAAA
1001 AAGAAGCTTT CTAA
```

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>:

m751.pep..

```
1  MAWSMFATTQ ADRAVRSATA PKEMWFHKKI IDEKTGKVSF DTRQIWSLND
51  LSKEELASIQ DTNGKVITVS NPGIFNNRED SLSNAAKQNR NSTNGSGVIA
101 VMNPPTGKYK SDSNNKIKDF LWLGSSLVSE LMYVGQDQLN NKVFQGYLPK
151 TNSEKLNQDI YREVQKMNG WSVDTSNHSR GGITASVSLK DWVNNQKQNG
201 IAPIRKARFY GTATNVQNDY ADVLQKNGYT YTGADGKTYN SGSYSIVHDK
251 DFGVGNKWIPF LLGTNDTTQG TCKGLCYSHS SYPAEVPKAG TKEFDDYVKI
301 WGEVEYDAQG KPINKSKPIL VEPNKTCDNE KYEKEAF*
```

a751.seq not found yet

a751.pep not found yet

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g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

```

m752.seq..
1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAATCAAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCTGAC TCTTTCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAATGATT TTGGATTGCG ACCGCATTGC
651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTGCAATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGCTCT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTG GAGCACTACA TTTCCGACAA ACAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTG GAGTAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

```

m752.pep
1  MKISRPEFT LLQOYMOHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51  DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAKESRK KIQKPIDFPF
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAIIILHE LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTYFYIYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALYVAP QDLLERLEKK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

```

m752-1.seq
1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAATCAAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCTGAC TCTTTCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAATGATT TTGGATTGCG ACCGCATTGC

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```

651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGTTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTT TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTTATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA AAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRRAVESRK KIQKPIDFPF
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLLSKLIM
151 EEAITSQALE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRODDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILLHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPQYAK SYLYAETDDL
351 DLTYYIYYQC DIIKRAVDL EHYISDKQKH QOEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDSLKL GEYRFLVPFK
451 SGNALXYVAP QDLERLEKK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCTT AACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTTAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTTCG GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TGCGCCAGTT ATTCCTAGT ACGACAGTAC
401 GCGCCTTGTA TCATAAAGG AGCGATAAGG GTTTGAGAA TTTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAI WLWYQSPTHR QVPIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLESD RHLRDNSDWN
101 CGDNIWLIQW FAPLGHSHQM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

1229

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```

m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTGT GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTGTC TGGGCATAAA TGCCCCACAG
451 GTTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAG GTTTTGATGC ATCCGAATAT
601 CTTGCTTGG CTGCCAATGA ATTTTATGTC ATGCAGACCA TCAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTCGGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCATAGT
851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTCA GTACTCTATC ATGACGAATA
951 CGATGTTCTG CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATT
1051 AACCTGACTA ACCACGGTAA GAAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAAATG ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```

m754.pep
1  MMKSILTVSG NMRKPRITY LDVWANDERI GTLEKGAMYR FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVRCND PLENEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQQYMAEIF HHGRFVSVSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIKQAGIA VAQTSLSLSEDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDT SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKPTY PSKNTLLDFA EKYCDLGRED ASEMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*

```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```

m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTACTCCGAT ATTAACACCA
101 TCTTGGCTAG ACATGGATTG GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTTTACC
251 GCCTTGAAAG TGATTTGAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAACACAG CTTTCCTTCA ACGTGTGTA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTTGAATT GGAAAGTCTT AACCTGAAAT TAAATTAA

```

1230

This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

```
m755.pep..
  1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSSVYLQ
  51 REGISEAHGT IAIQELTARF DWFYSCISNI KEYRLESIDLN AQFIADGVYQ
 101 AKQAFLLQVRV QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*
```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

```
m756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
  51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
 101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
 151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
 201 AGATATGCTT CAAGATATGC CCCCTAAAT CCGTTCGGCA ACGCTGGTAG
 251 CGTTGACGAC CCGTCTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
 301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
 351 TGCCGTCGAC CGTCTTGAG AATCCCAAGA ACGGATAACG TCCGCCATCC
 401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
 451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
 501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
 551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

```
m756.pep
  1 MTANFAQTLV EIQDSLRYRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
  51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTLLV GGALGYGYLE
 101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
 151 SREDISEANR RAERVYPYAE LVSDGNFTAV LSDIGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

```
a756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
  51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
 101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
 151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
 201 AGATATGCTT CAAGATATGC CCCCTAAAT CCGTTCGGCA ACGCTGGTAG
 251 CGTTGACGAC CCGTCTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
 301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
 351 TGCCGTCGAC CGTCTTGAG AATCCCAAGA ACGGATAACG TCCGCCATCC
 401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
 451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
 501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
 551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

```
a756.pep
  1 MTANFAQTLV EIQDSLRYRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
  51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTLLV GGALGYGYLE
 101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
 151 SREDISEANR RAERVYPYAE LVSDGNFTAV LSDIGD*
```

m756 / a756 99.5% identity in 186 aa overlap

```

      10      20      30      40      50      60
m756.pep MTANFAQTLVEIQDSLRYRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE
          |||||
a756      MTANFAQTLVEIQDSLRYRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE
          10      20      30      40      50      60
```

1231

	70	80	90	100	110	120
m756.pep	TLVRFGRDMLQDMPPKIRSATLVALTTLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756	TLVRFGRDMLQDMPPKIRSATLVALTTLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
a756	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
	130	140	150	160	170	180
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

```

m757.seq
1  ATGAAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAATAAAC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAATAACTG TCCAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGGCG ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

```

m757.pep (lipoprotein)
1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFSGLTI LTVDTKADK
101 ITAVRVVWNT DAMPQKAEKL SKAAAALIAA TAPEDRTMLR DTGDQIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPVS VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

```

m758.seq
1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCGGTT ACAGACCATC
101 AGGGCAAAC TGTGGAAATT CCGTCTGCT ACGGCGCGCA ATACGGCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCCGGTC GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGCGGCG TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAAGAA GGATTGAGCC
501 ATGA

```

1232

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLEI PVCYGG EYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1  ATGAACAATC TGACCGTGT CACCCGTTTC GATACCGATT TGGCGACGCT
 51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101  AGGGCAAAC TGTGGAATC CCCGCTGCTC ACGGCGGCGA ATACGGCCCG
151  GATTTGGCGG AAGTCGCTGC TTCCATCAG ACGGTTATTT CCGAAATCGT
201  CCGCCGCCAT ACGGCGCAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251  CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301  CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351  CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401  TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451  CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC
501  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLEI PVCYGG EYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

	10	20	30	40	50	60
m758.pep	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLEIPVCYGG EYGPDLAEVAAFHQ					
a758	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLEIPVCYGG EYGPDLAEVAAFHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m758.pep	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
a758	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
	70	80	90	100	110	120
	130	140	150	160		
m758.pep	GVYPFASPGGWQIIGRTELP LFRADLNPPTLLAAGDQVRFVAERIEPX					
a758	GVYPFASPGGWQIIGRTELP LFRADLNPPTLLAAGDQVRFVAERIEPX					
	130	140	150	160		

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1  ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51  TCTTTTGGCC GTTCCCTG CTTACTCATC CATTGTCCGC AACGATGTCG
101  ATTACCAATA TTTTCGCGAC TTGCGCGAAA ATAAAGGCGC GTTACCCGTA
151  GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGC AAAA TATTAGGCAG
201  GGTTCTCAAC GGCATCCCA TGCCCGACTT CCGCGTCAGC AACCGCCAAA
251  CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTC AAACAC
301  AACGTCGGCT ACGGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
351  AGAACAAAGCC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGACT
401  ACGACTACCA CCTTCCCGC CTCAACAAAC TGGTTACCGA AATCTCACCT
```

451 ACCGCACTCA GCAGCGTACC CTTGCTTGA AACGGCCAGC CAAAGGCCAA
 501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTTGTACGA CTCGGCTCAG
 551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGCGTACACG AACCGCCCCG
 601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAGTAT TGGGGTTCCA
 651 AAACCACGGC TTA CTCTGTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA
 701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCC CCCTGTTTGC CTTGACAAAG
 751 CATGAAAACC GCTGGGTGCT TGCGGGCGTA CTCAGCACCT ACGCCGGCTT
 801 CGATAATTTT TTAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT
 851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTGCGGCT GACCACCAAC
 901 GAACTCATAT GGCGCGACAA CGGTAATGGC AACAGCACCC TGCAAGGGCT
 951 CAACGAACGC ATCACCTGTC CCATTGCAAA CCCTTCGCTT GCCCCACAAA
 1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCCTA
 1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA
 1101 AGGCGCAGGC GCATTGCAGT TCGACAGCAA CTTACCCGTC GTCCGTAATA
 1151 ACCACACATG GCAAGGTGCA GCGGTTATCG TAGCCGACGG CAAACGCGTC
 1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGGCG
 1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCAGGGC GACATCAGCA
 1301 TCGGGGAAGG CACTGTGTA CTCGCCAAA AAGCTGCTTC AGACGGCAGC
 1351 AAACAAGCAT TCAACCAAGT CGGCATCACC AGCGGCAGGG GCACGGCCGT
 1401 CCTCGCGAC AGCCAGCAA TCAAACCGA AAACCTCTAT TTCGGCTTCA
 1451 GGGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCTT TACCATATC
 1501 CGCCATGCGG ACGGCGGCGC GCAAATCGTC AATCACAACC CTGACCAAGC
 1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTCTG
 1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGC GGTTTACGAA
 1651 TACATCAACC CGCACCGCAA CCGTCGACG GACTACTTCA TACTCAAAAC
 1701 CGGCGGCAAC CCGCGCAAT TTTTCCCGTT AAATATGAAA AACTCAACAA
 1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCCGCCGA ACAAGTCGCC
 1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTTGGG
 1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAG AAAACCAATG
 1901 AAGCAGCCAT AGAAAAAACC CGCATATCG CAAATGCCGC CGTATACGGC
 1951 CGGCCCGAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA
 2001 ACGCACCGAC AGCACGCTGT TGCTCAACGG CGGCATGAAC CTTAACGGGG
 2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTCAGGCAG GCCCGTACCC
 2101 CATGCCTACG ACCACAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG
 2151 GACCGACGGC AGCTTCAAGG CTGCACGGTT CACCCTGCGA AACCATGCCC
 2201 GACTGACGGC AGGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA
 2251 TACGATCTGT CCGGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA
 2301 ATGTACCGC TCCTACCATA GCGGCAGCAC CCACTGCACA CCCAACGCCG
 2351 TTTTAAAAGC CGAAAATAT CGTGCACTAC CTGCAACGCA AGTACGCGGC
 2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT
 2451 GTACGGCAGC ATCCGTGCCG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG
 2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGGCGC ACTGACGCTT
 2551 GACGCGCAC AAATTACCCT GAACCCGAT TTCGCCAATA ATACACAA
 2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTCCGCA
 2651 CATTCCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC
 2701 AAAGTGAAG GGGACAGCCG CGGCGCATTC CAAATCCACG TCAAAAACAC
 2751 CGGACAAGAA CCTCAAACAA CCGAATCGCT TGCACTTGTG AGCCTCAATC
 2801 CGAAACACAG CCACCAAGCC CGATTACCC TCCAAAACGG CTATGCCGAT
 2851 TTGGGTGCCT ACCGCTACAT CCTCCGCAA AACAAACACG GATACAGCCT
 2901 GTACAACCCG CTCAAAGAG CCGAACTTCA AATTGAAGCC ACGCGTGCGG
 2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC
 3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC
 3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT
 3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTCTGACG
 3151 CGTGCCCAA ACCTGTGTGC CGCACAAGGA TACAGTGCCG ATATCTGCCG
 3201 TCAGGTTGCC AAAGCCGCGC ACACGAACGA CCTGACACTC TTCGAAACCG
 3251 AACTGGATAC GTATATAGAA CGTGTAGAAA TGGCCGAATC CGAACTTGAC
 3301 AAAGCACGGC AAGGCGGCGA TGGCAGGCC GTCGAAACAG CCCGGCACGC
 3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAATCCAC AGTTTGAAAA
 3401 CCGGCGTTGC CGGCATCCGT ATGCCGAACC TGGCCGAAT GATCAGCCGG
 3451 TCGGCCAACA CCGCCGTTTC CGAACAGGCC GCCTACAATA CCGGCCGGCA
 3501 ACAGGCGGGA CGCCGCATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA
 3551 ACATCTGGCT GGAAACCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA
 3601 CACCGTCCCT ACCAACAAAC TACCAACTAT GCACATATCG GCATCCAAAC
 3651 CGGCATCACC GACCGTCTCA GTGTCGGTAC GATTTTAACC GATGAGCGCA
 3701 CAAACAACCG TTTTGATGAA GCGGTATCCG CCCGAAACCG CAGCAACGGC

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3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCGC CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CCGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCGTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCCG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCGCCAC AAACAGGCAG GAATCAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

```

m759.pep
1 MRFTHTPFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFTV
51 GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQYVNSVKH
101 NVGYGSIQFG NDTQNPEEQE YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLL NGQPKANAYL DTDREPYFVR LSGGTQQVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
251 HENRWVLAGV LSTYAGFDNF FNKYIVTQPE FIRSTIROYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQNSRHPM SEDAGKTLL
351 SSRFDNKTLM LADNINQAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FWQVSNPKGD RLSKLGAGTL IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGRLDL NGNNLAFTHI
501 RHADGGAQIV NHPDQAATL TLTGNPVLSP EHVEWVQWGN RPQGNAAVYE
551 YINPHRNRRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAYVG
651 RPEYRYNGAL NLHYRKPRTD STLLNNGGMN LNGEVLIEGG NMIVSGRPVP
701 HAYDHQAKRE PVLENEWTDG SFKARFTLR NHARLTAGRN TAHLDGDITA
751 YDLSGIDLGF TQGKTECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNDRSEL RLGKAHLYGS IRAGKDTAVR MEADSNWTL SSSHTGALTL
851 DGAQITLNPD FANNTNHNRF NTLTVNGTLD GFGTFRFLTG IVRKQNPAPL
901 KLEGDSRGAF QIHVKNTGQE PQTESLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNGYSLYNP LKEAELQIEA TRAEHERNQQ AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
1051 RAQNLCAAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESELD
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAEISR
1151 SANTAVSEQA AYNTGRQQAG RRIDRHLTDP QQQNIWLETG TQQTDYHSGT
1201 HRPYQQTNY AHIGITGIT DRLSVGTILT DERTNNRFE GVSARNRSG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTTHW AGIRLDKIVE
1351 LGQAKLTPAF SSDYYHTRQN SGSALSVNDR TLLQQAAGT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

```

g760.seq (partial)
1 AACAAACGCA ACACCCGTTA CGCCGCATTG GGCAAACGCG TGATGGAAGG
51 CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCTGCT GGTGCCCAA CACAGCGCAA ACCTGTGGAC
201 GACTACCAA GTTACGCCCG GGCTGACCGT CGGCGGCGGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT GCAGGGATGC ATGCAGGCGG TTATGCCACG
301 TTCGATGCGA TGGCGGCATA CCGCTTCACG CCCAAGCTGA AGCTGCAAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

```

g760.pep (partial)
1 NNRNTRYAAL GKRVMEGVET EISGAITPKW QIHAGYSYLH SQIKTAANPR
51 DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

```

1235

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1   ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAAAGCGG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCAGC CTGCCCAACC TGTTCCGCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTT GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGGTTCGGT ACGCACAAC AATATAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGCGAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGTCTCT CCGTCCCCTC CGAGAAAAAC AACCGGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GCGCGGGCT ATCTTTACCA GCAACGCGCG CTCGCGCCGT ACAACGGCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCCAA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTTAAATGC ACAGCCACGA CGTGTTCGCG
901 GATTTGAAAC ATTACTTCGG CAACGCGGCG TACGGCAAAG TCGGTATGCG
951 CTATTCCGAT CGGAAAGCCG ATTCCAATTA TACGTTTGCG GGCAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCGT TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTGT CAAAAGCGT CGCTTTAGAT
1201 GGTTCGCGC CTTTGCCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCCTC TGGAAGGTTT GTCGTTGATT
1351 GCAGCGGAC GTGTAGGACA TCACAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCTC CCAACTCTAC
1501 ACACGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA
1551 AGGCAACCAG TTTGAAATCG GCTACAAAG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTCGTTT TACCGCATGA AGGATAAAAA CGCCGCGCA
1651 CCGCTGGACT CAAACAACAA AAAAACCCTG TACGCCGAT TGGGCAAACG
1701 CGTGATGGAA GGTGTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTCGC GCGACGAAGG CATCTTCTG CTGATGCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATAGCGGC ATTACTTCAT CTGCAGGGAT ACATGCAGGC
1951 GGTATGCGCA CGTTCGATGC GATGGCGGCA TACCGTTCA CGCCAAACT
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCCC
2051 GCGTCGGCAG CGAGAGCACC TTTAACATT CCGGTTGCGA GCGCAGCCTG
2101 ACGGCAAACC TCGGTTACAG TTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1   MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKG QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQQVKDRNV DTFDQLARKT
101 PGLRVLSNDD GRSSVYARGY EYSEYNIDGL PAQMOSINGT LPNLFADFDRV
151 EVMRGPSGLF DSSGEMGGIV NLVRKPTKA FQGHAAAGFG THKQYKAED
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQORR LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHSHDVFA
301 DLKHYFGNGG YGKVMGRYSR RKADSNYTFA GSKLNNTGQA DVAGLGTDIK
351 QKAFVADASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSKVALD
401 GFRALPYNGI LQNRARAGNK FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKKI ESGDGKTLHK ASKTKFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNA
551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPKLKLQ INADNIFNRH YYARVGSEST FNIPGSEERSL
701 TANLRYSF*
```


1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRVSFYRMKDKNAAAPLDSNNKTRYAALGKRVMEGVETEISGAMTPKW					
g760	NNRNTRYAALGKRVMEGVETEISGAITPKW					
				10	20	30
	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIKTASNSRDEGIFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
g760	QIHAGYSYLHSQIKTAAANPRDDGIFLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	40	50	60	70	80	90
	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMAAAYRFTPKLKLQINADNIFNRHYYARVGSESTFNIPGSERSLTANL					
g760	AGMHAGGYATFDAMAAAYRFTPKLKLQINADNIFNRHYYARVGSTNTFNIPGSERSLTANL					
	100	110	120	130	140	150
	709					
m760.pep	RYSFX					
g760	RYSFX					

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

m761.seq

1	ATGAAAATAT	CATTTTCA	TTTATTA	CCCACGCTGA	TTATTGCTTC
51	CTTCCCTGTT	GCTGCCGCCG	ATACGCAGGA	CAATGGTGAA	CATTACACCG
101	CCACTCTGCC	CACCGTTTCC	GTGGTCGGAC	AGTCCGACAC	CAGCGTACTC
151	AAAGGCTACA	TCAACTACGA	CGAAGCCGCC	GTTACCCGCA	ACGGACAGCT
201	CATCAAAGAA	ACGCCGCAAA	CCATCGATAC	GCTCAATATC	CAGAAAAACA
251	AAAATTACGG	TACGAACGAT	TTGAGTTCCA	TCCTCGAAGG	CAATGCCGGC
301	ATCGACGCTG	CCTACGATAT	GCGCGGTGAA	AGCATTTTCC	TGCGCGGTTT
351	TCAAGCCGAC	GCATCCGATA	TTTACCGCGA	CGGCGTGCGC	GAAAGCCGAC
401	AAGTGCGCCG	CAGTACTGCC	AACATCGAGC	GCGTGGAAT	CCTGAAAGGC
451	CCGTCTTCCG	TGCTTTACGG	CCGCACCAAC	GGCGGCGGCG	TCATCAACAT
501	GGTCAGCAAA	TACGCCAACT	TCAAACAAAG	CCGCAACATC	GGAGCGGTTT
551	ACGGCTCATG	GGCAAACCGC	AGCCTGAATA	TGGACATTAA	CGAAGTGCTG
601	AACAAAAACG	TCGCCATCCG	TCTACCGGCG	GAAAGTCGGC	GCGCCAATTC
651	GTTCCGCAGC	GGCATAGACA	GCAAAAATGT	CATGGTTTCG	CCCAGCATTAA
701	CCGTCAAAC	CGACAACGGC	TTGAAGTGGA	CGGGGCAATA	CACCTACGAC
751	AATGTGGAGC	GCACGCCCGA	CCGCAGTCCG	ACCAAGTCCG	TGTACGACCG
801	CTTCGGACTG	CCTTACCGCA	TGGGGTTCGC	CCACCGGAAC	GATTTTGTCA
851	AAGACAAGCT	GCAAGTTTGG	CGTTCGGACC	TTGAATACGC	CTTCAACGAC
901	AAATGGCGTG	CCCAATGGCA	GCTCGCCAC	CGCACGGCGG	CGCAGGATTT
951	TGATCATTTT	TATGCAGGCA	GCGAAAATGG	CAACTTAATC	AAACGTAAC
1001	ACGCCTGGCA	GCAGACCGAC	AACAAAACCC	TGTCGTCCAA	CTTAACGCTC
1051	AACGGCGACT	ACACCATCGG	CCGTTTGTGA	AACCACCTGA	CCGTAGGCAT
1101	GGATTACAGC	CGCGAACACC	GCAACCCGAC	ATTGGGTTTC	AGCAGCGCCT
1151	TTTCCGCCTC	CATCAACCCC	TACGACCGCG	CAAGCTGGCC	GGCTTCGGGC
1201	AGATTGCAGC	CTATTCTGAC	CCAAAACCGC	CACAAAGCCG	ACTCCTACGG
1251	CATCTTTGTG	CAAAACATCT	TCTCCGCCAC	GCCCGATTTG	AAATTCTGTC
1301	TCGGCGGCCG	TTACGACAAA	TACACCTTTA	ATTCCGAAAA	CAAACCTACC
1351	GGCAGCAGCC	GCCAATACAG	CGGACACTCG	TTACGCCCCA	ACATCGGCGC
1401	AGTGTGGAAC	ATCAATCCCG	TCCACACACT	TTACGCCTCG	TATAACAAAG
1451	GCTTCGCGCC	TTATGGCGGA	CGCGGCGGCT	ATTTGAGCAT	CGATACGTTG
1501	TCTTCGCGCC	TGTTCAACGC	CGACCCCGAG	TACACCCGCC	AATACGAAAC
1551	CGGCGTGAAA	AGCAGTTGGC	TGGACGACCG	CCTCAGCACT	ACGTTGTCTG
1601	CCTACCAAAT	CGAACGCTTC	AATATCCGCT	ACCGCCCCGA	TCCAAAAAAC
1651	AACCCTTATA	TTTATGCGGT	TAGCGGCAAA	CACCGTTCGC	GCGGCGTGGA

1237

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1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACCTAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGTAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

m761.pep

```

1 MKISFHLALL PTLIASFPV AAADTDNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTD NKTLSNLTLL
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSASFASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPAPYG RGGYLSIDTL
501 SSAFVNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYYAVSGK HRSRGVELSA IGQIIPKKLY LRSLGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGAARVDAM LGWNHKNVNV TFAANLLNQ KYWRSDSMPG NPGYRTARVN
701 YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

a761.seq

```

1 ATGAAAATAT CATTTCATT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCTGTT GCTGCCGCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACCGCG CCTACGATAT GCGCGCGGAA AGCATTTTCC TCGCGCGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCGG TAGCACC GCCATCGAGC GCGTGGAAT CCTGAAAGGT
451 CCGTCTCCG TGCTTTATGG GCGTACCAAC GGGCGCGGTG TCATCAACAT
501 GGTCAAGCAA TACGCCAAT TCAAACAAAG CCGTAATATC GGTACGGTTT
551 ATGGTTTCGT GGCACACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
601 AACAAAAACG TCGCCATCCG TCTCACC GCGGCGGCG GCGCCAATTC
651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATT
701 CCGTCAAAT CGACAACGGC TTGAAGTGGA CCGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCGGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
801 CTTCCGACTG CCTTACCGCA TGGGGTTTCG CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTTCGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT
951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAT
1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCTCCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGTAA AACCACTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCGCTCT CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTCTGTC
1301 TCGGCGGCGG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTGAGCAT CGATACGTTG
1501 TCTTCGCGCG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC
1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCGGA TCCAAAAAAC
1651 AACCCTTATA TTTATGCGGT TAGCGGCAAA ACCCGTTCGC GCGGCGTGGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1238

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTCCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
1  MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51  KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDFGL PYRMGFAHRN DFKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTND NKTLSNLT
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFENSENKL
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDL
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGS LGV MQA KVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

m761.pep	10	20	30	40	50	60
a761	10	20	30	40	50	60
m761.pep	70	80	90	100	110	120
a761	70	80	90	100	110	120
m761.pep	130	140	150	160	170	180
a761	130	140	150	160	170	180
m761.pep	190	200	210	220	230	240
a761	190	200	210	220	230	240
m761.pep	250	260	270	280	290	300
a761	250	260	270	280	290	300
m761.pep	310	320	330	340	350	360
a761	310	320	330	340	350	360
	370	380	390	400	410	420

1239

```

m761.pep  NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
a761      NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
           370      380      390      400      410      420

           430      440      450      460      470      480
m761.pep  QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
a761      QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
           430      440      450      460      470      480

           490      500      510      520      530      540
m761.pep  YNKGFAFYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTLSAYQIERF
a761      YNKGFAFYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTLSAYQIERF
           490      500      510      520      530      540

           550      560      570      580      590      600
m761.pep  NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
a761      NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
           550      560      570      580      590      600

           610      620      630      640      650      660
m761.pep  RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYNRNKEVTTLPGFARVDAM
a761      RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
           610      620      630      640      650      660

           670      680      690      700
m761.pep  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761      LGWNHKNVNVTFAAANLFNQKYWRSDSMPGNPRGYTARVNYRFX
           670      680      690      700

```

g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1   ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTC GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGCC
201 AATTATTTAT CCTATTTTAT ATTTTITTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCTCT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1   MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
51  LFLLEIFNEV TKSIIYMAIIY PILYFFTIKK YYPYSRKVII LLSLALSIYF
101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1   ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTC GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGCC
201 AATTATTTAT CCTATTTTAT ATTTTITTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

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1240

301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
 351 TGAACCGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCTCT
 401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762.pep

1 MKWLLNMIMR PIKFSMVNTL LFIVICSSEF DLLVQLCTIL FHSQKIYFIT
 51 LFLLFIFNFV TKSIIYMAIIY PIIYFFTIKK YYPYSRKVII LLSLALSIYF
 101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762.pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSEFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSEFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762.pep	TKSIIYMAIIYPIIYFFTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
a762	TKSIIYMAIIYPIIYFFTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762.pep	PLHLYIPIIIINFFSLLVSNFILSFINKX					
a762	PLHLYIPIIIINFFSLLVSNFILSFINKX					
	130	140				

g763.seq not yet found

g763.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763.seq

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
 101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTGCCACTA
 151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
 201 GCGCGAGCAA CATTTCGGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG
 251 CAGTGC CGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCATGTA
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATT CTTCACCCG
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
 401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
 501 TTATTTCAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
 551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
 601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTTACGA
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
 701 AAAACCAAGT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAGC TGGAACGTTA
 801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
 901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
 951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
 1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
 1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
 1151 ATACCGAAAG CCGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
 1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
 1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCC
 1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
 1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAACGG TATTTGCGGA
 1401 ATAA

1241

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

m763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

a763.seq

```

1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGSTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTTCG CTGCGCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GCGCGAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTA CAGCGTGATG
251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATT CTTCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACAGTGT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCCAGC TGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTGCG CGCTTTTATC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAGACA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACC GGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC
1301 AAGCAGAACA GAAATCGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAACGCG TATTGCGGA
1401 ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

a763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*
```

m763 / a763 99.8% identity in 467 aa overlap

```

m763.pep      10      20      30      40      50      60
                MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a763          10      20      30      40      50      60
                MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
```

1242

	70	80	90	100	110	120
m763.pep	LPEAWRAAQHSAD	FQASHYQRDAV	RRARQQQAKAA	FLPHVSANASYQ	RQPPSISSTRET	Q
a763	LPEAWRAAQHSAD	FQASHYQRDAV	RRARQQQAKAA	FLPHVSANASYQ	RQPPSISSTRET	Q
	70	80	90	100	110	120
	130	140	150	160	170	180
m763.pep	GWSVQVGQTLF	DAAKFAQYRQSR	FDTQAAEQRFDA	AREELLKVAESY	FNVL	LSRDTVAA
a763	GWSVQVGQTLF	DAAKFAQYRQSR	FDTQAAEQRFDA	AREELLKVAESY	FNVL	LSRDTVAA
	130	140	150	160	170	180
	190	200	210	220	230	240
m763.pep	HAAEKEAYAQQV	RQAQALFNKGAAT	ALDIHEAKAGYD	NALAQEI	IAVLA	EAKQTYENQLNDY
a763	HAAEKEAYAQQV	RQAQALFNKGAAT	ALDIHEAKAGYD	NALAQEI	IAVLA	EAKQTYENQLNDY
	190	200	210	220	230	240
	250	260	270	280	290	300
m763.pep	TDLDSKQIEAID	TANLLARYLPKLE	RYSLDEWQRIALS	NNHEYRMQQLAL	QSSGQALRAA	
a763	TGLDSKQIEAID	TANLLARYLPKLE	RYSLDEWQRIALS	NNHEYRMQQLAL	QSSGQALRAA	
	250	260	270	280	290	300
	310	320	330	340	350	360
m763.pep	QNSRYPTVSAHV	GYQNNLYTSSAQ	NNDYHYRGKGM	SVGVQLNLPLYT	TGGELSGKIH	EAEA
a763	QNSRYPTVSAHV	GYQNNLYTSSAQ	NNDYHYRGKGM	SVGVQLNLPLYT	TGGELSGKIH	EAEA
	310	320	330	340	350	360
	370	380	390	400	410	420
m763.pep	QYGAAEAQLTAT	ERHIKLAVRQAY	TESGAARYQIMAQ	ERVLESSRLKLK	STETGQ	QYGIR
a763	QYGAAEAQLTAT	ERHIKLAVRQAY	TESGAARYQIMAQ	ERVLESSRLKLK	STETGQ	QYGIR
	370	380	390	400	410	420
	430	440	450	460		
m763.pep	NRLEVIRARQEVA	QAEQKLAQARYK	FMLAYLRLVKES	GLGLET	VF	FAEX
a763	NRLEVIRARQEVA	QAEQKLAQARYK	FMLAYLRLVKES	GLGLET	VF	FAEX
	430	440	450	460		

1243

g764.seq not found yet

g764.pap not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

```

m764.seq
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GGCCTTTTTG CCCGCGCATT TGGAAC TGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GGCGGCGCGT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GGCGGCGCGA GCAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GGCGCAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GGCGCAGGAG CAGAAGCTGG TTTCGGTGGG GGCGATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTC GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGC GGCCATTGCA CAGCGCGAGC
851 AGAATCGGT GCTGAATACG CAGAACTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAGT
1101 TTTGTGATTG AACAAAGACA TCGGTTTGTG GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GGCGGTGCTG GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

```

m764.pap
1  MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEQAFLE PAHLELTDP
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDGQHVQKGE TLAELEAVGT DSDVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE OKLVSVGAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRQQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGLTGT
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEK
451 TGRRVLDYL LSPLQTKLDE SFRER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

```

a764.seq (partial)
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GGCCTTTTTG CCCGCGCATT TGGAAC TGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GGCGGCGCGT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GGCGGCGCGA GCAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GGCGCAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GGCGCAGGAG CAGAAGCTGG TTTCGGTGGG GGCGATCGAG CAGCAGAAAA

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1244

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701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAAAT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

```

a764.pep (partial)
  1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAFLE PAHLELTDTP
 51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVKGQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQALRGHQ AELQSAKAE QKLVSVAIE QKKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

m764.pep	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
a764	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
m764.pep	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDQHVKGQE					
a764	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDQHVKGQE					
m764.pep	130	140	150	160	170	180
	TLAELEAVGTSDSDVVQSEQALQAAQLSKLRYEAVLALESRTVPHIDMAQARSLGLSDAD					
a764	130	140	150	160	170	180
	TLAELEAVGTSDSDVVQSEQALQAAQLSKLRYEAVLALESRTVPHIDMAQARSLGLSDAD					
m764.pep	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQALRGHQAEQKLSVGAIEQQKTADYRRL					
a764	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQALRGHQAEQKLSVGAIEQQKTADYRRL					
m764.pep	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA					
a764	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA					
m764.pep	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
a764	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
m764.pep	370	380	390	400	410	420
	DKMDVEVLVLNKDIGFVEQQDAVVKIESFPYTRYGYLTGKVKSVDHAVSHEQLGLVYT					

1245

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|||||
a764      DKMDVEVLVLNKKDIGFVEQGDVAVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
              370      380      390      400      410      420

              430      440      450      460      470
m764.pep  AVVSLDKHTLNIDGKAVNLTAGMNVTAIEIKTGKRRVLDYLLSPLQTKLDESFRERX
              |||||
a764      AVVSLDKHTLNIDGK
              430

```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```

m765.seq
1  ATGTTAAGAT  GCCGTCCGAA  ATCCGTTTTG  GATTCAGACG  GCATTTTTTT
51  GAAATTTAAT  TTTTAAAGGA  GTAAACCTAA  ATATGAAATT  TCCTTCCTTC
101 CTTCCTTTAA  ACGGATACTC  TGCCTGTCGG  CAGTAATCTC  GGTATTGGGG
151 GCTTGTCGGG  TCGTTGCTGA  TGTTTACGGT  CATGATCCG  CCACAATGAA
201 CGCTGCGGCT  GCCAAAGATT  ATATGAAAC  GGTGAGTTA  AACAACTCTG
251 CCGGCAATGT  CGATACCACA  TCCAGAACAG  CCGCAGGGT  GCAGGCAGTA
301 TTTCGACGTA  TGCTGCCTTA  TGCCGATGCG  GCAAATAATA  CCAGCCATAA
351 GTTTGACTGG  AAAATGACGG  TTTTCAAAA  CGATGAGCTG  AACCGTGCGG
401 CAATGCCCGG  TGGAAAAATG  GCGTTTTATA  CGGGGATAGT  CGACAACTC
451 AAGCTGACCG  ATGACGAAAT  TGCCGCCATT  ATGGGCGATG  AAATGACGCA
501 CGCCCTGCAT  GAACACGGTA  AAAATAAGGT  CGGGCAGCAA  ATCTTGACCA
551 ATACGGCGGC  GCAGATAGGC  ACGCAGATTA  TATTAGACAA  AAAACCGGAT
601 ACTAATCCGG  AATTGGTCGG  ATTGGGTATG  GATATTTTGG  GGACGTACGG
651 TCTTACCTTG  CTTATAGCC  GCAGCTTGA  AGAAGAAGCC  GATGAGGGGG
701 GAATGATGTT  GATGGCGCAG  GCAGGCTATC  ATCCGCGCGC  CGCTGTCAGG
751 GTTTGGGAAA  AAATGAATCA  GGAACACGAC  CAAAACGGCT  TTATTATATG
801 TATTACCTCT  ACTCATCCGA  CAAACAATGC  CCGTATAGAA  AATCTAAAC
851 GGTGTGTGCC  GACCGTTATG  CCGGTTTATG  AGCAAAGTGT  CAGAAATAAG
901 GGGCGCGTTA  ATAAAAACG  TCGCGGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```

m765.pep
1  MLRCRPKSVL  DSDGIFLKFN  FLRSKPKYEI  SFLPSFKRIL  CLSAVISVLG
51  ACAVVADVVG  HDSATMNAAA  AKDYMKTVEL  NKSAGNVDTT  SRTARRVQAV
101 FRRMLPYADA  ANNTSHKFDW  KMTVFKNDEL  NAWAMPGGKM  AFYTGIVDKL
151 KLTDEIAAI  MGHETHALH  EHGNKVGQQ  ILTNTAAQIG  TQILDKKPD
201 TNPELVGLM  DILGTYGLTL  PYSRLEEAA  DEGGMLMAQ  AGYHPAAVR
251 VWEKMNQEND  QNGFIYAITS  THPTNNARIE  NLKRLLEPTV  PVYEQSVRNK
301 GRVNNKRRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```

a765.seq
1  ATGTTAAGAT  GCCGTCCGAA  ATCCGTTTTG  GATTCAGACG  GCATTTTTTT
51  GAAATTTAAT  TTTTAAAGGA  GTAAACCTAA  ATATGAAATT  TCCTTCCTTC
101 CTTCCTTTAA  ACGGATACTC  TGCCTGTCGG  CAGTAATCTC  GGTATTGGGG
151 GCTTGTCGGG  TCGTTGCTGA  TGTTTACGGT  CAGGATCCG  CCACAATGAA
201 TGCTGCGGCT  GCCGAAGATT  ATATGAAAC  GGTGAGTTG  AACAACTCTG
251 CCGGCAATGT  CGATACTACA  TCCAAAACAG  CCGTAGGGT  GCAGGCAGTA
301 TTTCGACGTA  TGTTGCCTTA  TGCCGATGCG  GCAAATAATA  CCAGCCATAA
351 GTTTGACTGG  AAAATGACGG  TTTTCAAAA  CGATGAGCTG  AACCGTGCGG
401 CAATGCCCGG  CGGAAAAATG  GCGTTTTATA  CGGGGATAGT  CGATAAACTT
451 AAGCTGACCG  ATGGCGAAAT  TGCCGCCATT  ATGGGCGATG  AAATGACGCA
501 TGCCCTGCAT  GAACACGGTA  AAAATAAGGT  CGGGCAGAAA  ATCTTGACTA
551 ATATGGCGGC  GCAGATAGGC  ACGCAGATTA  TATTAGACAA  AAAACCGGAC
601 ACTAATCCGG  AATTGGTCGG  ATTGGGTATG  GATATTTTGG  GGATGTACGG
651 CATTACCTTG  CTTATAGCC  GCAGCTTGA  AGAAGAAGCC  GATGAGGGGG
701 GAATGATGTT  GATGGCGCAG  GCAGGCTATC  ATCCGCGCAG  CGCTGTCAGG
751 GTTTGGGAAA  AAATGAATCA  GGAACACGAC  CAAAACGGCT  TTATTATATG
801 TATTACCTCT  ACTCATCCGA  CAAACAATGC  CCGTATAGAA  AATCTAAAC
851 GGTGTGTGCC  GACCGTTATG  CCGGTTTATG  AGCACAGTGT  TAGAAATAAG
901 GGGCGCGTTA  ATAAAAACG  TCGCGGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```

a765.pep
1  MLRCRPKSVL  DSDGIFLKFN  FLRSKPKYEI  SFLPSFKRIL  CLSAVISVLG

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1246

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51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRMLPYADA ANNTGHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDEGIAAI MGHEMTHALH EHGKKNKVGQK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSL EEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAIT STHPTNNARIE NLKRLLPTVM PVYEH SVRNK
301 GRVKNRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

```

              10      20      30      40      50      60
m765.pep      MLRCRPKSVLDSGIFLKFNFLRSKPKYEISFLPSFKRILCLSAVISVLGACAVVADVYG
              |||||
a765           MLRCRPKSVLDSGIFLKFNFLRSKPKYEISFLPSFKRILCLSAVISVLGACTVVADVYG
              10      20      30      40      50      60

              70      80      90     100     110     120
m765.pep      HDSATMNAAAAKDYMKTVELNKSAGNVDTTSRTARRVQAVFRRMLPYADAANNTSHKFDW
              :|||
a765           QDSATMNAAAAKDYMKTVELNKSAGNVDTTSRTARRVQAVFRRMLPYADAANNTGHKFDW
              70      80      90     100     110     120

              130     140     150     160     170     180
m765.pep      KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDDEIAAIMGHEMTHALHEHGKKNKVGQQ
              |||||
a765           KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDGEIAAIMGHEMTHALHEHGKKNKVGQK
              130     140     150     160     170     180

              190     200     210     220     230     240
m765.pep      ILTNAAQIGTQIILDKKPDNTNPELVGLGMDILGTYGLTLPYSRSL EEEA DEGGMMLMAQ
              |||
a765           ILTNAAQIGTQIILDKKPDNTNPELVGLGMDILGMYGITL PYSRSL EEEA DEGGMMLMAQ
              190     200     210     220     230     240

              250     260     270     280     290     300
m765.pep      AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPTVMPVYEQSVRNK
              |||||
a765           AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPTVMPVYEH SVRNK
              250     260     270     280     290     300

              310
m765.pep      GRVKNKRRRX
              |||||
a765           GRVKNKRRRX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTG TGCGATAAAC
101 CCATTCCTCA AGAACAGCCG GGAAAAATTG AGGTTTGGA ATTTTCGGC
151 TATTTTTCG TACATTGCCA TCATTTCGAT CCTTGTGTTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCTG
301 GGTTCGAAAT ATCAGGCAAA CTCTGCTGTG TTAAAGCAG TTTACGAACA
351 AAAAATCCGT TTGGAACA GGGCTGTTGC CGGGAATGG GCTTTATCTC
401 AAAAAGGTTT TGACGGCAAA AAACGTATGC GCGCCTATGA TTCCCCCGAA
451 GCTGCCGCCG TCGCATTAAA AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAGAATT GGTGGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQP GKIEVLEFFG
51  YFCVCHHFD PLLKLKGLAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

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101 GLKYQANSV FKAUYEQKIR LENRAVAGKW ALSQKGFDDK KLMRAYDSPE
 151 AAAVALKMQK LTEQYGDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCTCTCA AGAACAGTCG GGTAATAATTG AGGTTTGTGA ATTTTTCGGC
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAACTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTTGAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CCGCTGCCGT CAATTGTCTG
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCTGTG TTTAAAGCAG TTTACGAACA
 351 AAAAATCCGC TTGGAACA GGTGGGTTGC CGGAAATGG GCTTTGTCTC
 401 AAAAAGGCTT TGACGGCAAA AAATGATGC GCGCTATGA TTCCCCCGAA
 451 GCTGCCCGCG CCGCATTAAT AATGCAGAAA CTGACGGAAC AATACCGCAT
 501 CGACAGCAGC CCGACCGTTA TTGTCCGCGG AAAATACCGC GTTATCTTCA
 551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAAGATT GGTGCCAAA
 601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep
 1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG
 51 YFCVHCHHFD PLLKLKGLAL PSDAYLRTEH VVWQPEMLGL ARMAAAVNLS
 101 GLKYQANPAV FKAUYEQKIR LENRSVAGKW ALSQKGFDDK KLMRAYDSPE
 151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLL SAVLSAQAYALTEGEDYLV LDKPIPQEQSGKIEVLEFFGYFCVHCHHFD					
m767	MKLKHLLPLL SAVLSAQAYALTEGEDYLV LDKPIPQEQSGKIEVLEFFGYFCVHCHHFD					
	10	20	30	40	50	60
g767.pep	PLLKLKGLALPSDYLRTHEVVWRPEMLGLARMAAAVKLSGLKYQANSVFKAUVEQKIR					
m767	PLLKLKGLALPSDAYLRTEHVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAUVEQKIR					
	70	80	90	100	110	120
g767.pep	PLLKLKGLALPSDYLRTHEVVWRPEMLGLARMAAAVKLSGLKYQANSVFKAUVEQKIR					
m767	PLLKLKGLALPSDAYLRTEHVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAUVEQKIR					
	70	80	90	100	110	120
g767.pep	LENRAVAGKWALSQKGFDDGKKLMRAYDSPEAAAVALKMQKLTEQYGDSTPTVIVGGKYR					
m767	LENRSVAGKWALSQKGFDDGKKLMRAYDSPEAAAAALKMQKLTEQYRIDSTPTVIVGGKYR					
	130	140	150	160	170	180
g767.pep	LENRAVAGKWALSQKGFDDGKKLMRAYDSPEAAAVALKMQKLTEQYGDSTPTVIVGGKYR					
m767	LENRSVAGKWALSQKGFDDGKKLMRAYDSPEAAAAALKMQKLTEQYRIDSTPTVIVGGKYR					
	130	140	150	160	170	180
g767.pep	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
	190	200	210			
g767.pep	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCTCTCA AAAACAGTCG GGCATAATTG AGGTTTGTGA ATTTTTCGGC
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAATTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGTTCTG GCAAGAATGG CTGCTGCCGT CAAGCTGTCA
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTTAAAGCAG TTTACGAACA
 351 AAAAATCCGC TTGGAACA GGTGGGTTGC CGAATAATGG GCTTTGTCTC
 401 AAAAAGGCTT TGACGGCAAA AAATGATGC GCGCTACGA CTCTCCTGCG

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451 GCAGCGGCTG CTGCATCAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAAGAATT GGTGCGCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
1  MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPKQOS GKIEVLEFFG
51  YFCVHCHHFD PLLLLKGKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
101 GLKYQANPAV FKAVYEQKIR LENRSVAEKW ALSQKGFDDG KLMRAYDSPA
151 AAAAAASKMQQ LTEQYRIDST PTVVVGKYYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

```

m767/a767 96.7% identity in 214 aa overlap

      10      20      30      40      50      60
a767.pep MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPKQSGKIEVLEFFGYFCVHCHHFD
m767      MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPKQSGKIEVLEFFGYFCVHCHHFD
      10      20      30      40      50      60

      70      80      90     100     110     120
a767.pep PLLLLKGKALPSDAYLRTEHVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVYEQKIR
m767      PLLLLKGKALPSDAYLRTEHVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVYEQKIR
      70      80      90     100     110     120

      130     140     150     160     170     180
a767.pep LENRSVAEKWALSQKGFDDGKLMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGKYYR
m767      LENRSVAGKWALSQKGFDDGKLMRAYDSPAAAAALKMQQLTEQYRIDSTPTVIVVGKYYR
      130     140     150     160     170     180

      190     200     210
a767.pep VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
m767      VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
      190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
1  ATGAATATCA AACAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCACGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTAGCGAA
151 GGTCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
201 CATATACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
301 TATACAAATG TTGCCAATCA CGCGGTTAT GAAGACCTGC TCAAAAAGG
351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
1  MNIKQLITAA LIASAAFATQ AAPQKPVSA QTAQHSAVVI DVRSEQEFSE
51  GHLHNAVNI PVDQIVRIYE AAPDKDTPVN LYCRSGRRAE AALQELKKA
101 YTNVANHGGY EDLLKGMK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
1  ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATCCGCG CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTAGCGAA
151 GGGCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC

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251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
 51 GHLLHNAVNI VDQIVRRIE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGKMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAALIASAAFATQAA	PQKPVSAQAQHS	AVWIDVRSEQEFSE	GHLLHNAVNI		
m768	MNIKHLITAALIASAAFAAQAA	PQKPVSAQAQHS	AVWIDVRSEQEFSE	GHLLHNAVNI		
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	VDQIVRRIE	AAPDKDTPVNLYCRSGRRAE	AALQELKKAG	YTNVANHGGY	EDLLKKGKMKX	
m768	VDQIVRRIE	AAPDKDTPVNLYCRSGRRAE	AALQELKKAG	YTNVANHGGY	EDLLKKGKMKX	
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCGC AAAAACCCTG ATCCGCGGCC CAAACCGCGC
 101 AACATTACAG CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCGC
 201 CATACACGAA GCCGCGCCCG ACAAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC
 301 TATACGAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSVWI DVRSEQEFSE
 51 GHLLHNAVNI VDQIVRRIE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGKMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAALIASAAFAAQAA	PQKPVSAQAQHS	AVWIDVRSEQEFSE	GHLLHNAVNI		
m768	MNIKHLITAALIASAAFAAQAA	PQKPVSAQAQHS	AVWIDVRSEQEFSE	GHLLHNAVNI		
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	VDQIVRRIE	AAPDKDTPVNLYCRSGRRAE	AALQELKKAG	YTNVANHGGY	EDLLKKGKMKX	
m768	VDQIVRRIE	AAPDKDTPVNLYCRSGRRAE	AALQELKKAG	YTNVANHGGY	EDLLKKGKMKX	
	70	80	90	100	110	120

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq

```

1 TTGATAATGG TTATTTTTTA TTTTATTTT TGTGGGAAGA CATTATGCC
51 TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 CCGAAGAaAC ACCgtgCGAA CCGGATTGTA GAAGCCGTCC CGAGTTCAGG
151 CTTTCATGAAG CCGAGGTCAA ACCGATCGAC AGGGAGAAGG TACCGGGGCA
201 GGTGCGGGAA AAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 AAAATCCCGA ATTGTTGTCT CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTACCTAC AACAGGCGCG
351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
401 AGGGCAGGGT GAAGGAGGCG GTTTCCTTTC ACCGGGAATT GATTGCCGCC
451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATGTGTTGA
501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
551 AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
601 TTGCGCGAAC GCGATGCGTG GAAGGTAAAC GCGGTTTCA GCGTTACCCG
651 CGAACACAAT ATCAACCAAG CCCCAGAAAC GCAGCAGTAC GGCAATTGGA
701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
751 GAGAAAAAAT GGTGCTGAA AACGGCTGG TACACGACGG CGGGCGGCGA
801 CGTGTCGGCG AGGGTTTATC CCGGGAATAA GAAATTCAAC GATATGACGG
851 CAGGTGTTTC CCGCGGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG
901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
951 CGCCACCGCG GCACGCTTT ATTTCAACCG TTGGCAAACC CCGAGATGGC
1001 AAACGCTGTC TTCGGCGGAG TGGGGCGGTT TGAAGAATAC CGCGCGGCGG
1051 CGTTCGGACA ATACCCATTT GCAAATTTCC AATTGCTGGG TGTTTTACCG
1101 GAATGCGCGC CAATATTGGA CCGGCGGTTT GGATTTTAC CGCGAGCGCA
1151 ACCCCGCCGA CCGTGGCGAC AATTCAACC GTTACGGCCT GCGCTTTGCC
1201 TGGGGGCAGG AATGGGGCGG CAGCGGCTG TCTTCGCTGT TCCGCTCGG
1251 CGTGGCGAAA CGGCATTATG AAAAACCCGG CTTCTTCAGC AGTTTTAAAG
1301 GGGAAAGCGC CAGGGATAAA GAATCGGACA CATCCTTGAG CCTTTGGCAC
1351 CGGGCATTGC ATTTCAAAGG CATCACGCCG CGCCTGACGC GTCGCACCGC
1401 CGAAACGTGG AGCAACGATG TGTTTAACGA ATACGAGAAA AACAGGCGCT
1451 TTGTCGAGTT TAACAAAACG TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep

```

1 LIMVIFYFYF CGKTFMPARN RWMLLPLLAS AAYAEETPCE PDLRSRPEFR
51 LHEAEVKPID REKVPQVRE KGKVLQVDGE TLLKNPELLS RAMYSAVVSN
101 NIAGIRVILP IYLLQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
151 QPDAPAVRMR LAAALFEDRO NEAAADQFDR LKTEDLPQOL MEQVELYRKA
201 LRERDAWKVN GGFSVTREHN INQAPKQQQY GNWTFPPQVD GTAVNYRFGA
251 EKKWSLKNW YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 LAVFHERRTY GNDAYSANG ARLYFNWQT PRWQTLSSAE WGRLEKNRRA
351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
401 WQGEWGGSL SSLFRLGVAK RHYEKPFFS SFGERRRDK ESDTSLSLWH
451 RALHFKGITP RLTLSHRETW SNOVFNEYEK NRAFEVFNKT F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq

```

1 TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCTGCACG
51 AAACAGATGG ATGCTGTGTC TGCTTTTATT GGCAGCGCGC GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CCGGGCAGGT
201 GCGGGAAAAA GGAAGAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GTTGTCCTCG CCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGCGG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTTACC GGAATTGAT TGCGGCCCAA
451 CCCGACGCGC CCGCCGTCCG TATGCGTTTG CCGGCAGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCTG AAGCGGAAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTGC AGCTGTACCG CAAGGCATTG
601 CCGGAACGCG ATGCGTGAA GGTAAATGGC GGCTTCAGCG TCACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG CGGCGCAGCT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CCGCATCGGT TTTGCCGACC GCGCGAAGA TGCCGGGCTG
901 GCAGTGTTC ACGAACGCC CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTCCAAT TCCTGCTGTG TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCAG GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCG CCGCCTGTCT TCCTGTTGCG GCCTCGGCGC

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1251

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1251 GGC GAAACGG CATTATGAAA AACCCGGCTT TTTCAGCGGT TTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCAG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCAGCA
1401 AACCGCGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

```

m769.pep
  1 LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLRSRPEFRL
 51 HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPOLM EQVELYRKAL
201 RERDAWKVNG GFSVTRHNI NQAPKQQYQ KWTFFPKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGGGSL SLLRLGAAKR HYEKPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

```

m769/g769 95.1% identity in 492 aa overlap

      10      20      30      40      50      59
g769.pep LIMVIFYFCGKTFMPARNRWMLL-PLLASAAYAEETPCEPDLRSRPEFRLHEAEVKPI
      |||
m769      LIMVIFY--FCGKTFMPARNRWMLLPLLASAAYAEETPREPDLRSRPEFRLHEAEVKPI
      |||
      10      20      30      40      50

      60      70      80      90      100     110     119
g769.pep DREKVPQVREKKGKVLQVDGETLLKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQD
      |||
m769      DREKVPQVREKKGKVLQIDGETLLKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQD
      |||
      60      70      80      90      100     110

      120     130     140     150     160     170     179
g769.pep KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAAALFEDRQNEAADQFD
      |||
m769      KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAADQFD
      |||
      120     130     140     150     160     170

      180     190     200     210     220     230     239
g769.pep RLKTEDLPPQLMQVELYRKALRERDAWKVNGGFSVTRHNIINQAPKQQYGNWTFPKQV
      |||
m769      RLKAENLPPQLMQVELYRKALRERDAWKVNGGFSVTRHNIINQAPKQQYKWTFFPKQV
      |||
      180     190     200     210     220     230

      240     250     260     270     280     290     299
g769.pep DGTAVNYRFGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV
      |||
m769      DGTAVNYRLGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA
      |||
      240     250     260     270     280     290

      300     310     320     330     340     350     359
g769.pep GLAVFHERRTYGNDAYSANGARLYFNWQTPRWQTLSSAEWGRLKNTRRARSNDNTHLQI
      |||
m769      GLAVFHERRTYGNDAYSYTNGARLYFNWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQI
      |||
      300     310     320     330     340     350

      360     370     380     390     400     410     419
g769.pep SNSLVFYRNARQYWTGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGGSLSLFLRGVA
      |||
m769      SNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGGSLSLRLGAA
      |||
      360     370     380     390     400     410

      420     430     440     450     460     470     479
g769.pep KRHYEKPGEFFSKGERRRDKESDTSLSLWHRALHFKGITPRLTLSHRETWSNDVFNEYE
      |||

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m769      KRHYEKPGFSGFKGERRRDKELNLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
           420      430      440      450      460      470

           480      490
g769.pep  KNRAFVEFNKTFX
           |||||
m769      KNRAFVEFNKTFX
           490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTT TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACC GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 GCGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCATTACC GGAATTGAT TGTCGCCCAA
451 CCCGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCGGCAT TGTTTAAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACGGG ATGCGTGGAA GGTAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GCGCGAAAGA TGCCGGGCTG
901 GCAGTGTTC ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGCGCGGT
1051 TCCGACAATA CCCATTGCA AATTTCGAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCAGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCGTTCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCCTGTCT TCGCTGTTGC GCCTCGGCGC
1251 GCGCAACCGG CATTATGAAA AACCCGGCTT TTTACGCGGT TTTAAAGGGG
1301 AAAGCGCGAG GGATAAGAAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCAGCA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGCTTG
1451 TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLLPLLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSVVVSN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVMRML AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTRHNI NQAPKROQYG KWTFFKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRDN FNRYGLRFAW
401 GQEWGGSGLS SLLRLGAAGR HYEKPGFSG FRGERRRDE LNTSLSLWHR
451 ALHFRGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

```

m769/a769  99.8% identity in 490 aa overlap

           10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTTFMPARNRWMLLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
           |||||
m769      LIMVIFYFCGKTTFMPARNRWMLLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
           10      20      30      40      50      60

           70      80      90      100     110     120
a769.pep  ERVPQVREKGVKVLQIDGETLLKNPELLSRAMYSVVVSNNIAGIRVILPIYLQQAQQDKM

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|||||
m769      EKVPGQVREKGVQLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM
          70      80      90      100     110     120

          130     140     150     160     170     180
a769.pep  LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
          |||||
m769      LALYAQGILAQADGRVKEAISHYRELIAAQPDAFAVRMRLAAALFENRQNEAAADQFDRL
          130     140     150     160     170     180

          190     200     210     220     230     240
a769.pep  KAENLPPQLMQVQLYRKALRERDAWKVNGGFSVTRHNNINQAPKROQYGKWTFFPKQVDG
          |||||
m769      KAENLPPQLMQVQLYRKALRERDAWKVNGGFSVTRHNNINQAPKROQYGKWTFFPKQVDG
          190     200     210     220     230     240

          250     260     270     280     290     300
a769.pep  TAVNYRLGAEEKKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
          |||||
m769      TAVNYRLGAEEKKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
          250     260     270     280     290     300

          310     320     330     340     350     360
a769.pep  AVFHERRTYGNDAISYTNGARLYFNRWQTPKWQTLSSAEWGRCLKNTRRARSNDNTHLQISN
          |||||
m769      AVFHERRTYGNDAISYTNGARLYFNRWQTPKWQTLSSAEWGRCLKNTRRARSNDNTHLQISN
          310     320     330     340     350     360

          370     380     390     400     410     420
a769.pep  SLVFYRNARQYWMGGLDFYREARNPADRGDNFNRYGLRFAWGQEWGGGSLSLRLGAAKR
          |||||
m769      SLVFYRNARQYWMGGLDFYREARNPADRGDNFNRYGLRFAWGQEWGGGSLSLRLGAAKR
          370     380     390     400     410     420

          430     440     450     460     470     480
a769.pep  HYEKPGFFSGFKGERRRDKEKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYEKN
          |||||
m769      HYEKPGFFSGFKGERRRDKEKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYEKN
          430     440     450     460     470     480

          490
a769.pep  RAFVEFNKTFX
          |||||
m769      RAFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCCG
51  CAGCGCGCAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTCGACGA TCCCACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCGC GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGC GTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCGTGCG CAAACCGAAA
301 GAAGTTTTC ACGCGGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTG GTTTACAGCG
401 ATAAATCGT CCAAGGATCG CCGAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCAGCG GCATACCGCA AACCGACGGG GTGCAAGCCG ATACTTCGGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTTC CAACCGATA AAAATCCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1  MNRLLLLSAA VLPTACSGSE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KGGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKRGTFEA FKSRIQVRY DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FGSGIPQTDG VQADTSGKLL AGACIIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCCG
51  CAGCGCGCAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

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101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACAACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCTCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

m770.pep

```

1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKS RQIVRY DPKRKT FAYL VYSDKIIQS PKNLSAVSC
151 FGGGIPQTDG VQADTSNLL AGACMISNPI ENLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

m770/g770 93.5% identity in 186 aa overlap

	10	20	30	40	50	60
g770.pep	MNRLLLLSAAVLPTACGSGETDKIGRASTVFNILGKNDR I EVEGFDDPDVQGVACYISYA					
m770	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDR I EVEGFDDPDVQGVACYISYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
g770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKKEVFKRGTFGFAFKSRQIVRY					
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKKEVFKHGASFAFKSRQIVRY					
	70	80	90	100	110	120
	130	140	150	160	170	180
g770.pep	DPKRKFAFAYLVYSDKIVQSGPKNLSAVSCFGSGIPQTDGVQADTSKLLAGACIISNPI					
m770	DPKRKTFAFAYLVYSDKIIQSGPKNLSAVSCFGGGIPQTDGVQADTSNLLAGACMISNPI					
	130	140	150	160	170	180
g770.pep	KNPDKRX					
	:					
m770	ENLDRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

a770.seq

```

1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51  CAGCGGGCAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACAACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCTCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

a770.pep

```

1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKS RQIVRY DPKRKT FAYL VYSDKIIQS PKNLSAVSC

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151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap.

	10	20	30	40	50	60
a770.pep	MNRLLLLSAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA					
m770	MNRLLLLSAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKVEFKHGASFAFKSRQIVRY					
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKVEFKHGASFAFKSRQIVRY					
	70	80	90	100	110	120
	130	140	150	160	170	180
a770.pep	DPKRRTFAYLVYSDKIIQGSFPKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
m770	DPKRRTFAYLVYSDKIIQGSFPKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
	130	140	150	160	170	180
a770.pep	ENPKRXX					
m770	ENLDRXX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

1	ATGGATTAT	TATCGGTTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTGGC
51	GGTGTGACG	ATGCTGCTT	TGGCGGCAGT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCACCT	CACGCCCGAA	AACATCCGCA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACCC	ACCGGAAAT	CTCGTTGAT	GCGGATATAC	GGCGCAGGCT
201	TCTGCCCCG	CCGACCGTCA	TCCTGAAAA	CCTGACCATT	ACCGAACCCG
251	ACGGCGGCCG	GGTCGCCGTT	TCCGTCAAAG	AAACCAAAAT	CGGATTGAGC
301	TGGAAAAACC	TGTGGTCGGA	TCGGATACAG	GTTGAAAAAT	GGGTGGTTTC
351	GGGTGCGGAT	CTTGCCCTGA	CGCGCGACAG	AAACGCGGCT	TGGAACATCC
401	AAGACCTGTT	CGACGGCGCG	AAACACTCCG	CCTCAGTCAA	CCGCATTATC
451	GTCGAAAACA	GCACCGTCCG	CCTCAATTC	CTGCAGCAAC	AGCTTATCCT
501	GAAGGAAATC	AGCCTCAACC	TGCAATCCCC	CGATTCTGCG	GGGCAGCAGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGGAGAA	AGCTGTCCGT	CCCGTGGAAA
601	AGCAGGGGGC	TGTTCCCTTC	AGACGGCATC	GGCAGCGCCG	AAATCTCACC
651	GTTCCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATCACCATT
701	CCACCACCGG	CAGCCCTTCT	GTCCGCTTCA	ACGCCGGCGG	AGCGGATGCC
751	GCCGGCCTCG	GCCTGCGTGC	AGACACTTCC	TTCCGCAACC	TCCACCTGAC
801	CGCGCAAAATC	CCCGCACTGG	CACTCAAAAA	CAACAGCATC	AAAACCGGCA
851	CGGTCAACGG	CACGTTTACC	GCCGGCGGCG	AATATGCCCG	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAAC	ACCGCGCCTT	CAAACCAATT
1001	TCTCCCTCGG	CTCGCCGTTG	GTTTGGAGTC	GGGACAACGG	GCTGGACGCC
1051	CCGCGCCTGC	ACATATCGAC	CCTTCAGGAT	ACCGTCGACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGCG	TCGACGGTTC	GCTGTCCATA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	ACCCGTGGCC
1201	GCAAAATTCA	AATATACGCG	GGAAGGCGCA	CCGCACCTGG	AAGCCGCCGC
1251	CGCGCTGCAA	AAATTAAACC	TCGCCCCCTA	TCTTGACGAA	TTTCGGCAAC
1301	AAAACGGCAA	AATATTCCCC	GACATCTCCG	GCAGGCTGTC	CGGCAACGTC
1351	GAGGCACACC	TCAAAATCGG	CAGCATCCAA	CTCCCCGGCT	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGACCATATC	GGGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAAACCCC	GTCCCGCCAC	TTACCGCTTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	TGCGGTCAATC	GACCTGACCG	CAAGCGGCGA	AAACCGCAAA
1651	CAGCTTATCC	GCTCGCTGCA	AGGCAGCCTG	TCGCTGAATA	TTTCCAACGG
1701	CGCGTGGCAC	GGCATCGATA	TGGACAGCAT	TTTAAAAAAC	GGCCTTTCCG

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1751 GGAAATCTC GGGCAGCACA CCCTTCTACC GATTACGCT CAACAGCGAA
1801 ATTTAGACG GCATCAGCCG CCACATCGAT ACCGAACTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CTTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCGATTA
2001 CGGCAGGCTG ACCGGCGGCA TCAATTCGCG CAAAGAGAAA CAGAAAATCC
2051 TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
3051 TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

g771.pep

```

1 MDLLSVFHKY RLKYAVAVLT MLLLAAVGLH ASVYRTFTPE NIRSRLQOSI
51 ANTHRKISFD ADIRRRLLPR PTVILKNLTI TEPDGGRVAV SVKETKIGLS
101 WKNLWSDRIQ VEKVVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRII
151 VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQOFESSGIL VWRKLSVPWK
201 SRGLFSLDGI GTPEISPFHF EASTSLDGHG ITISTTGSFS VRFNAGGADA
251 AGGLGLRADTS FRNLHLTAQI PALALKNNIS KTGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNLDA
351 PRHLISTLQD TVDRLPQPRF ISRLDGSLSI PNLQWNWAEI NGTFDRQPVA
401 AKFKYTRREGA PHLEAAAALO KLNLPYLDE FRQNGKIFP DILGRLSGNV
451 EHLKIGISIQ LPGLQLDDME TYLHADKDH IALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QONASNIQIQ PLLQDLFGFH SFGNGDAVI DLTASGENRK
551 QLIRSLQSSL SLNISNGAWH GIDMDSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHD TELFSDSLYV TSNGYTNLDT QELSEDVLR NAVHPKNKPI
651 PLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDLLE QWQWLKPKPE
701 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

m771.seq

```

1 ATGGATTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGCTGACG ATACTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCCTGA AACATCCGCA GCCGCCTACA ACAAGCATT
151 GCACACACAC ACCGAAAAT CTCGTTTGAT GCGGACATTC AGCGCAGGCT
201 CCTGCCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
251 GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGAAAAAATC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGGCGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAAACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAACA GCACCGTCCG CCTCAATTC CTGCAGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCTGTC GGGCAGCCGT
551 TTGAAAGTTC GGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC TGTTCTTTTC AAACGGCATC GGCCCGCCCG AAATCTCACC
651 GTTCCATTTC GAAGCTTCCA CTTGCTGGA CCGACACGGC ATTACCATTT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 CGCGGCCCTG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAATC CCCGCGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTATC GCCGGCGGCG AATATGCCCG ATGGGACGGT
901 TCCTTCAAA TCACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGGC
1051 CCGCGCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCGGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCCTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCT GACACCTCG CCAAGCTGTC CGCGGACATC
1351 GAGGCGCACC TGAATTCGG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC CGCTCAGCC
1451 GTTTCAAGTC AGGGCTTTAC GGCGGCCATA CCGAAGGCGG CATCAGCATC
1501 GCGAACACCC GTCCCGCCAC TTACCGCTG CAACAGAATG CAAGCAACAT
1551 CCAATCCAA CGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTATC GACCTGACCG CGGGCGGCGA AACCCGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCACCGG
1701 TGATATGGAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAACTGCG CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTACG
1801 CTCAACAGCG AAATTTTCTA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTCTCTCGAC AGCCTCTATG TTACAGCAAA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCAGC ACGGTGGACA AACCGTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTCC CGCAAAGAGA
2051 AACAGAAAAT CCTCGAAGAC ACCCTGCTGG AACAAATGGA GTGGCTCAAA
2101 CCTAAAGAAC CGTA

```

1257

This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

```
m771.pep
1  MDLLSVFHKY RLKYAVAVLT ILLLAAGVLH ASVYRTFTPE NIRSRLQOSI
51  ANTHRRKISFD ADIQRRLPR PTVILKNLTI TEPGGDQTAV SVQETKIGLS
101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFLSNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTV
401 AKFRYTHEDA PHEAAVALQ KNLTPYLDD VRQONGKIFP DTLAKLSGDI
451 EAHKIGKVQ LPLQLDDME TYLHADKGHI ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQGS LSNISGAWH GIDMDNLKN GISGKTADNA APSTPFHRT
601 LNSEISDGI RHIDTELFSD SLYVTSNGYT NLDTEQSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLEQWQWLK
701 PKEP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

```
m771/g771 90.3% identity in 704 aa overlap
              10      20      30      40      50      60
g771.pep MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLQOSIAHTRKISFD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQOSIAHTRKISFD
          10      20      30      40      50      60

              70      80      90      100     110     120
g771.pep ADIRRRLLPRPTVILKNLITITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWVSGAD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 ADIQRRLPRPTVILKNLITITEPGGDQTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE
          70      80      90      100     110     120

              130     140     150     160     170     180
g771.pep LALTRDRNGAWNIDLFDGAKHSASVNRIIVENSTVRLNLFQQLILKEISLNLQSPDSS
          |||||:|:|||||:|:|:|||||:|||||:|||||:|||||:|||||:
m771 LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNLFQQLILKEINLNLQSPDSS
          130     140     150     160     170     180

              190     200     210     220     230     240
g771.pep GQPFESSGILVWRKLSVPWKSRGLFLSDGIGTPEISPFHFEASTSLDGHGITISTTGSPS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 GQPFESSGILVWGLSVPWKSRGLFLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS
          190     200     210     220     230     240

              250     260     270     280     290     300
g771.pep VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGTFTAGGEYARWDG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG
          250     260     270     280     290     300

              310     320     330     340     350     360
g771.pep SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPVWSDNGLDAPRLHISTLQD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
          310     320     330     340     350     360

              370     380     390     400     410     420
g771.pep TVDRLPQPRFISRLDGSLSIPNLQNWNAELNGTFDRQPVAAKFKYTREGAPHLEAAALQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 TVNRLPQPRFISRLDGSLSVPLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
          370     380     390     400     410     420

              430     440     450     460     470     480
g771.pep KNLNAPYLDEFRRQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDHI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 KNLNTPYLDDVRQNGKIFPDTLAKLSGDI EAHKIGKVQLPGLQLDDMETYLHADKGHI
```

1258

	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771.pep	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNGLSGKISG---STPFYRFT					
m771	DLTAGGETRKLIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771.pep	LNSEISDGISRHIDTELFSDSLVYTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLVYTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

```

a771.seq
1  ATGGATTAT  TATCGGTCTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTAGC
51  CGTGCTGACG  ATACTGCTTT  TGGCGGCAAT  CGGGCTGCAC  GCTTCCGTAT
101 ATCGCATCTT  CACACCTGAA  AACATCCGAA  GCCGCCTCCA  ACAAGCATT
151 GCCCATACGC  ACCGGAATAA  CTCGTTTGAT  GCGGATATAC  AGCGCAGGCT
201 TCTGCCCCGG  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCCG
251 GCGGCGACCG  GACTGCCGTT  TCCGTCCAAG  AAACCAAAAT  CGGATTGAGC
301 TGGAAAAACC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351 GAGTCCGGAA  CTTGCCCTGA  CGCGCGACGG  GAAAGGTGTT  TGAACATCC
401 AAGACCTGAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATTATC
451 GTCGAAAACA  GCACCGTCCG  CCTCAATTTC  CTGCAGGAAC  AGCTTATCCT
501 GAAGGAAATC  AACCTCAACC  TGCAATCCCC  CGATTCTCG  GGGCAGCCGT
551 TTGAAAGTTC  GGGCATACTG  GTTTGGGGAA  AGCTGTCCGT  CCCGTGGAAA
601 AGCAGGGGGC  TGTTCCTTTC  AGACGGCATC  GGCACGCCCA  AAATCTCACC
651 GTTCCATTTT  GAAGCTTCCA  CTTGCGTGGA  CGGACACGGC  ATTACCATT
701 CCACGACCCG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751 GCGGCGCTCG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801 CGCCCAATC  CCTACGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851 CCGTCAACGG  CGCATTTACC  GCCGCGCGCG  AATATGCCCA  ATGGGACGGT
901 TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951 CAACGCCGAA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCAC  CAGACCAACT
1001 TCTCCCTCAA  TTCGCCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACGCG
1051 CCGCGCCTGT  ATGTATCGAC  CCTTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101 ACCCCGTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151 AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACGCCCA  AACCGTTGCC
1201 GCGAAATTCA  GATACACACA  TGAAGACGCA  CCGCATCTGG  AAGCCGCCGT
1251 CGCACTGCAA  AAATTGAACC  TGACCCCTCA  TCTTGACGAC  GTGCGGCAAC
1301 AAAACGGCAA  AATATTTCCC  GACACCTCG  CCAAGCTGTC  CGGCGACATC
1351 GAGGCGCAC  TGAAAATCGG  AAAAGTCCAA  CTTCCCGGCC  TGCAACTGGA
1401 CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGGCCATATC  GCGCTCAGCC
1451 GTTTCAGTGC  AGGGCTTTAC  GCGCGCCATA  CCGAAGGCGG  CATCAGCATC
1501 GCCAACACCC  GTCCCGCCAC  TTACCGCCTG  CAACAGAATG  CAAGCAACAT
1551 CCAAATCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601 GCAACGGCGA  CGCGGTCTAT  GACCTGACCG  GGGCGGCGGA  AACCAGAAAA
1651 GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGCTAAATA  TTTCCAACGG
1701 TGCATGGCAC  GGTATCGACA  TGGACAATAT  CCTGAAAAAC  GGCATTTCGG
1751 GCAAAACTGC  CGACAATGCC  GCACCCAGCA  CACCTTCCA  CCGATTACAG
1801 CTCACAGCG  AAATTTAGA  CGGCATCAGC  CGCCACATCG  ATACCGAACT
1851 CTTCTCCGAC  AGCCTCTATG  TTACCAGCAA  CGGCTATACC  AATCTGGATA
1901 CGCAGGAATT  GTCTGAAGAT  GTCTTATCC  GCAACGCCGT  CCATCCGAAA
1951 AACAAACCGA  TTCCCTGAA  AATCACCGGT  ACGGTGGACA  AACCGTCCAT
2001 TACCGTCGAT  TACGGCAGGC  TGACCGGCGG  CATCAATTCC  CGCAAAGAGA
2051 AACAGAAAA  CCTCGAAGAC  ACCCTGCTGG  AACATGGCA  GTGGCTCAAA
2101 CCTAAAGAAC  CGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

1259

a771.pep
 1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQQSI
 51 AHTRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
 101 WKNLWSDQIQ IEKVVVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
 151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
 201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
 251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTV
 401 AKFRYTHEDA PHLEAAVALQ KNLNTPYLDD VRQNGKIFP DTLAKLSGDI
 451 EAHKIGKVQ LPGLQLDDME TYLHADKGGHI ALSRFKSGLY GGHTGGISI
 501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
 551 ELIRSLQGS SLNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
 601 LNSEISDGIS RHIDTELFSD SLVYTSNGYT NLDTOELSED VLIRNAVHPK
 651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK
 701 PKEP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

	10	20	30	40	50	60
a771.pep	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPE	NIRSRLQQSI	AHTRKISFD			
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPE	NIRSRLQQSI	AHTRKISFD			
	10	20	30	40	50	60
	70	80	90	100	110	120
a771.pep	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLS	WKNLWSDQIQIEKVVVSSAE				
m771	ADIQRRLPRPTVILKNLTITEPGGDQTA	SVQETKIGLSWKNLWSDQIQIEKVVVSSAE				
	70	80	90	100	110	120
	130	140	150	160	170	180
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLN	FLQEQILKEINLNLQSPDSS				
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLN	FLQEQILKEINLNLQSPDSS				
	130	140	150	160	170	180
	190	200	210	220	230	240
a771.pep	GQPFESSGILVWGKLSVPWKS	RGLFLSDGIGTPKISPFHFEASTSLDGHG	ITISTTGSPS			
m771	GQPFESSGILVWGKLSVPWKS	RGLFLSNGIGPPEISPFHFEASTSLDGHG	ITISTTGSPS			
	190	200	210	220	230	240
	250	260	270	280	290	300
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTLALRNNSI	KIETVNGAFTAGGEYAQWDG				
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSI	KIETVNGAFTAGGEYARWDG				
	250	260	270	280	290	300
	310	320	330	340	350	360
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPL	VWTENKGLDAPRLYVSTLQD				
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPL	VWTENKGLDAPRLYVSTLQD				
	310	320	330	340	350	360
	370	380	390	400	410	420
a771.pep	TVNRLPQPRFISRLDGSLSV	PNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ				
m771	TVNRLPQPRFISRLDGSLSV	PNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ				
	370	380	390	400	410	420
	430	440	450	460	470	480
a771.pep	KNLNTPYLDDVRQNGKIFPDTLAKLSGDI	EAHLKIGKVQLPGLQLDDMETYLHADKGGHI				
m771	KNLNTPYLDDVRQNGKIFPDTLAKLSGDI	EAHLKIGKVQLPGLQLDDMETYLHADKGGHI				
	430	440	450	460	470	480

1260

	490	500	510	520	530	540
a771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKEILIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRET					
m771	DLTAGGETRKEILIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRET					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKPEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKPEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

g772.seq

1	GTGTTTCGGCA	CGGTCTTGCG	GAATGATGCC	GAATGCCTGC	AAATCATCGT
51	CGTCGGCAAG	TTCTTTCAGG	TTGTTGCGTA	TGGTTTTGCG	CGCTTGGCGG
101	AAGGCGAGTT	TCACGAGTTT	GGCGAAATGA	TCGAAATCGT	CCGCCTTGCC
151	GATACGGTGT	TTCAACGGAA	TCATGCGCAC	CACTGCGGAA	TCGATTTTCG
201	CGCGGGGATC	GAACGATTCG	GGCGGCACGT	CAATCAGCAG	CTCCATATCG
251	AAAAAATATT	GCAGCATCAC	ACCCAAGCGA	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATGCGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCAAT
351	CGCGGACATC	GTCCGCCACC	TCCGCCAGTT	TGAACAAAAG	CGGCGTGAG
401	ATGTTATACG	GCAGGTTGCC	GACGATTTTC	TTTTTGCTG	AGATGCCGTT
451	GAATCAAAC	TGCAACACGT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTCGAT	TTGCAACAAC
551	TGCGGCGGTT	TCAGCTTTTT	CGCCAAAGGT	TCGTAATTCG	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA
651	CAATATCGCT	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC
701	TTGCGGGGCT	TGTGTTCTTT	CATCGTGTTC	CCTCTTCGCT	TGAACCCCG
751	CCCTTTAGGG	CGGCAGGATC	AGACTCTGTT	TGGGCGGGGC	GTAACCCCTT
801	CCAAATCAGG	ACGACACATA	GGCGGTGCT	TTATGTGTCG	TCCTGTGTGT
851	TGGAACATAA	ATGTGTTTAC	AGTATCCGTT	TGATGTCGGC	ATTGTAA

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

g772.pep

1	VFGTVLRTDA	DCLQIIVVGK	FFQVVAYGFA	ALAEGEFHQF	GEMIEIVRLA
51	DTVFHRNHAH	HCGIDFRRGI	ERFGRHVNOQ	LHIEKILQHH	TQATVVVAFR
101	RGNHALDHFF	LQHKVHIGDI	VRHLRQFEQK	RRGDVIRQVA	DDFLFA*DAV
151	EIKLQHVAFV	NHQFIRKRQR	FQTAYDVAVD	FDNVOAVQLF	RQRFGNCRQT
201	RADFNHDIIR	LRAHGVDNIA	DNPRVLQKIL	PETLAGFVFF	HRVSSSVETP
251	PFRAAGSDSV	WAGRNPFQIR	TTHRAVLYVS	SCVLEHRCVY	SIRLSMSAL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

m772.seq

1	ATGTTTCGGCG	CGGTCTTGCG	GATTGATGCC	GAATGCCTGC	AAATCATCGT
51	CGCCTGCAAG	CTCTTTCAGA	TTGTTGCGTA	TGGTTTTGCG	CGCTTGGTGG
101	AAGGCGAGTT	TCACGAGTTT	GGCAAAATGC	TCGAAATCGT	CCGCCTTGCC
151	GATGCGGTGT	TTCAACGGAA	TCATACGGAC	GACGGCGGAA	TCCACTTTCG
201	CGCGAGGGTC	GAACGATTCG	GGCGGTACGT	CAATCAGCAT	TTCCATATCG
251	AAAAAATATT	GCAGCATCAC	GCCCAAGCGG	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATACGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCAAT
351	CGACGACATC	GTCCGCCACC	TCCGCCAGCT	TGAACAAAAG	CGGTGTGGAA
401	ATGTTGTACG	GGAGGTTGCC	GACGATTTTC	TTTTTGCTG	CGATGCCGTT
451	GAATCAAAC	TGCAATACAT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTCGAT	TTGCAACAAC
551	TGCGGCGGTT	TCAGCTTTTT	CGCCAAAGGT	TCGTAATTCG	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA
651	CAATATCGCT	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC

1261

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701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

```

m772.pep
1  MFGAVLRIDA DCLQIIVACK LFIQIVAYGFA ALVEGEFHEF GKMLEIVRLA
51  DAVFHRNHTD DGGIHFRRRV ERFGRYVNOH FHIEKILQHH AQAQVVAFR
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEQK RCGNVVREVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RADFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLVVS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

m772/g772 85.2% identity in 298 aa overlap

	10	20	30	40	50	60
g772.pep	VFGTVLRTDADCLQIIVVGKFFQVVA	YGFALAEGEFHQFGEMIEIVRLADTVFHRNHAH				
m772	MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD					
	10	20	30	40	50	60
g772.pep	HCGIDFRRGIERFGRHVNQQLHIEKILQHHTQATVVVAFRRGNHALDHFFLQHKVHIGDI					
m772	DGGIHFRRRVERFGRYVNOHFHIEKILQHHAAQAAVVVAFRRGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
g772.pep	VRHLRQFEQKRRGDVIRQVADDFLAFXDAVEIKLQHVAFVNHQFIRKQRQFQTAYDVAVD					
m772	VRHLRQLEQKRCGNVVREVADDFLFACDAVEIKLQYIAFVNHQFIRKQRQFQTAYDVAVD					
	130	140	150	160	170	180
g772.pep	FDNVQAVQLFRQRFGNCRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
m772	FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
g772.pep	HRVSSSVETPPFRAAGSDSVWAGRNPFQIRTTTHRAVLVSSCVLEHKCVYSIRLMSALX					
m772	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLVSSCVLKHKCVYSIRLMSALX					
	250	260	270	280	290	299

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

```

a772.seq
1  ATGTTCCGGC CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51  CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGGTTTTCGG GCGTTGGTGG
101 AAGCGGAGTT TCACGAGTTT GGCGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGGCCGAA TCCACTTTCG
201 GCGCGGGGTC GAACGATTTC GCGGCGACGT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGCAGCATA AAGTGCAATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGTTGCC GACGATTTTC TTTTGCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTCAGACGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGACCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAATTCTG CCCGAAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ACGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

1262

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

```
a772.pep
  1  MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GEMLEIVRLA
 51  DTVFHRNHAD DGRIFHRRGV ERFGRHVNOH FHIEEILQHH AQAQVVVAFR
101  RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGVVVGQVA DDFLFACDAV
151  EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGRNRQT
201  RTDFNNDIIR LRAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251  PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

```
m772/a772 95.6% identity in 298 aa overlap

      10      20      30      40      50      60
a772.pep MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD
m772     MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHAD
      10      20      30      40      50      60

      70      80      90     100     110     120
a772.pep DGRIFHRRGVVERFGRHVNOHFHIEEILQHHAAQAAVVVAFRRGNHTIDHFFLQHKVHIDDI
m772     DGGIHFRRRVERFGRYVNOHFHIEKILQHHAAQAAVVVAFRRGNHTLDHFFLQHKVHIDDI
      70      80      90     100     110     120

      130     140     150     160     170     180
a772.pep VRHLRQLEQKRRGNVVGQVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD
m772     VRHLRQLEQKRCGNVVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD
      130     140     150     160     170     180

      190     200     210     220     230     240
a772.pep FDNVQAVQLFRQRFGRNRQTRTDFNNDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF
m772     FDNVQAVQLFRQRFGRNRQTRADFNNDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF
      190     200     210     220     230     240

      250     260     270     280     290     299
a772.pep HRVSFSVETPPFRAVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX
m772     HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRVLYVSSCVLKHKCVYSIRLMSALX
      250     260     270     280     290
```

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

```
m773.seq
  1  ATGGGATTGG GTGCAACGAC TTTGTGCGGT TCGGGTGCTA TAGGCGGAGG
 51  TCTGTGCAGT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101  CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATTG
151  TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201  TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAACTAG
251  CCGTATGGGG ATTGGAAACG CTGATTACGC GCAAATTGGG AAAGTTGGCA
301  ACGGGTGTGA AAAGTTCCCT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351  TATCCTGTCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
401  GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGGCTT GTCTGCCAAT
451  GCAAGGTTAC CTAAAAATTT TAAAACATTT GATTATTTTG ATCGTGGTAC
501  AGGCACGGCA ATCAGTGCCA AAAGTTCTGA TACGCAAACT ACGGCACGCC
551  TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601  ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
651  CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCGCA CAACTAATA
701  AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751  AACATTACAG TCAAAATTAC GGAGATCGAA TAA
```

1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
  1  MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TOASEGSRQL
 51  FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA
101  TGVKTSITPK TADVQRNLS QSEVGKWK GIEGQGPWE DYVGKGLSAN
151  ARLPKNFKTF DYFDRGTGTA ISAKTLDTQT TARLSKEQL YSTMKGVIDK
201  TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEQRLQL QRVVEYGKSO
251  NITVKITEIE *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
  1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
 51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101  CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151  GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201  GGAAATGTTA AACGGGAAAG TCAAAGCATT GGAGCATACG AAAATACACC
251  CTTCCGGCAG GACATACGTC CAAAACCTCG ACGACCGCAA ATTGAAAGAG
301  CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC
351  CGCACAAAAC CTCTACAATC AGGCACTCAA AACTATCAA AACGGCAGGT
401  TTTCTGCCGC AGCCGCCCTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451  AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAGCA GGGCGCGTAT
501  GGGGAACCTG GAATCTGTCA TCGAAATCGG AGGCGGTTAC GCCAACCGTT
551  TCAAAGACAG CCCAACCGCG CCCGAAGTCA TATTCAAAT CCGCGAATGC
601  CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GCGCGAGCCT
651  GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701  TACGCAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
  1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTOENASD GIPYPVPTLQ
 51  DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRITYV QKLDRLKE
101  HYLNTGEGSA SAHTVETAQN LYNQALKHYQ NGRFSAAL LKGADGGDGG
151  SIAQRSMYLL LQSRARMGNC ESVEIGGRY ANRFKDSPTA PEVIFKIGEC
201  QYRLQOKDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
  1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCGCCCTC
 51  CTGTGCTTCC GTTTTACCCG TTCCGGCAGG CAGCCAAACC GAAATGTCGA
101  CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151  GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201  GGAAACCTTA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT
251  CTTCCGGCAG GGCATACGTC CAAAACCTCG ACGACCGCAA GTTGAAGAG
301  CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTCGAAAC
351  CGCACAAAAC CTCTACAATC AGGCACTCAA AACTATAAA AGCGGCAAGT
401  TTTCTGCCGC TGCTCCCTG TTGAAGGGCG CGGACGGAGG CGACGGCGGC
451  AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAGCA GGGCGCGTAT
501  GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGCGGTTAC GCCAACCGTT
551  TCAAAGACAG CCCAACCGCG CCTGAAGCCA TGTTCAAAAT CCGCGAATGC
601  CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GCGCGAGCCT
651  GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701  TCGCAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
  1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
 51  DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDRLKE
101  HYLNTGEGSA SAHTVETAQN LYNQALKHYK SGKFSAAAL LKGADGGDGG
151  SIAQRSMYLL LQSRARMGNC ESVEIGGRY ANRFKDSPTA PEAMFKIGEC
201  QYRLQOKDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFIIWLSVSASCASVLPVPEGSRT	EMPTQENASDGIPYPVPTLQDRDL	DYLEGKI			
m774	MKIKLPLFIIWLSVSASCASVSPV	PAGSQTEMSTRENASDGIPYPVPTLQDRDL	DYLEGKI			
	10	20	30	40	50	60
g774.pep	VRLSNEVEMLNGKVKALEHTKIHPSGR	TYVQKLD	DRKLKEHYLNTEGGSASAHTVETAQN			
m774	VRLSNEVETLNGKVKALEHAKTHSSG	RAYVQKLD	DRKLKEHYLNTEGGSASAHTVETAQN			
	70	80	90	100	110	120
g774.pep	LYNQALKHYQNGRFSAAAALLKGADGGD	GGG	SIQRSMYLLQSRARMGN	CESVIEIGGRY		
m774	LYNQALKHYKSGKFSAAAALLKGADGGD	GGG	SIQRSMYLLQSRARMGN	CESVIEIGGRY		
	130	140	150	160	170	180
g774.pep	ANRFKDSPTAPEVIFKIGECQYRLQ	QKDIARATWRS	LIQTYPGSPA	KRAAAAVRKR		
m774	ANRFKDSPTAPEAMFKIGECQYRLQ	QKDIARATWRS	LIQTYPGSPA	KRAAAAVRKR		
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

1	ATGAAGACCA	AATTACCGCT	TTTATCATT	TGGCTGTCCG	TATCCGCCGC
51	CTGTTCTTCC	CCTGTTTCCC	GCAATATTCA	GGATATGCGG	CTCGAACCGC
101	AGGCAGAGGC	AGGTAGTTCG	GACGCTATTC	CCTATCCCGT	TCCCACTCTG
151	CAAGACCGTT	TGGATTATCT	GGAAGGCACA	CTCGTCCGCC	TGTCGAACGA
201	AGTGGAAACC	TTAAACGGCA	AAGTCAAAGC	ACTGGAGCAT	GCGAAAACAC
251	ACCCTTCCAG	CAGGGCATA	GTCCAAAAC	TCGACGACCG	CAAGTTGAAA
301	GAGCATTACC	TCAATACCGA	AGGCGGCAGC	GCATCCGCAC	ATACCGTCGA
351	AACCGCACAA	AACCTCTACA	ATCAGGCACT	CAAACACTAT	AAAAGCGGCA
401	GGTTTCTG	CGCTGCCTCC	CTGTTGAAAG	GCGCGGACGG	AGGCGACGGC
451	GGCAGCATCG	CGCAACGCAG	TATGTACCTG	TTGCTGCAAA	GCAGGGCGCG
501	TATGGGCAAC	TGCGAATCCG	TCATCGAAAT	CGGAGGGCGT	TACGCCAACC
551	GTTTCAAAGA	CAGCCCAACC	GCGCCTGAAG	CCATGTTCAA	AATCGGCGAA
601	TGCCAATACA	GGCTTCAGCA	AAAAGACATT	GCAAGGGCGA	CTTGGCGCAG
651	CCTGATACAG	ACCTATCCCG	GCAGCCCGGC	GGCAAAACGC	GCCGCCGCAG
701	CCGTGCGCAA	ACGATAG			

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

1	MKTKLPLFII	WLSVSACSS	PVSRNIQDMR	LEPQAEAGSS	DAIPYPVPTL
51	QDRLDYLEGT	LVRLSNEVET	LNGKVKALEH	AKTHPSSRAY	VQKLD
101	DRKLKEHYLN	TEGGSASAHT	VETAQN	LYNQALKHY	KSGRFSAAA
151	LLKGADGGDG	GSIAQRSMYL	LLQSRARMGN	CESVIEIGGR	YANRFKDSPT
201	APEAMFKIGE	CQYRLQKDI	ARATWRS	LIQTYPGSPA	KRAAAAVRKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKTKLPLFIIWLSVSACSSPVSRNIQDMR	LEPQAEAGSSDAIPYPVPTLQDRDL	DYLEGT			
m774	MKIKLPLFIIWLSVSASCASVSPV	PAGSQTEMSTRENASDGIPYPVPTLQDRDL	DYLEGK			
	10	20	30	40	50	

1265

```

              70      80      90      100      110      120
a774.pep      LVRLSNEVELNGKVKALEHAKTHPSSRAYVQKLDLDRKLEHYLNTEGGSSAHTVETAQ
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774          IVRLSNEVELNGKVKALEHAKTHSSGRAYVQKLDLDRKLEHYLNTEGGSSAHTVETAQ
              60      70      80      90      100      110

              130      140      150      160      170      180
a774.pep      NLYNQALKHYKSGRFSAAASLLKGADGGDGGGSIQSRMYLLQSRARMGNCSVIEIGGR
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774          NLYNQALKHYKSGKFSAAASLLKGADGGDGGGSIQSRMYLLQSRARMGNCSVIEIGGR
              120      130      140      150      160      170

              190      200      210      220      230      239
a774.pep      YANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARKRAAAVRKRX
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774          YANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARKRAAAVRKRX
              180      190      200      210      220      230

```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```

m790.seq
1   ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAGTC CTTAACGATG TCCAAGGCGA TACGACCATC AACAAACCATC
401 ATACGCATAC GCACAACAC AGCGATGCCG ATGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCG
551 CCCCCTCGCA GTACACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGAGA CTTGCTGGTG GTCGAGCCGC GTATGTCGCC
651 TCGCGACGAA GACATCGCGC TGATTGAACT GTCCGACAAG CGGCTGGTCTG
701 TCGCGCACCT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
751 GGCAGGCCGT CTGAAGCCTT TGACCTGCCC GAAGGCAGCA CGATTTTAGG
801 TGTGGTGCTG GAGTCAAAAA ACGGTTTATG TCCGCGCAC AGGCAAGAAG
851 GCGTGTTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTATGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

```

m790.pep
1   MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSIV LNDVQGDTTI NNHHTHTNH SDADGKALSM
151 RLTPRPLLSL RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMCPADE DIALIELSDK RLVVAHLVID IAGRMILIYQT
251 GRPSEAFDLP EGSTILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGMI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```

a790.seq
1   ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATATAT CTTAACGATG TCCAAGGCGA TACGACCATC AACAAACCATC
401 ATACGCATAC GCACAACAC AGCGATGCCG ACGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCG
551 CCCCCTCACA ATATACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGTCGCC
651 TCGCGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTCTG
701 TCGCGCACCT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG

```

1266

```

751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGTCT GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTGAT TCGGATTACC GCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTCGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
  1 MARRSKTFEE AAAEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRSR
  51 YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
 101 ITTQAYNEMT KSVAGSNSII LNDVQGDTTI NNHHTHTHNN SDADGKALSM
 151 RLTPRPLLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
 201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID IAGRMLIYQT
 251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
 301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

```

a790/m790 98.2% identity in 342 aa overlap

      10      20      30      40      50      60
a790.pep MARRSKTFEEAAAEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW
          |||
m790     MARRSKTFEEAAAEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW
          |||

      10      20      30      40      50      60

      70      80      90     100     110     120
a790.pep GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSII
          |||
m790     GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSIV
          |||

      70      80      90     100     110     120

      130     140     150     160     170     180
a790.pep LNDVQGDTTINNHHHTHNNHSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA
          |||
m790     LNDVQGDTTINNHHHTHNNHSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA
          |||

      130     140     150     160     170     180

      190     200     210     220     230     240
a790.pep SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMRPADE DIVLIELSDKRLVVAHLVID
          |||
m790     SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMCPADE DIALIELSDKRLVVAHLVID
          |||

      190     200     210     220     230     240

      250     260     270     280     290     300
a790.pep IAGRMLIYQTGRPSEALDLP EGSVILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGTI
          |||
m790     IAGRMLIYQTGRPSEAFDLPEGSTILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGMI
          |||

      250     260     270     280     290     300

      310     320     330     340
a790.pep SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
          |||
m790     SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAX
          |||

      310     320     330     340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
  1 ATGTTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTA CTGTTT
  51 TGGTTTGGTT TTTGGTTTGT GTGTATTTGG AGTGGGCTCG GTTGCCATTG
 101 CTATTTTGGT AACGTATCCG AAACGCGCGT CTTTGGATTC TTTGCAGCAT
 151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GAGAAGTCAT
 201 CCGTATGTAT GGGGAGCAGC GGCGCGAATT TACAAAAATC GGCGATTTC
 251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
 301 CCGCATTGGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGGCAA
 351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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1267

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401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCCGCAA ATCTATTCA ATAAGAATGT CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCCAAG CTCGCTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAACT GCATTATGAG CGGTTTGTTT GGAATAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCGATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTGCAT CGCGGCAGCA GCTACCGCGG TCGGAAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCATAAAAT GGTTCGCCCC GTTGTGTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTGCGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGAG CGGTCGATAA TGAGAAAATG
1201 GGGGAGGACC GTATCCGCAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CGCGCTCCAC AGTGGTTAAC GATGCGCGGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GGCAGGAGCA TATAGTGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTCTCGC ACGTGATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAAATG CAACCTTTGG TGGCAGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGTTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAACG ACAATAAAGA
2001 TCGTGGTTT GTCGGTTTAA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGCTACGG CGGTACGATT
2101 CGGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAAATGC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

```

g791.pep
1 MVNYYSAMIK KILTTFCGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLQG RAYGFASAAQ IYFNKNVRDL
201 TLAEAAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFKYVTTV
301 RTDHRKAATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMPPA VVLDVTKKKK VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPQLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRAGYGGTI
701 AVFVWVDYMR FALKGKQGGK MKMPEGVVSS NGEYYMKERM VTDPLMLDN
751 SGIAPQPSRR AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

```

m791.seq
1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTTT GTGTATTGAG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAAGTCCCGT CTTGGATTTC TTTGACGAT
151 TACCAGCCTA AAATGCCGTT GACTATTAT TCAGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGCAATT TACAAAAATC GGCATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGTGGATGTT TTTGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

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1268

```

451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC AATCAGATTTA CCTCGGTGAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC AATAAGATGT CCGAGATTG
601 ACTTTGCGCG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAGT GCATTACGAG CGGTTTGTTT GGAAATCGA
801 TCAGAGTGCG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TGCGGAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCAGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTTACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAG GATGCGCCGA TTTCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGCG TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTCTCGC ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAATG CAACCTTTGG TGGCTGGGCA
1851 AATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCATATAT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACCGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTAA ACCCTGATGT GGTTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGC CTGAAGGTGT GGTACGACG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGCGCGA TGACGAAGTC CGCCAAGATA
2351 TGAGGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

m791.pep

```

1  MNVYYSAMIK KILTTTCFGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWG ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTKRF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMPVA VVLDVTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGWR AVVQEPLLQG ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVNV DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGVAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVT A VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVSS NGEYMKERM VTDPLGLDN
751 SGIAPQPSRR AKEDDGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

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g791/m791 97.3% identity in 805 aa overlap

```

          10      20      30      40      50      60
g791.pep  MNVYYSAMIKKILTTTCFGLFFGFCVFGVGLVAIAAILVTYPKLPSLDSLQHYQPKMPLTIY
          |||
m791      MNVYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAAILVTYPKLPSLDSLQHYQPKMPLTIY
          10      20      30      40      50      60

          70      80      90      100     110     120
g791.pep  SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVVDVWGVARAAVGNVVS
          |||
m791      SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVVDVWGVARAAVGNVVS
          70      80      90      100     110     120

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1269

	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAAGLGLPKAPSAYNPIVNPERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAGLGLPKAPSAYNPIVNPERAKLRQKYILNNMLE					
	190	200	210	220	230	240
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKEYGEDAYTQGFVKVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKEYGEDAYTQGFVKVYTTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFDRGSSYRGAENYIDLKSKSEDVEETVSQYLSGLYTVDKMPVA					
m791	RADHOKVATEALRKALRNFDRGSSYRGAENYIDLKSKSEDVEETVSQYLSGLYTVDKMPVA					
	310	320	330	340	350	360
	370	380	390	400	410	420
g791.pep	VVLDVTKKKNVVIQLPGGRRVALDRLALGFAARAVDNEKMGEDRIIRGAVIRVKNNGGRW					
m791	VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIIRGAVIRVKNNGGRW					
	370	380	390	400	410	420
	430	440	450	460	470	480
g791.pep	AVVQEPQLLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPQLLQALGSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
	550	560	570	580	590	600
g791.pep	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
	610	620	630	640	650	660
g791.pep	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
m791	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
	610	620	630	640	650	660
	670	680	690	700	710	720
g791.pep	TTNDNKDAWFGFNPVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKGKQKG					
m791	TTNDNKDAWFGFNPVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKGKQKG					
	670	680	690	700	710	720
	730	740	750	760	770	780
g791.pep	MKMPEGVVSSNGEYYMKERMVTDPLGLDLSGIAQPSSRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVVSSNGEYYMKERMVTDPLGLDLSGIAQPSSRAKEDDGGAAEGGRQAADDEV					
	730	740	750	760	770	780
	790	800				
g791.pep	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```

1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51  TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AACTGCCGT CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTAT TCGGCGGATG GGGAAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GGCATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGT GCGCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCTTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC ATAAGATGT CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCGCTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCCGCGAT
751 CAGGCGTTGA ATGAGGAAC GCATTACGAG CGGTTTGTTC GGAANAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACCGTGA AGATGCCTAT ACGCAGGTT TTAAGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CGCGGCAGCA GCTACCGCGG TCGGGAATG TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCG GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CCGCAGCGCG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCGCG CGGTCAATAA TGAANAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACACCGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAGGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTCTCGC ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCAAATG CAACCTTGG TGCCCGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGG AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCG TAAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGACC GTATATATCG
2051 GCTTCAGCAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTACGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC GGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAAGAG ATGACGGGGG
2301 CGCGGAGAAA GCGGACGGC AGCGGCGGGA TGACGAAGTC GCGCAAGATA
2351 TGCAGGAAAC GCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep

```

1  MVNYYSAMIK KILTTCEGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEORREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTKRF
151 NEVLLAYKIE QLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVROE LYEKYGEDAY TQGFVKYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMPPA VVLDVTKKKK VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIIRGAV IRVKNNGGRW AVVOEPLLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIIT LRQALTASKN MVSIRILMSI GVGYAQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR YSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNP QAIIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGQKGG MKMPEGVVSS NGEYMKERM VTDPLGLTLDN
751 SGIAPQPSRR AKEDDGGAEE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

a791/m791 99.9% identity in 805 aa overlap

10 20 30 40 50 60

1271

a791.pep	MVNYYSAMIKKILTTCFGLVFGFCVFGVGLVAIAILVITYPKLPSLDSLQHYQPKMPLTIY
m791	MVNYYSAMIKKILTTCFGLVFGFCVFGVGLVAIAILVITYPKLPSLDSLQHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
m791	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
m791	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
m791	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
m791	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
m791	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
m791	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
m791	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
m791	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
m791	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
m791	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
m791	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
m791	730 740 750 760 770 780

1272

	730	740	750	760	770	780
	790	800				
a791.pep	RQDMQETPVLPSNTGSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX	790	800			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

```

1  ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCCTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTGT
251 CCggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGGAAAGAGC GGCATTACG GCAATGATGG AAGCTGTTC CGACAAAAAC
451 AGGATTTTCG AACTGTATTT AACTCAATC GAATGGCACT ACGGCGtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAACCG GCcgcaGACC
551 TGACcAAACA GCAGgcggcG aaactgacgg tactcgtccc cgccccgttt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcattgggt cgccaaatta ccccaaacg aaacggactg
701 attgttcag atatggaat gccgcctgaa ctggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

```

1  MFRIVKWLIA LPVGIFIFFN AYVYGNIIY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVEGAE AASRYFYKPP AADLTQQAA KLTVLVPAPF
201 YYSDHPKSKR LRNKTNIVLR RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

```

1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCCTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAAAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCCTTTTCG
251 CCGGGCAGCG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTTC CGACAAAGAC
451 AGGATTTTTC AACTGTATTT AACTCAATC GAATGGCACT ACGGCGTTTT
501 CGGCGCGGAA GCCGCGTCCC GGTATTTTTA TCAAATACCC CGCGCCAAGC
551 TGACCAACA GCAGGCGGCA AACTGACGG CGCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAAA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

```

1  MFRIIKWLIA LPVGIFIFFN AYVYGNIIY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIONAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVEGAE AASRYFYQIP AAKLTQQAA KLTARVPAPL
201 YYADHPKSKR LRNKTNIVLK RMGSAELPES DTD*

```

g792 / m792 90.4% identity in 230 aa overlap

	10	20	30	40	50	60
g792.pep	MFRIVKWLIALPVGIFIFFNAYVYGNIIYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
m792	MFRIIKWLIALPVGIFIFFNAYVYGNIIYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
	10	20	30	40	50	60
	70	80	90	100	110	120
g792.pep	WVPYNRISTNLKKALIASD	VRFAGHGGFD	GDGIQNAIRRN	NRNSGEVKAG	GSTISQQLAK	

[illegible]

```

a792.seq
1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCGTATTGTT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCGCTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCATC GGATTACGCG TGGATTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCTTGATTGC TTCGAAGAT GCCCGTTTCG
251 CGGGGACGCG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATACGGCGC
301 AACCGBAACA GCGGCAAAAT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAA AACTGTTTTT TAAACGAAG CCGCAGCTAT ATCCGCCAAG
401 GCGGAAGAAG GCGGATTACC CGGATGATGG AACCGCTTAC CGACAAGAAC
451 AGGATTTTTG AACTGTATTT AAACCTAATC GAATGGCACT ACGGCGTTTT
501 CGGCGGGGAA GCGCGTCTCC GGTATTTTTA TCAAAATACC GCCGCCAAGC
551 TGACCAAAAC CGAGGCGGCA AACTGACGG CGCGCGTCCC CGCCCGCTCG
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCGCAACA AAACCAATAT
651 CGTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC CATACGGACT
701 GA

```

a792.pep

1	MFRIIKWLIA	LPVGIFIFFN	AYVYGNIIY	RAVAPHRTAF	MSMRMKQFEQ
51	EGRDVALDYR	WMPYKRISTN	LKKALIASED	ARFAGHGDFD	WGGIQNAIFR
101	NRNSGKVKAG	GSTISQQLAK	NLFLNESRSY	IRKGEEAAIT	AMMEAVTDKD
151	RFELYLNSI	EWHYGVFGAE	AASRYFQIP	AAKLTKQQA	KLTAIVPAPL
201	YYADHPKSKR	LRKNTINVL	RMGSAAELPS	DTD*	

	10	20	30	40	50	60
a792.pep	MFRIIKWLIALPVGIFIFFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQEGRD	VALDYR			
m792	MFRIIKWLIALPVGIFIFFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQEGRD	VALDYR			
	10	20	30	40	50	60
	70	80	90	100	110	120
a792.pep	WMPYKRISTNLKKALIASEDARFAGHG	GGFDWGGIQNAIRNRNRNSGKVAGGS	TISQQLAK			
m792	WMPYKRISTNLKKALIASEDARFAGHG	GGFDWGGIQNAIRNRNRNSGKVAGGS	TISQQLAK			
	70	80	90	100	110	120
	130	140	150	160	170	180
a792.pep	NLFLNESRSYIRKGEEAAITAMMEAVT	DKDRIFELYLNSIEWHYGVFGAEAA	SRYFYQIP			
m792	NLFLNESRSYIRKGEEAAITAMMEAVT	DKDRIFELYLNSIEWHYGVFGAEAA	SRYFYQIP			
	130	140	150	160	170	180
	190	200	210	220	230	
a792.pep	AAKLTQQAAKLTARVPAPLYADHPKSK	RLRNKTNIVLRRMGSAELPESD	TDX			
m792	AAKLTQQAAKLTARVPAPLYADHPKSK	RLRNKTNIVLRRMGSAELPESD	TDX			
	190	200	210	220	230	

q793.seq

1274

```

1  ATGTTGATTA  AAAGCGAATA  TAAGCCCCGG  ATGCTGCCCA  AAGAAGAGCA
51  GGTCAAAAAG  CCGATGACCA  GTAACGGACG  GATTAGCTTC  GTCCTGATGG
101 CAATGGCGGT  CTTGTTTGCC  TGTCTGATTG  CCCGCGGGCT  GTATCTGCAG
151 ACGGTAACGT  ATAACCTTTT  GAAAGAACAG  GCGGACAACC  GGATTGTGCG
201 GACTCAAGCA  TTGCCGGCTA  CACGCGGTAC  GGTTCGGAC  CGGAACGGTG
251 CGGTTTTTGG  GTTGAGCGCG  CCGACGGAGT  CCCTGTTTGC  CGTGCCCTAAA
301 GATATGAAGG  AAATGCCGTC  TGCCGCCCAA  TTGGAACGCC  TGTCCGAGCT
351 TGTGCGATGT  CCGGTCGATG  TTTTGAGGAA  CAAACTCGAA  CAGAAAGGCA
401 AGTCGTTTAT  TTGGATCAAG  CGGCAGCTCG  ATCCCAAGGT  TGCCGAAGAG
451 GTCAAAAGCCT  TGGGTTTGGA  AAACCTTTGA  TTTGAAAAAG  AATTAAAACG
501 CCATTACCCG  ATGGGCAACC  TGTTGCACA  CGTCATCGGA  TTTACCGATA
551 TTGACGGCAA  AGGTCAGGAA  GGTTTGGAAC  TTTGCGTTGA  AGACAGCCTG
601 TATGGCGAAG  ACGGCGCGGA  AGTTGTTTGG  CGGGACCGGC  AGGGCAATAT
651 TGTGGACAGC  TTGGACTCCC  CGCGCAATAA  AGCACCGCAA  AACGGCAAAG
701 ACATCATCCT  TTCCCTCGAT  CAGAGGATTC  AGACCTTGGC  CTATGAAGAG
751 TTGAACAAGG  CCGTCAATA  CCATCAGGCA  AAAGCCGGAA  CGGTGGTGGT
801 TTTGGATGCC  CGCACGGGGG  AAATCCTCGC  CTTGGCCAAT  ACGCCCGCCT
851 ACCATCCCAA  CAGACCCGGC  CGGGCAGACA  GCGAACAGCG  GCGCAACCGT
901 CCGGTAACCG  ATATGATCGA  ACCTGGTTCG  GCAATCAAAC  CGTTGCGTAT
951 TGCGAAGGCA  TTGGATGCGG  GCAAAACCGA  TTTGAACGAA  CGGCTGAATA
1001 CGCAGCCTTA  TAAATCCGGA  CCGTCTCCCG  TGCGCGATGA  TACCCATGTT
1051 TACCCCTCTT  TGGATGTGCG  CGGCATTATG  CAGAAATCGT  CCAACGTCGG
1101 CACAAGCAAA  CTGCTGCGC  GTTTCGGCGC  CGAAGAAATG  TATGACTTCT
1151 ATCATGAATT  GGGCATCGGT  GTGCGTATGC  ACTCGGGCTT  TCCGGGGGAA
1201 ACTGCAGGTT  TGTGTAGAAA  TTGGCGCAGG  TGGCGGGCCA  TCGAACAGGC
1251 GACGATGTCT  TTCGGTTACG  GTCTGCAATT  GAGCCTGCTG  CAATTGGCGC
1301 GCGCCTATAC  CGCACTGACG  CACGACGGCG  TTTTGCTGCC  GCTCAGCTTT
1351 GAGAAGCAGG  CGGTTGCCCC  GCAAGGCAAA  CGCATATTCA  AAGAATCGAC
1401 CCGCGCGCAG  GTACGCAATC  TGATGGTTTC  CGTAACCGAG  CCGGGCGGCA
1451 CCGGTACGGC  GGGTGGCGTG  GACGTTTCG  ATGTCGGCGC  TAAAACCGGC
1501 ACGGCGCGCA  AGTTCGTCAA  CGGGCGTTAT  GCCGACAACA  AACACGTCGC
1551 TACCTTTATC  GGTTTTGCCC  CCGCAAAAAA  CCCCCTGTGT  ATTGTGGCGG
1601 TAACCATCGA  CGAACCGACT  GCCCACGGCT  ATTACGGCGG  CGTAGTGGCA
1651 GGGCCGCCCT  TCAAAAAAAT  TATGGGCGGC  AGCCTGAACA  TCTTGGGCAT
1701 TTCCCGGACC  AAGCCACTGA  CCGCGCGAGC  CGTCAAAACA  CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

```

g793.pep
1  MLIKSEYKPR  MLPKEEQVKK  PMTSNGRISF  VLMAMAVLFA  CLIARGLYLQ
51  TVTYNFKLEQ  GDNRIVRTQA  LPATRGTVSD  RNGAVLALSA  PTESLFAVPK
101 DMKEMPSAAQ  LERLSELVDV  PVDVLRNKLE  QKGKSFIIWK  RQLDPKVAEE
151 VKALGLENFV  FEKELKRHYP  MGNLFAHVIG  FTDIDGKQGE  GLELSLEDSL
201 YGEDGAIEVVL  RDRQGNIVDS  LDSPRNKAPQ  NGKDIILSLD  QRIOTLAYEE
251 LNKAVEYHQA  KAGTVVVLDA  RTGEILALAN  TPAYDPNRPQ  RADSEQRNR
301 AVTDMIEPGS  AIKPFVIAKA  LDAGKTDLNE  RLNTQPKYIG  PSPVRDDTHV
351 YPSLDVRGIM  QKSSNVGTSK  LSARFGAEEM  YDFYHELIG  VRMHSGFPGE
401 TAGLLRNWRR  WRPIEQATMS  FGYGLQLSL  QLARAYTALT  HDGVLLPLSF
451 EKQAVAPQ GK  RIFKESTARE  VRNLMVSVTE  PGGTGTAGAV  DGFDVGAFTG
501 TARKFVNGRY  ADNKHVATFI  GFAPAKNPRV  IVAVTIDEPT  AHGYYGGVVA
551 GPPFKRIMGG  SLNILGISPT  KPLTAAAVKT  PS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

```

m793.seq
1  ATGTTGATTA  AGAGCGAATA  TAAGCCTCGG  ATGCTGCCCA  AAGAAGAGCA
51  GGTCAAAAAG  CCGATGACCA  GTAACGGACG  GATCAGCTTC  GTCCTGATGG
101 CAATAGCGGT  CTTGTTTGCC  GGTCTGATTG  CTCGCGGACT  GTATCTGCAG
151 ACGGTAACGT  ATAACCTTTT  GAAAGAACAG  GCGGACAACC  GGATTGTGCG
201 GACTCAAAAC  TTGCCGGCTA  CACGCGGTAC  GGTTCGGAC  CGGAACGGTG
251 CGGTTTTTGG  GTTGAGTGCG  CCGACGGAGT  CCCTGTTTGC  CGTGCCCTAAA
301 GAGATGAAGG  AAATGCCGTC  TGCCGCACAA  TTGGAACGCC  TGTCCGAGCT
351 TGTGCGATGT  CCGGTTGATG  TTTTGAGGAA  CAAGCTCGAA  CAGAAAGGCA
401 AGTCGTTTAT  CTGGATTAA  CGGCAGCTCG  ATCCCAAGGT  TGCCGAAGAG
451 GTCAAAAGCCT  TGGGTTTGGA  AAACCTTTGA  TTTGAAAAAG  AATTAAAACG
501 CCATTACCCG  ATGGGCAACC  TGTTGCACA  CGTCATCGGA  TTTACCGATA
551 TTGACGGCAA  AGGTCAGGAA  GGTTTGGAAC  TTTGCGTTGA  AGACAGCCTG
601 CATGGCGAAG  ACGGCGCGGA  AGTCGTTTGG  CGGGACCGGC  AGGGCAATAT
651 TGTGGACAGC  TTGGACTCCC  CGCGCAATAA  AGCCCCGAAA  AACGGCAAAG
701 ACATCATCCT  TTCCCTCGAT  CAGAGGATTC  AGACCTTGGC  CTATGAAGAG
751 TTGAACAAGG  CCGTCAATA  CCATCAGGCA  AAAGCCGGAA  CGGTGGTGGT
801 TTTGGATGCC  CGCACGGGGG  AAATCCTCGC  CTTGGCCAAT  ACGCCCGCCT
851 ACATCCCAA  CAGGCCCGGC  CGGGCAGACA  GCGAACAGCG  GCGCAACCGT
901 GCGGTAACCG  ATATGATCGA  ACCCGGTTTC  GCAATCAAAC  CGTTTGTGAT
951 TGCGAAGGCA  TTGGATGCGG  GCAAAACCGA  TTTGAACGAA  CGGCTGAATA

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1275

```

1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACCTCGGCAC
1101 AAGCAAACGT TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCCGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCGACCG
1451 GTACGCGGGG TCGGCTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCCGT TTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCGGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

```

m793.pep
1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNLFKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKFSFIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYPMGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPKIG PVPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRRW RPIEQATMSF GYGLQLSLLQ LARAYTALTH DGVLLPVSE
451 KQAVAPQGKR IFKESTAREV RNLMVSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGCVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*

```

g793/m793 98.5% identity in 582 aa overlap

```

g793.pep      10      20      30      40      50      60
MLIKSEYKPRMLPKEEQVKKPMTSNGRISFVLMAIAVLFACLIARGLYLQTVTYNLFKEQ
|||||
m793          10      20      30      40      50      60
MLIKSEYKPRMLPKEEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNLFKEQ
|||||

g793.pep      70      80      90     100     110     120
GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVPKDMKEMPSAAQLERLSELVDV
|||||
m793          70      80      90     100     110     120
GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV
|||||

g793.pep     130     140     150     160     170     180
PVDVLRNKLEQKGKFSFIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG
|||||
m793         130     140     150     160     170     180
PVDVLRNKLEQKGKFSFIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG
|||||

g793.pep     190     200     210     220     230     240
FTDIDGKGQEGLELSLEDSLYGEDGAEVVLDRQGNIVDSLDSPRNKAPQNGKDIILSLD
|||||
m793         190     200     210     220     230     240
FTDIDGKGQEGLELSLEDSLHGEDGAEVVLDRQGNIVDSLDSPRNKAPKNGKDIILSLD
|||||

g793.pep     250     260     270     280     290     300
QRIQTLAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR
|||||
m793         250     260     270     280     290     300
QRIQTLAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR
|||||

g793.pep     310     320     330     340     350     360
AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKIGPSPVRDTHVYPSLDVRGIM
|||||
m793         310     320     330     340     350
AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKIGPSPVRD-THVYPSLDVRGIM
|||||

g793.pep     370     380     390     400     410     420
QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMS
|||||
m793         360     370     380     390     400     410
QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMS
|||||

```


1276

```

          430      440      450      460      470      480
g793.pep    FGYGLQLSLLQLARAYTALTHDGVLLPLSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE
            |||
m793        FGYGLQLSLLQLARAYTALTHDGVLLPLSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE
          420      430      440      450      460      470

          490      500      510      520      530      540
g793.pep    PGGTGTAGAVDGFVDGAKTGTARKFVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
            |||
m793        PGGTGTAGAVDGFVDGAKTGTARKFVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          480      490      500      510      520      530

          550      560      570      580
g793.pep    AHGYYGGVVAGPPFFKIMGGSNLILGISPTKPLTAAAVKTPSX
            |||
m793        AHGYYGGVVAGPPFFKIMGGSNLILGISPTKPLTAAAVKTPSX
          540      550      560      570      580

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

```

a793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCCGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAACA TTGCCGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTTGATG TTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AAACTTTGT TTTGAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGAAC TTTGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTGG CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGAATCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGACCAAGG CCGTCAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 CCGTAAACCG ATATGATCGA ACCCGTTTCG GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAATG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCCTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCGCA AGGCAAACGC ATATCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GGCGGCACCG
1451 GTACGGCGGG TGCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGGCGAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGCGCT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```

a793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQT LPATRGTVSD RRGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYP MGNLFHIVIG FTDIDGRQOE GLELSLEDSL
201 HGEDGAEEVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPG RADSEQRRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFEHELIGIV RMHSGFPGET
401 AGLLRNRRW RPTEQATMSF GYGLQLSLLQ LARAYTALTH DGVLLPVSE
451 KQAVAPQGKR IFKESTAREV RNLMVSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYYGGVVAG
551 PPFFKIMGGS LNILGISPTK PLTAAAVKTP S*

```

a793/m793 100.0% identity in 581 aa overlap

1277

a793.pep	10	20	30	40	50	60
	MLIKSEYKPRMLPKKEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
m793	MLIKSEYKPRMLPKKEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
	10	20	30	40	50	60
a793.pep	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
a793.pep	130	140	150	160	170	180
	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
m793	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
	130	140	150	160	170	180
a793.pep	190	200	210	220	230	240
	FTDIDGKGQEGLELSLEDSLHGEGDAEVVLRDRQGNIVDSLDSPRNKAPKNGKDIIISLD					
m793	FTDIDGKGQEGLELSLEDSLHGEGDAEVVLRDRQGNIVDSLDSPRNKAPKNGKDIIISLD					
	190	200	210	220	230	240
a793.pep	250	260	270	280	290	300
	QRIQTLAYEELNKAVEYHQAAGTGVVLDARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQAAGTGVVLDARTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
a793.pep	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVRDTHVYPSLDVRGIMQ					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVRDTHVYPSLDVRGIMQ					
	310	320	330	340	350	360
a793.pep	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFFGETAGLLRNWRRWRPIEQATMSF					
m793	KSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFFGETAGLLRNWRRWRPIEQATMSF					
	370	380	390	400	410	420
a793.pep	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALHDGVLLPVSFQAVAPQGGKRIFKESTAREVRNLMVSVTEP					
m793	GYGLQLSLLQLARAYTALHDGVLLPVSFQAVAPQGGKRIFKESTAREVRNLMVSVTEP					
	430	440	450	460	470	480
a793.pep	490	500	510	520	530	540
	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
	490	500	510	520	530	540
a793.pep	550	560	570	580		
	HGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
m793	HGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

1	gtgcgtttca	ATCATTTCAT	AATGGTAACG	ATTATTATAT	ATGTGATTTT
51	CCCTGCAAAC	AAGCCGGTCC	GCCGCCCGG	CGTCCCACT	TATCCGGCTT
101	TGCCTTATAA	TTGCTTTTTT	TATGTAACAG	ATTCACCTAT	GAATTTCCCC
151	AAAACAGCGG	CCTCCCTGCT	GCTGCTTCTC	GCCTCCCTCG	CCGCACACGC
201	GCTCGATACC	GGCCGCATTC	CGCAAAACGA	AATCGCTGTA	TATGTCCAAG
251	AGCTTGACAG	CGGAAAAGTC	ATCATTGACC	ACCGTGCCGG	CATACCCGTC
301	AATCCCGCGT	CCACGATGAA	GCTCGTTACC	GCGTTTGCCG	CCTTCAAAC
351	CTTCGGCAGC	AATTACCGCT	GGGCGACCGA	GTTTAAAGC	AACGGTACGG
401	TAAACGACGG	CACGCTTGAC	GGAAACCTGT	ATTGGGCGGG	CAGCGGCAGC
451	CCCGTTTCA	ATCAGGAAA	CCTGCTTGCC	GTCCAACGCC	AGTTGCGCGA
501	CAAAGGCATC	CGCAATATCA	CGGGGCGCCT	GATGCTCGAC	CACAGCCTGT

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551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAAATCC GACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGGCGCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTGCGTCAA AAAACTGATG CGGCATCTT TTTGCGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCGCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGCGGCGAC GGCAACTGC CCGCGTTTC
1101 CGAACAGCGC GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCACAAATG TTGGAACGG CTTATTTTCA
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCGGCGGCG
1501 GACGCGTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

```

g794.pep
1  VRENHFIMVT IIIYVISPAN KPVRRPGVPT YPALPYNCFF YVTDSPMNF
51  KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFES NGTVNDGTLT GNLWAGSGD
151 PVFNQENLLA VORQLRDKGI RNITGRMLLD HSLWGEVSP DHFEADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVMFMA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAOTLAVAH SKPMKEILD MNKRSNLLIA
351 RSVFLKLGDD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMAQM LETAYFSPFA QDFIDTLPIA GTDGLTRNRF KQSGGLLRK
451 TGTLNNVRAL AGYWLGDKEP AVVVIINSGR AVSLLPDLN FVAKNIISGG
501 DGWLDKLMC KERRA*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

```

m794.seq
1  GTGCGTCTCA ATCATTTTCA TATGATAGCG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAGACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAATC ATCATTGACC ACCGCTCGGA TGTCCCCGTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CTTCAAAAC
351 CTTGCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTAT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGAT GCTCAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCATATCA CGGGACACCT GATGCTCGAC CAGACCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTTC AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAACTGATG CGTGCATCTT TTTGCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCGG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGCGGCGAC GGCAACTGC CCGCGTTTC
1101 CGAACAGCGC GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGCTGTGC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCACAAATG TTGGAACGG CTTATTTTCA
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTTAC CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TCGTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGGCGGCG
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

```

m794.pep
1  VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51  KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV

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1279

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101 NPASTMKLVT AFAAFKTFGS NYRWATEFES NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLD AQKQLREQGI LNTIGHLMLE HSLWGEVGSF DDFEADSGSP
201 FMTFPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSNTLKL LRGNIPESEL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSDNLIA
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLTRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDKLMC KERRA*

g794/m794 95.5% identity in 515 aa overlap

      10      20      30      40      50      60
g794.pep VRFNHFIMVTIIIVISPAKPVRRPGVPTYPALPYNCFYVTDSPMNFPKTAASLLLLL
m794      VRLNHFIMIAIIIVISPAKPARHRSVPTYPALPYNCFYVTDLPMMNFPKTAASLLLLL
      10      20      30      40      50      60
g794.pep ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFAAFKTFGS
m794      ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
      70      80      90      100     110     120
g794.pep ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
m794      ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
      70      80      90      100     110     120
g794.pep NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRLRDKGIRNITGRMLLD
m794      NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQKQLREQGIILNITGHMLLD
      130     140     150     160     170     180
g794.pep NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRLRDKGIRNITGRMLLD
m794      NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQKQLREQGIILNITGHMLLD
      130     140     150     160     170     180
g794.pep HSLWGEVGSFDDFEADSGSPFMTFPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
m794      HSLWGEVGSFDDFEADSGSPFMTFPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
      190     200     210     220     230     240
g794.pep HSLWGEVGSFDDFEADSGSPFMTFPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
m794      HSLWGEVGSFDDFEADSGSPFMTFPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
      190     200     210     220     230     240
g794.pep QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
m794      QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
      250     260     270     280     290     300
g794.pep QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
m794      QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
      250     260     270     280     290     300
g794.pep NRWLLGGGRISDGIGIADTPGAQTLAVAHAKPMKEILTMNKRSDNLIARSVFLKLGGD
m794      NHWLLGGGRISDGIGIADTPGAQTLAVAHAKPMKEILTMNKRSDNLIARSVFLKLGGD
      310     320     330     340     350     360
g794.pep NRWLLGGGRISDGIGIADTPGAQTLAVAHAKPMKEILTMNKRSDNLIARSVFLKLGGD
m794      NHWLLGGGRISDGIGIADTPGAQTLAVAHAKPMKEILTMNKRSDNLIARSVFLKLGGD
      310     320     330     340     350     360
g794.pep GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVARTARMAQMLETAYFSPFA
m794      GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVARTARMAQMLETAYFSPFA
      370     380     390     400     410     420
g794.pep GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVARTARMAQMLETAYFSPFA
m794      GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVARTARMAQMLETAYFSPFA
      370     380     390     400     410     420
g794.pep QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKTGTLNNVRALAGYWLGDKPMVAVVVIINSGR
m794      QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKTGTLNNVRALAGYWLGDKPMVAVVVIINSGR
      430     440     450     460     470     480
g794.pep QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKTGTLNNVRALAGYWLGDKPMVAVVVIINSGR
m794      QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKTGTLNNVRALAGYWLGDKPMVAVVVIINSGR
      430     440     450     460     470     480
g794.pep AVSLLPDLNDFVAKNIISGGDGWLDKLMCKERRAX
m794      AVSLLPDLNDFVANNIISGGDGWLDKLMCKERRAX
      490     500     510

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

```

a794.seq
1  GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCTCAT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACA GGTCCGATTC CGCAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCCGTC

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1280

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301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTCGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCGGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGGCCGA TATTTTCGCC AAAACAACCT TGAATAATAC CGCCTCCCAA
751 GCTGCCGTGC CTTCGATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGAAGCCTG
851 TCGGTGTCGG GATGTTTCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCCG GAAGGCGCGC AGACGCTTGC CGTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAACCT CGGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCA GCGTCTGCCG TCCGGCGTGA ACTTGGCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAACCGTT CAGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCAATG TTGGAACGG CTTATTTTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGTGGGCGCA
1401 CAACCGCATG GCGGTGGTCG TCATCATCAA CAGCGGCGCG CCGGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGGCGGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

a794.pep

```
1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51 KTAASLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRSDVPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLG GNLWAGSGD
151 PVFNQENLLA VQRQLREQGI RNITGHLMLD HSLWGEVGSF DDFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILTD MNKRSNLI
351 RSVFLKLGDD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENSGSLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLPLDLN FVANNIISGG
501 DGWLDKLMC KERRA*
```

a794/m794 98.6% identity in 515 aa overlap

	10	20	30	40	50	60
a794.pep	VRLNHFIMIAIIIYVISPAN	KPARRHSVPTYPALPYNCFF	YVTDLPMNFPKTAAS	LLLL		
m794	VRLNHFIMIAIIIYVISPAN	KPARRHSVPTYPALPYNCFF	YVTDLPMNFPKTAAS	LLLL		
	70	80	90	100	110	120
a794.pep	ASLAHALDTGRIPONEIAV	YVQELDSGKVIIDHRSDVPV	NPASTMKLVTAF	AFAFKTFGS		
m794	ASLAHALDTGRIPONEIAV	YVQELDSGKVIIDHRSDVPV	NPASTMKLVTAF	AFAFKTFGS		
	130	140	150	160	170	180
a794.pep	NYRWATEFKSNGTVNDGTL	DGNLYWAGSGDPVFNQENLL	AVQRQLREQGIR	NITGHLMLD		
m794	NYRWATEFKSNGTVNDGTL	DGNLYWAGSGDPVFNQENLL	DAQQLREQGIL	NITGHLMLD		
	190	200	210	220	230	240
a794.pep	HSLWGEVGSPPDDFEADSG	SFMTPPNPTMLSAGMVMVRAE	RNAADSTDILTDPPLPHIFA			
m794	HSLWGEVGSPPDDFEADSG	SFMTPPNPTMLSAGMVMVRAE	RNAAGSTDILTDPPLPHIFA			
	250	260	270	280	290	300
a794.pep	QNNLKITASQAACPSIKKLM	RASFSDNTLKLRGNIPESCL	GKPVGVRMFALDELIRQSFT			
m794	QNNLKITASQAACPSIKKLM	RASFSDNTLKLRGNIPESCL	GKPVGVRMFALDELIRQSFT			
	310	320	330	340	350	360
a794.pep	NHWLLGGGRISDGIGISDTP	EGAQTLAVAHSKPMKEILTD	MNKRSNLIARSVFLKGGD			

g900.seq

g900.pcp

m900.seq

1 ATGCCGCTCTG AAACGCGGCA GCGGAGGTT CGACGGCAT CGGGTTTCATT
51 TCAACGGGCG GATGcGCACC GCATcG. TA CTTTGTCCAA TAATTGCGGT
101 GCTTCTTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTGATTTCG

1282

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151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CCGCGTTGAT TTTCGCCGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATCCACC GTTTCAGACG GCGTGGAGAA
301 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATTT TTGGGTTTTT
401 tTGTCGTTTT CCCAAAGCGG AATGTGTTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CGGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTGAAGCG GCCGGCGATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTGG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCTGCCCC GTTTTCTGCA
701 TTTGCCTGCA CGGCGGCTTT GTAGGCATGG CCGCGGTTCA TCAAACCTT
751 GGCAGTGATG CAGGTCAGAA TCCAGTTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTGAGTCC GCAGCgAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
901 GCATTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTCCGTAT
951 CGAGGTTTTG CGCCGCGCGG ACGGCGGGG GATGCGGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCGGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

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This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

```

m900.pep
  1 MPSETRQAEV RTASGSFORA DADRIXVFVQ *FACFFTRFR RACLQNLFDL
 51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPR NGVAVGFGHF
151 ASVQTDQEFV VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTEIRVFLP VFCICLHGGF VGMGAVHQTL
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHRLRV
301 AFDDTVVIGE EEEGFGIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QOTFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

```

m900/g900

      10      20      30      40      50
m900.pep  MPSETRQAEVRTASGSFORADADRIXVFVQX*FACFFTRFRACLQNLFDLRRVGGQ
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900      MPSEMPSETWQAEVRTALGLFORADADRIAYFIQQFARFFARFLRACLQNLFDLRRIRGQ
          10      20      30      40      50      60

      60      70      80      90     100     110
m900.pep  LVVAFARFGEFGVDFFRRQKFFGFTPRQAVGKHFRKFHRFRRRGEFGVDFKQWAFVGLFRL
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900      CVVAFQAQFCQFGVDFFRRKFFRLAPSAVAGKHLRKFRFRRRRGEFGFIDFKQRAVGLFRL
          70      80      90     100     110     120

      120     130     140     150     160     170
m900.pep  ARLFHIGDDFVDRFLGFFVVFPRKNGVAVGFGHFASVQTDQEFDFVDFHFGQGEFPEA
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900      ARLFHVGNDFVDRFLGFFVVFPRKNGIAGVFGHFASVQTDQEFDFVDFHFGQGEFLET
          130     140     150     160     170     180

      180     190     200     210     220     230
m900.pep  VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTEIRVFLPVFCICL
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900      VGEAAGNVARHFDVLDLVAPDGHFVGVEHQNVGSHQNRITEQTHFHTEIGVFLPVFRIGL
          190     200     210     220     230     240

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	240	250	260	270	280	290
m900 . pep	HGGFVGMGAVHQ	TLGSDAGQNPVQ	FHHFGSVALAVE	GGALGVESAGKP	SGGNGLGGLVNH	
	:	:	:	:	:	:
g900	NGGFVGVGAVHQ	TLGGDAGQNPVQ	LHHFGNVALAVE	GGALGVESAGKP	SGGNGLGGLVNH	
	250	260	270	280	290	300
	300	310	320	330	340	350
m900 . pep	LRLVAFDDTVV	IGEEEEFGIEVL	RRLADGGADG	ADVVAQMRDAG	GGYAGQNSFF	FAHKNVL
g900	LLLVAFD	DAVVIGEEEEFG	IGVLRRLADGG	ADGADVVAQMR	GAGGYAGQNS	FFFAHKNVL
	310	320	330	340	350	360
	360	370	380			
m900 . pep	AASMP	SEREKDVPII	PDLPPTSSRQ	TFPYX		
	:	:	:	:	:	:
g900	TAAMP	SEREKDAPII	PDLPHTSSRQ	TFPYX		
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2703>:

a900 . seq	(partial)
1	GAGGTCGGA CGGCATTGGG TTTATTTCAA CGGGCGGATA CCGACCGCAT
51	CACGTACTTT GCCCAATAAT TCGCGTGCTT CTTTACGCGC TTTTTCGCGC
101	CCTGCCTGCA AAATCTCTTC GATTTCGGAA GGGTCGGCGG TCAGCTCGTT
151	GTAGCGTTCG CGCGGTTCCG CGAGTTCGGC GTTGATTTC CCGCCAAAA
201	GTTTTTTTGC CTCGCCCAA GCCAAGCCGT CGGCAAGCAT TTTCGTAAT
251	TCTGCCGTTT CAGACGGCGT GGAGAAAGCT TTGTAGATT CAAACAGAGG
301	GCTTTCGTCG GGCTTCTTCG GCTCGCCCGG CTCCTTCATA TTGGTGATGA
351	TTTTGTGAC CGATTTTGG GTTTTTTGT CGTTTTCCCA AAGCGGAATG
401	GTGTTGCCGT AGGATTGGA CATTTTTCGT CCGTCCAAAC CAACCAAGAG
451	TTTCGCGTTT TCGTCGATT TCACTTCGGG CAGTGTGAAG AGTCCCGGA
501	AGCGGTGGTT GAAGCGGCCG GCAATATCGC GTGCCATTTC AACGTGTTGG
551	ATTTGGTCGC GACCGACTGG AACTTCATGG GCATTGAACA TGAGAATGTC
601	GGCAGTCATG AGGATAGGGT AGCTGTACAA ACCCATTTCC ACGCCGAAAT
651	CGGGGTCTTC CTGCCCGTTT TCCGCATTG CCGTGCACGGC GGCTTTGTAG
701	GCGTGCGCG GGTTCATCAA ACCCTTGGCG GTGATGCAGG TCAGAATCCA
751	GTTCAATTCC ATCACTTCGG GAATGTCGCT TTGACGGTAG AAGGTGGTGC
801	GCTCGGGGTC GAGTCCGAG GCAAGCCAAG TGGCGGCAAC GGCTTGGGTG
851	GATTGGTGAA TCATCTCCG CTCGTGGCAT TTGATGATAC CGTGGTAATC
901	GGCGAGGAAG AGGAAGGATT CGGTATCAGG GTTTTGCGCC GCGCGGACGG
951	CGGGGCGGAT AGCACCACG TAGTTGCCCA GATGCGGGAT GCCGGTGGTG
1001	GTTACGCCGG TCAGAACTCG TTTTGTGCTC ATAAAAATGT CCTTGCGGCA
1051	TCAATGCCGT CTGAAAGGGA AAAAGATGCG CCGATTATAC CCGATTTGCC
1101	ACCTACATCC AGCCGACAAC AGACTTTTCC ATATTAA

This corresponds to the amino acid sequence <SEQ ID 2704; ORF 900.a>:

a900 . pep	(partial)
1	EVRTALGLFQ RADTDRTYF AQ*FACFFTR FLRAQLQLNF DLRRVGGQLV
51	VAFAFGEFG VDFRRQKFFC LAPSQAVGKH FRKFCRFRRR GESFVDFKQR
101	AFVGLRLRLR LFHIGDDFVD RFLGFFVVFV KRNGVAVGFG HFASVQTNQE
151	FDVFVDHFG QCEEFFPEAVV EAAGNIACHF NVLDLVATDW NFMGIEHENV
201	GSHEDRVAVQ THFHAIEGVF LPVERICLHG GFVGVGAVHQ TLGGDAGQNP
251	VQFHHFGNVA LTVEGGALGV ESAGKPSGGN GLGGLVNHRL LVAFD
301	EEEEEGFIR VLRRADGGAD STDVVAQMRD AGGGYAGQNS FFAHKNV
351	SMPSEREKDA PIIPDLPTS SRQOTFPY*

m900/a900 88.4% identity in 378 aa overlap

	10	20	30	40	50	60
m900 . pep	MPSETRQAEV	RTASGSFQRA	DADRIXYFVQ	XFACFFTRFR	RRAQLQLN	FDLRRVGGQLV
a900	EVRTALGLFQ	RADTDRTYF	FAQXFACFF	TRFLRAQLQ	NLFDLRRV	GGQLVVA
	10	20	30	40	50	
	70	80	90	100	110	120

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m900.pep	FARFGEFGVD	FRRQKFFG	FTPRQAVG	KHFRKFHR	FRRRGEGF	VD	FKQWAF	VGLFRL	LARLF		
a900	FARFGEFGVD	FRRQKFFC	LAPSQAVG	KHFRKF	FCRFRRRG	ESFVDF	KQRAFV	GLLRL	LARLF		
	60	70	80	90	100	110					
m900.pep	HIGDDFVDR	FLGFFV	VFPKRNGV	AVGFGH	FASVQT	DQEF	VD	FIDF	HFGQGE	EFPEAV	VEA
a900	HIGDDFVDR	FLGFFV	VFPKRNGV	AVGFGH	FASVQT	NQEF	VD	FVDF	HFGQCE	EFPEAV	VEA
	120	130	140	150	160	170					
m900.pep	AGDVARHFD	VDLVLV	APDGHF	VGVEHQ	NIGSHQ	NRITEQ	THFHT	EIRVFL	PVFCIC	LHGGF	
a900	AGNIACHFN	VDLVLV	ATDWNF	MGIEHEN	VGSHED	RVAVQT	HFHAEI	GVFLP	VFRI	LHGGF	
	180	190	200	210	220	230					
m900.pep	VGMGAVHQ	TLGSDA	GNPVPQ	FHHFGS	VALAVE	GGALGV	ESAGK	PSGGN	GLGGLV	NHLRLV	
a900	VGVGAVHQ	TLGSDA	GNPVPQ	FHHFGN	VALTVE	GGALGV	ESAGK	PSGGN	GLGGLV	NHLRLV	
	240	250	260	270	280	290					
m900.pep	AFDDTVVI	GEEEEG	FGIEVL	RRADGG	ADGADV	VVAQMR	DAGG	GYAGQ	NSFFA	HKNVLA	ASM
a900	AFDDTVVI	GEEEEG	FGIRVL	RRADGG	ADSTDV	VVAQMR	DAGG	GYAGQ	NSFFA	HKNVLA	ASM
	300	310	320	330	340	350					
m900.pep	PSEREKDV	PIIPDL	PPTSSR	QQTFF	PYX						
a900	PSEREKDA	PIIPDL	PPTSSR	QQTFF	PYX						
	360	370									

g901.seq not found yet
g901.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

m901.seq

1	ATGCCCGATT	TTTCGATGTC	CAATTTGGCC	GTTGCCTTTT	CCATCACATT
51	GGCTGCCGGT	TTGTTTACCG	TATTAKGyAG	TGGCTTGGTG	ATGTTTTC
101	AAACGCCCAA	TCCGCGTGTG	TTGTCGTTTG	GTTTGGCGTT	TGCCGGCGGT
151	GCGATGGTAT	ATGTTTCCCT	GACGGAGATT	TTCAGTAAGT	CCAGCGAGGC
201	GTTGCTGAA	ATTTATGATA	AAGACCACGC	GTTTGGCGCG	GCGACCATGG
251	CATTTTGGC	CGGATGGGC	GGCATTGCGC	TGATTGACCG	TCTGGTGCCG
301	AACCCGCATG	AACTTTTGA	CGCGCAAGAC	CCGTCGTTTC	AAGAAAGCAA
351	ACGCCGCCAT	ATCGCGCGAG	TCGGCATGAT	GGCGGCGTTT	GCGATTACTG
401	CGCACAAATT	CCCCGAAGGC	TTGGCGACGT	TTTTTGCCAC	ATTGAAAAAT
451	CCAGCAGTCG	GGATGCCTTT	GGCCTTGGCG	ATTGCCATCC	ATAATATTCC
501	GGAGGGCATT	TCCATCGCCG	CGCCGGTTTA	TTTTGCCACC	CGCAGCCGTA
551	AGAAAACGGT	GTGGGCGTGT	CTGCTATCCG	GCTTGGCCGA	GCCGTTGGGG
601	GCGGCTTTGG	GCTATTTGGT	TTTGCAGCCG	TTTTTGTCGC	CTGCCGTGTT
651	TGGTTTCGTA	TTCCGCGTGA	TAGCCGGTGT	GATGGTGTTT	TTGGCGTTGG
701	ACGAGCTGnt	GCCGGCTGCC	AAACGCTATT	CAGACGGCCA	TGAAACCGTT
751	TACGGCCTGA	CAACGGGTAT	GGCGGTGATT	GCCGTCAGCC	TGGTATTGTT
801	CCATTTTTAA				

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

m901.pep

1	MPDFSMSNLA	VAFSITLAAG	LFTVLXSGLV	MFSKTPNPRV	LSFGLAFAGG
51	AMVYVSLTEI	FSKSSEAFAE	IYDKDHAFAA	ATMAFLAGMG	GIALIDRLVP

101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELPAA KRYSDGHETV
 251 YGLTTGMAVI AVSLVLFHF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq
 1 ATGCCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCCTTT CCATTACGTT
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTCCCA
 101 AAACGCCCAA TCCGCGCGTG TTGTCGTTG GTTTGGCATT TGCCGGCGGT
 151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTCGGCGC GCGACCATGG
 251 CATTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
 301 AACCCGCATG AAACCTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GGCGGCGTTT GCGATTACTG
 401 CGCACAAATT CCCCGAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAT
 451 CCAGCAGTCG GGATGCCTTT GGCTTGGCG ATTGCCATCC ATAATATTC
 501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGGCCAC CGCAGCCGTA
 551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTGGGG
 601 GCGGCTTGG GCTATTTGGT TTGTCAGCCG TTTTGTGCG CTGCCGTGTT
 651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGTTT TTGGCGTTGG
 701 ACGAGCTGCT GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAACCGTT
 751 TACGGCTGA CAATGGGCAT GCGGTGATT GCCGTCAGCC TGGTATTGTT
 801 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep
 1 MPDFSMSNLA VAFSITLAAG LFTVLGSLV MFSKTPNPRV LSFGLAFAAG
 51 AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP
 101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELPAA KRYSDGHETV
 251 YGLTMGMAVI AVSLVLFHF*

m901/a901 98.9% identity in 269 aa overlap

	10	20	30	40	50	60
m901.pep	MPDFSMSNLA VAFSITLAAG LFTVLGSLV MFSKTPNPRV LSFGLAFAAG AMVYVSLTEI					
a901	MPDFSMSNLA VAFSITLAAG LFTVLGSLV MFSKTPNPRV LSFGLAFAAG AMVYVSLTEI					
	10	20	30	40	50	60
m901.pep	FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP NPHE TLDAQD PSFQESKRRH					
a901	FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP NPHE TLDAQD PSFQESKRRH					
	70	80	90	100	110	120
m901.pep	IARVGMMAAF AITAHNFPEG LATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
a901	IARVGMMAAF AITAHNFPEG LATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
	130	140	150	160	170	180
m901.pep	RSRKTWAC LLSGLAEPLGAALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELPAA					
a901	RSRKTWAC LLSGLAEPLGAALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELPAA					
	190	200	210	220	230	240
m901.pep	KRYSDGHETV YGLTMGMAVI AVSLVLFHF					
a901	KRYSDGHETV YGLTMGMAVI AVSLVLFHF					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

g902.seq

```

1  ATGCCGTCGG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTTGATTTC
151 ACGCCGCGCC TGTTCCGCGT CGGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCCTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCAATG
251 GCGCGGATGT GGTTCAAAAT GGCGGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGGCGGC TTTTgCggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTcAGAc ggCTTTTGGT CTCGGcgatg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TCGTGcgcg CGcgcccgtg aacggcaaGg
551 gcggaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg
601 atcgctcgtc tgccaaccca AacggGTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTcCTGC
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTTcTtgg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCGAG TCCGACGTTg taacgcgcg
801 catCCGCCAT CtggtcggGG TCGCTGCCGG CAATCTGCAC GGCAACGATG
851 CCGccttcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTcCT
901 GAGCGTCGGA TCGCTGCCCA GCATTTCGCA CACCGCCAA CCTGCGCCAA
951 ACGCCCGACA GAGGCGGCGG AAGGGTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCga TGGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

g902.pep

```

1  MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQON GGSAFcQTQG
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAfG LGDEFVTRLA FVHLRARAPV NGKGGNAaIF GDFGDGGQVL
201 IVVVPQTGF EGNgyARRLD HRLQNGNQR LVLHQRATGL DVAHFLGGAA
251 HIDVDDLrPE SDVVTrRIRH LFGVAAGNLH GNDAAFIgKI TAVQGFSGIP
301 ERRIAGQHfA HRPTCAKRPT EAAEGFVGNA RHRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

m902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATT TGGCGGTAGG
51  CGCACGCCCA ACTGTGCGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TgTCTgTTCG CCGTcGGGCA TTTcGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTGCGCGT AAAACGCGTG TATGGCGCGG
251 ATGTGGTTCA AAATAGCGGC GCGCATTCT GCCAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTCCGGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGCGCGC GGTTTGTTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAAGTA ATGTCGCGCT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC GATGAGTTcG TAACGCGCTT
501 CGCCTTTGTA CATTTCGTA CCGGTGCGTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CCGCACCGCG CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGcGCaAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

m902.pep
 1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
 51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFQQTQGRR
 101 QNTVFGIMFQ IAEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD
 151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAAFGD FGDDGQVLMV
 201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHQRATGLDI ADFFSGTAHV
 251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
 301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRCDDGVVDK IAADVHNGSA
 351 FQKSTPLYIF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

m902.pep	10	20	30	40	50
	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT CLFAVGHF				
g902	10	20	30	40	50
	MPSEPERRHGNTALPFP IAA RPTVGFSGKPFKITGKCVLRRRIVQAVDFTPRLFAVGHF				
m902.pep	60	70	80	90	100
	VDVPAYVFACDAHTGGVAVKRVY GADVQNSG GAFQQTQGRRQNTVFGIMFQIAEPRPA				
g902	60	70	80	90	100
	ADVVPAYVFACDAHTDGLTIKRVHGADVQNGGSAFCQTQGRRXNAVFGIMLQIAEKPRPA				
m902.pep	120	130	140	150	160
	LRAAPYHNAVGGGLFEDGLGFLRRSNVAVD PDRDVQTAFGFGDEFVTRFAFVHLRTRASV				
g902	120	130	140	150	160
	LRAAPYHDAVGGGLFEDGGGFLRRSDVAVD PGRDVQTAFGLGDEFVTRLAFVHLRARAPV				
m902.pep	180	190	200	210	220
	DGKGGDAAFGD FGDDGQVLMVVVPTQTGFEGNGYACRTDDG FQNGGNQRLV LHQRATGL				
g902	180	190	200	210	220
	NGKGGNAAFGD FGDDGQVLIVVPTQTGFEGNGYARRLDHRLQNGGNQRLV LHQRATGL				
m902.pep	240	250	260	270	280
	DIADFFSGTAHV DVDKLRPKADV VTRGIRHLLRIASGNLHGNNA AFIGKIAA VQGFSSIS				
g902	240	250	260	270	280
	DVAHFLGGAHIDVDDL RPESDVVTRIRHLFGVAAGNLHGNDAA FIGKITAVQGFSGIP				
m902.pep	300	310	320	330	340
	ERRVAGQHFAHRPTCAKISAKS AERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLY				
g902	300	310	320	330	340
	ERRIAGQHFAHRPTCAKRPT EAAEGFVGNARHRRKCDGVVDKI TADVHNGPAFQKSAPLY				
m902.pep	360				
	IFX				
g902	360				
	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

1 TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTG GGGCGGTAGG
 51 CGCAGCCCCA ACTGTCGGTT TTTTCGGCAA GTCTTCAAG ATAACCTGCA

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```

101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TGTCTGTTTCG CCGTCGGGCA TTTCTGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAACTCA AGGCAGGCGG
301 TAAACACCG TGTCGGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTTTGTTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAGGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTTGCGTG CGCGTGCGTC CGTGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCCGCCGCTT
651 TGACCACCGC CTCCAAATG GCGGCAACCA GCGGCTCGT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAAACG CCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCTT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGCGCAAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGGC
1051 TTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

```

a902.pep
1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51 CLFAVGHEVD VPAYVFACDA HTGGVAVKRV HGSDEVVQNSG GTFCQTQRRR
101 *NTVFGVMFQ IAEEPRSLR AAPYHNAVCG GLFEDGLGFL RRGNAVDPD
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGGNAAFI GD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNAHR RRCDDGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

m902/a902 94.7% identity in 360 aa overlap

```

          10      20      30      40      50      60
m902.pep  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAVGHEVD
          |||
a902       LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAVGHEVD
          10      20      30      40      50      60

          70      80      90      100     110     120
m902.pep  VPAYVFACDAHTGGVAVKRVYGVADVVQNSGGAFQCQTQRRQNTVFGIMFQIAEEPRPALR
          |||
a902       VPAYVFACDAHTGGVAVKRVHGSDEVVQNSGGTFCQTQRRXNTVFGVMFQIAEEPRSLR
          70      80      90      100     110     120

          130     140     150     160     170     180
m902.pep  AAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASVDG
          |||
a902       AAPYHNAVCGGLFEDGLGFLRRGNVAVDPDRDVQTAFGFGNQVVSRAFAFVHLRARASVDG
          130     140     150     160     170     180

          190     200     210     220     230     240
m902.pep  KGGDAAIFGDFGDDGQVLMVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGLDI
          |||
a902       KGGNAAIFGDFGDDGQVLMVVPTQTGFEGNGYARRFDHRLQNGGNQRLVLHQRATGLDI
          190     200     210     220     230     240

          250     260     270     280     290     300
m902.pep  ADFFSGTAHVVDVKLRPKADVTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER
          |||
a902       ADFFSGTAHVVDVKLRPKADVTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER
          250     260     270     280     290     300

          310     320     330     340     350     360
m902.pep  RVAGQHFAHRPTCAKISAKSAERFVGNAHRRCDDGVVDKIAADVHNGSAFQKSTPLYIF

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|||||
a902   RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
              310      320      330      340      350      360

m902.pep   X
            |
a902       X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcG gatgaggCAA GCCCCTGCTT
51  TCCTATTTCT GAGGTGGAAAT TGGTGGGTGA aGaaacggct aAATTCGGgt
101 tTGCCTcaa ccaTGCCTTG tgccAAACAC ATTTTgtttc cGgcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAatcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAaccctga tgccggGCTA TCtgcgctcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTT CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTGGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgttcc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAC GTCTGCTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTCGG CTTCAACCGC CTGTTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAAACTGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAATCG ACTGTACAAC GGCGTAAAAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTGCGAGTA CGGCAGATT TAAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG ACAAACTGGC
1251 TATCGGCGGA CACCACCCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTTAAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGTTATCGG GCCAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA TATATTACC
1501 GGCCGTGCAT TGA AAAAGCC cgaatatatt cAGACGAAGA Aatgggtaac
1551 999gtTTCAG gtgggttatt cgTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51  LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAFAQ NKFPTRSNDL LNLRLDLEQL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DGHKKEGGSN NYAVHYSAPP
251 GKWTWAFNHN GYRYHQAVSG LSEVYDYNK SYNTDFGNR LLYRDAKRKT
301 YLSVKLWTRE TKSYYDAEL TVQRRKTTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTFFQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVVRGFDGE MSLPAERGWY WRNDLSWQFK
451 PGHQLYLGLAD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIPT
501 GRALKKPEYF QTKKWVTGFQ VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAAATGT
51  CCGTTTCGAG CAACCATTTG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AACACCGTG TACTCGGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

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1290

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151 CGCAAATTTT CTTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAaCCACAGA ATATGGATTG GGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCAATC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAAACC TGCGTCGTTT
501 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCA
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTGCTTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTtTATG
701 TTTTCATATG ACGCGGTTTG GCGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAACAAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCCAGGTA CATCTCGTAT GAAAATCATT
1201 ACTGCCAGTT TGGACGCAGC CGCCCATTT AyTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCCAAGATAA ATTGTCAATC GGCAGCCGCT ACACCGTTTC CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTTCATCCG ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

m903.pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV
51  RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRVEKRDG KSAEGSISAF NNFPLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTDAT
251 GTETESGSR SSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSLAERM LWRNRLHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRLAYL RWQLDGKLSY KRGTMGRQSM PAPEENGDI LPGTSRMKII
401 TASLDAAAPF XLGKQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

              10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
              |:::| |:::| |:::| |:::|
g903      MATQVGGANSDEASPCFP ISEVELVGEETAKFRFALNHA
              10      20      30

              70      80      90     100     110     120
m903.pep  MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG
              : : | | : | | : : : : | | | | : : | | : : | :
g903      LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGYTTTRILAAPQDLNSGKQLTLMPGYLR
              40      50      60      70      80      90

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1291

	130	140	150	160	170	180
m903.pep	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRDVEQGLENLRLPSVKTDIQIIPSE					
g903	SIRIDRSNDQTHAGRIAAFQNKFPTRSDLLNLRDLEQGLENLKCLPTAEADLQIVPVE					
	100	110	120	130	140	150
	190	200	210	220	230	
m903.pep	EE-GKSDLQIKWQONK-PIRFSIGIDDAGGKTGKYQGNVALSFDNPLGLSDLFVVSYGR					
g903	REPNQSDVVVQWRXLLPYCVSVGMDNSGSEATGKYQGNITFSADNPFGLSDMFVNYGR					
	160	170	180	190	200	210
	240	250	260	270	280	290
m903.pep	GLAHKTDLTATGTETESGSRYSVHYSVPVKWLFNFHNGHRYHEATEGYSVNYDYNG					
g903	SIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAFNHNGYRYHQAVSGLSEVYDYNG					
	220	230	240	250	260	270
	300	310	320	330	340	350
m903.pep	KQYQSSLAERMLWRNRLHKTSGVMKWLTRQTYKIDDAEIEVQRRRSAGWEAELRHRY					
g903	KSYNTDFGNRLLYRDAKRKTYLSVKLWTRETKSYIDDAELTVQRRKTTGWLAELSHKGY					
	280	290	300	310	320	330
	360	370	380	390	400	410
m903.pep	LNRWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIIITASLDAAAPFXLGKQOFF					
g903	IGRSTADFKLKYKHGTGMKDALARPEEAFGE---GTSRMKIWTASADVNTFPQIGKQLFA					
	340	350	360	370	380	390
	420	430	440	450	460	470
m903.pep	YATAIQAWNKTPPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYQNTLTWYFHPNHQFY					
g903	YDTSVHAQWNKTPPLTSQDKLAIGGHHTVIRGFDGEMSLPAERGWWYRNDLSWQFKPGHQLY					
	400	410	420	430	440	450
	480	490	500	510	520	530
m903.pep	LGADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTV					
g903	LGADVGHVSGQSAKWLSGQTLAGTAIGRQIKLGGNLHYDIFTGRALKKPEYFQTKKWV					
	460	470	480	490	500	510
	540					
m903.pep	YGFNLNYSFX					
g903	TGFQVGYSEFX					
	520					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2719>:

a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTTAACTG	ATGCAAATGT
51	CCGTTTCGAG	CAACCATTTG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAATTTT	CTTTTCTTCC	TTCTGTGCTC	ATGAAAGAAA	CAGCTTTTAA
201	AACTGGGATG	TGTTTAGGTT	CCAATAATT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGGCTACC	TCACTTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATT	GGAATTCTG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	AGGGCAGTAT	TAGTGCATT	AATAACAAAT	TCCCTTATA	TAGGAACAAA
451	ATTCTCAATC	TTCGCGATGT	AGAGCAGGGC	TTGGAAGAAC	TGCGTCGTTT
501	CCGAGTGTT	AAAACAGATA	TTCAGATTAT	ACCGTCCGAA	GAAGAAGGCA
551	AAAGCGATTT	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTCAGT

1292

```
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTATG
701 TTTCATATGG ACGCGGTTTG GTGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACGG CGGCGGTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCCGAT TGGATGCAGC GGCCCGGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTGTAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA
```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

a903.pep

```
1 MQRQQHIDAE LLTDANVRFE QPLEKNYYVL SEDETPCTRV NYISLDDKTA
51 RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEKRDG KSAEGSISAF NKNKFLYRNL
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGK
301 YQSSLAERM LWRNRFHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRAYLN RWQLDGKLSY KRGTGMRQSM PAPEENGGGT IPGTSRMKII
401 TAGLDAAAPF MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*
```

m903/a903 98.4% identity in 547 aa overlap

	10	20	30	40	50	60
m903.pep	MQRQQHIDAE	LLTDANVRFE	QPLEKNYYVL	SEDETPCTRV	NYISLDDKTV	RKFSFLPSVL
a903	MQRQQHIDAE	LLTDANVRFE	QPLEKNYYVL	SEDETPCTRV	NYISLDDKTV	RKFSFLPSVL
	70	80	90	100	110	120
m903.pep	MKETAFKTM	CLGSNNLSRL	QKAAQQILIV	RGYLTSAII	QPQNMDSGIL	KLRVSAGEIG
a903	MKETAFKTM	CLGSNNLSRL	QKAAQQILIV	RGYLTSAII	QPQNMDSGIL	KLRVSAGEIG
	130	140	150	160	170	180
m903.pep	DIRYEKRDG	KSAEGSISAF	NKNKFLYRNL	KILNLRDVEQ	GLENLRLPSV	KTDIQUIPSE
a903	DIRYEKRDG	KSAEGSISAF	NKNKFLYRNL	KILNLRDVEQ	GLENLRLPSV	KTDIQUIPSE
	190	200	210	220	230	240
m903.pep	EEGKSDLQI	KWQONKPIR	FSIGIDDAGG	KTTGKYQGNV	ALSFDNPLGL	SDLFYVSYGR
a903	EEGKSDLQI	KWQONKPIR	FSIGIDDAGG	KTTGKYQGNV	ALSFDNPLGL	SDLFYVSYGR
	250	260	270	280	290	300
m903.pep	AHKTDLTDA	TGTETESGSR	SYSVHYSVPV	KKWLFSFNH	NGHRYHEATE	GYSVNYDYNKG
a903	AHKTDLTDA	TGTETESGSR	SYSVHYSVPV	KKWLFSFNH	NGHRYHEATE	GYSVNYDYNKG

1293

	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKTSVGMKWLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
a903	YQSSLAERMLWRNRFHKTSVGMKWLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTGMRQSMPEENGDDILPGTSRMKIITASLDAAPFXLGKQOFFYA					
a903	RWQLDGKLSYKRGTGMRQSMPEENGDDILPGTSRMKIITASLDAAPFXLGKQOFFYA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYQNTLTWYFHPNHQFYLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

g904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTGCGGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCGCCCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGC GCGCGGCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTCCG CCAAACCTGC GCCTACTTCG TCGAACAATT CCGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTCGCCG TTTTGTGTTT
651 TTTGTTCAA CACGCgggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CCTTTGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGTAAGG CAGGATCAGC GGGCAGGTCG GCGGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCGAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAGGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGCCG CCTTGAAGC GCACgacGct
1201 gCCGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCTCGTTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

g904.pep

```

1  MMQHNRFFAV GAGGDDGDRR AADFFNPFI CFIQRQCVV AFHADSRFAP

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1294

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51 AGHGFVNRF A GFHRIARTARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
101 HTGNAVDLDG AFQGGGIKPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGIG FDDAQNIQIH LRTYARACRS RAGETVGRGN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNNRR NARRDFFDNR HHVFRFNRSG
251 VMQVLELDV IGKDGIOFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF AGLVERDVVR QDQRAGRRDF QTAFDVVFHAC RVQLVDFAAQ
351 GFGGNDNART DEAIQSFVQD TARNQAQNGF FAADDQGMAR IVAALEAHDA
401 AGFFRQPVND FTFTLVAPLC ADYNYIFSHS HITRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

```

m904.seq
1 ATGATGCAGC ACAATCGTTT CTTCTCGGTC GGGGCCGgTG GAGACGATGG
51 CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCG
101 TTTTCGGGCA ATGCGCCGTA GTCTTCACG CCGAAAGTGG ATTCGCGCCA
151 CGCGGGCATG GTTTCGTAAA TCGGCTTGCA GGTTCACACC GCATCGGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC ATAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TAGTAATACA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTTCTG CCAAACCTAC GCCTACTTCG TCGAACAATT CCGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCGCGC CTGCCGAAGC TCGCGCCGCC
551 AGACAGTTGG ACGAGGTAAC GAAGGGATAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TCTCGTTCAA CACGCGGGAC ACGTCGGTAA TCATCGCGCG AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGCTCGGC
751 ATTGTGCAGA TGTTCAGTT GGACATTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTCTCA GGATGCAGCA AATCGCGCGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CCTTGCCGCG GCG.ATcTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCGAACC GATGAAGCAG TCCTAACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AATGGTTTTT TTTGCGCGCG
1151 ACAACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACCaCGCC
1201 GCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTAsT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

```

m904.pep
1 MMQHNRFVSFV GAGGDDGDRR AADFFNPFI CFCVFGQCAV VLHAESGFAP
51 AGHGFVNRLA GFHRIARTARQ DVGFAAVGQF IADADIDGFN AVHYIEFSNT
101 HTGNAVDLDG AFQGGGIKPA AAACASGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGIG FDDAQNIQIH LRTYARACRS CARQTVGRGN EGISAVVDVQ
201 QRTLRAFQKQ FFAVFVFLVQ HAGHVGNNRR NARRDFFDNR HHVFRFNRSLG
251 IVQMLQLDIV IGKDGIOFFT QFXRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAAXIF AGLVERDVVR QDQRAGRRDF QTAFDVVFHAC RVQLVDFAAQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMAR IVAALEAHHA
401 AGFFRQPVND FTFTLVAPLC ADXNYIFSHS HITRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

```

m904/g904
10 20 30 40 50 60
m904.pep MMQHNRFVSFV GAGGDDGDRR AADFFNPFI CFCVFGQCAV VLHAESGFAP AGHGFVNRLA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g904 MMQHNRFVAV GAGGDDGDRR AADFFNPFI CFCVFGQCAV VAFHADSRA FAPAGHGFVNRLA
10 20 30 40 50 60
70 80 90 100 110 120

```

1295

m904 . pep	GFHRIGTARQDVGF	AAVQGFIADADIDG	FNNAVHYIEFSNTH	TGNAVDLDGAFQGG	GGIKPA
g904	GFHRIR	TARQDVGF	AAAWQFVADADIDG	FNNAVHYIEFGNAHT	TGNAVDLDGAFQGGG
	70	80	90	100	110 120
m904 . pep	AAACASGYRTEFVS	AFCQTYAYFVEQFGR	ERARTDARGIGFDDA	QNIIOHLRTYARACRS	
g904	AAARAAGYRTEFVS	ALRQTCAYFVEQFGR	ERARTDARGIGFDDA	QNIIOHLRTYARACRS	
	130	140	150	160	170 180
m904 . pep	CARQTVGRGNEGISA	VVDVQRTLRAFQKQFF	AVFVFLVQHAGHVG	NHRRNARRDFFDNR	
g904	RAGETVGRGNEGISA	VVDVQRTLRAFQKQFF	AVFVFLVQHAGHVG	NHRRNARRDFFDNR	
	190	200	210	220	230 240
m904 . pep	HHVFRFNRLGIVQML	QLDIVIGKDGIOFFTQ	FXRMQOIGGANGAACH	FVFGVGRADAAAGR	
g904	HHVFRFNRLGIVQML	QLDIVIGKDGIOFFTQ	FXRMQOIGGANGAACH	FVFGVGRADAAAGR	
	250	260	270	280	290 300
m904 . pep	ADFAFAARI	FAGLVERDVVRQDQ	RAGRRDFQTA	FDVFHACRVQLVDF	FAQQGF
g904	ADFAFAARCF	FAGLVERDVVRQDQ	RAGRRDFQTA	FDVFHACRVQLVDF	FAQQGF
	310	320	330	340	350 360
m904 . pep	DEAVQTFMQDAARNQ	AQNGFFAADNQMARIVA	ALEAHHAAGFFRQ	PVNDFTFTLVAPLC	
g904	DEAIQSFVQDTARNQ	AQNGFFAADNQMARIVA	ALEAHHAAGFFRQ	PVNDFTFTLVAPLC	
	370	380	390	400	410 420
m904 . pep	ADXYNIFSHSHITYRYX				
g904	ADYYNIFSHSHITYRYX				
	430				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

1	ATGATGCAGC	ACAATCGTTT	CTTCGCGGTC	GGGGCCGGTG	GAGACGATGG
51	CGACCGGCGC	ACCGCAGACT	TCTTCAATCC	GTTTCAAATA	TGCTTTGGCA
101	TTGGCAGGTA	ATGCGTCGTA	GCTTTTCACG	CCGAAAGTGG	ATTCGCTCCA
151	ACCGGCGCATG	GTTTCGTAAA	TCGGCTTGCA	GGCTTCTACC	GCATCAGAGC
201	CGCAAGGCAG	GATGTCGGTT	TTGCCGCCGT	CGGGCAATTC	GTAGCCGACG
251	CAGATATTGA	TGGTTTCAAC	CCCGTCCATT	ACATCGAGTT	TGGTAATACA
301	CATACCGGAA	ATGCCGTTGA	TTTGATGGA	GCGTTTCAGG	GCGGCGGCAT
351	CAAACCGACC	GCAGCGGCGT	GCGGTCCGG	TTACCGAACC	GAATTCGTGT
401	CCGCGTTCTG	CCAAACCTGC	TCCGACTTCG	TCGAACAATT	CGGTCGGGAA
451	CGGGCCCGAA	CCGACGCGCG	TGGTATAGGC	TTTGACGATG	CCCAAAACAT
501	AATCCAGCAT	TTGAGGCGCT	ACGCCCAGCG	CTGCCGAAGC	CGCGCCGGCG
551	AGGCAGTTGG	ACGAAGTAAC	GAAGGGGTAA	GTGCCGTAGT	CGATGTCCAA
601	CAACGCACCT	TGCGCGCCTT	CAAACAGCAG	TTTTTCGCGG	TTTTTGTTTT
651	TTTCGTTCAA	CACGCGGGAC	ACGTCGGTAA	TCATCGCGGT	AATGCGCGGC
701	GCGACTTTTT	CGATAACCGC	CATCACGTCT	TCCGCTTTCA	CCGACTCGGC
751	ATTGTGCAGA	TGTTGCAGTT	GGACGTTGTA	ATAAGCAAAG	ACGGCATCCA
801	GTTTTTCACG	CAGTTTTTCA	GGATGCAGCA	AATCGGCGGC	GCGAATGGCG
851	CGGCGTGCCA	CTTTGTCTTC	GTAGGCAGGG	CCGATGCCGC	GGCCGGTTCG
901	GCCGATTTTG	CCTTTGCCGC	GCGATGCTTC	TCGGGCTTGG	TCGAGCGCGA

а904.рор

m904/a904 91.3% identity in 436 aa overlap

430

1297

```

m904.pep    ADXYNIFSHSHITYRYX
             || ||||| ||||| |||
a904        ADYYNIFSHSHITXRYX
             430

```

g906.seq not found yet
g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
51  GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
1  MKYIVSISLA MGLAACSFGG FKPNPWDAAS FWELKNYANP YPGSASAALD
51  QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPYPENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGcaAC GCCGCCGCCT
51  GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG
101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTGACa ATCCGAAAGA
201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGGA AGATTCTGTC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAOREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
51  GTTGTGTGCC GCCGGTGCCT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGGA AGGTTCTGTC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTkTGG AAAAActACA TCGGCAAAACC GGCGCACAAc
451 CTGTTGACa TCCGCACCAa CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CGCGCGCTT GCCCGCTTTA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
1  MRKPTDTLPV NLQRRRLCA AGALLSPLA HAGAOREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVA RGLMQVMPXW KNYIGKPAHN

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

q907/m907

		10	20	30	40	50	60
g907.pep		MKKPTD	TLPVNLQRRRL	CAAGALLISPLAHAGA	QREETL	ADDDVASVMRSSVGSVNP	PRL
		:					
m907		MRKPTD	TLPVNLQRRRL	CAAGALLSPLAHAGA	QREETL	ADDDVASVMRSSVGSVNP	PRL
		10	20	30	40	50	60
		70	80	90	100	110	120
g907.pep		VFDNPKEGERWLSAMSARLARFV	PEDEGERRLLVNIQYESSRAGL	DTQIVLGLIEVESGY			
m907		VFDNPKEGERWLSAMSARLARFV	PEEEERRLLVNIQYESSRAGL	DTQIVLGLIEVESAF			
		70	80	90	100	110	120
g907.pep		RARIIS					
m907		RQYAI	SGVGARGLMQVMPXWKNYIGKPAHNL	FDIRTNLRYGCTILRHRYRNLEKGNIV	RAL		
		130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

```

a907.seq
1  ATGAAAAAAC  CGACCGATAC  CCTACCCGTC  AATCTGCAAC  GCCGCGCGCT
51  ATTGTGTGCT  GCCGGCGCGC  TGTGTCTCAG  CCGCGTGCCA  CAAGCGCGCG
101 CGCAACGTGA  AGAAACGCTT  GCCGACGATG  TGCGTTCGT  GATGAGGAGC
151 TCTGTCGGCA  GCATAAATCC  GCCGAGGCTG  GTGTTGACA  ATCCGAAAGA
201 GGGCGAGCGT  TGGCTGTCCG  CGATGTCTGC  TCGGTTGGCA  AGGTTCTGTC
251 CCGATGTGCA  GGAGCGGCGC  AGGCTGCTGC  TCAATATCCA  GTACGAAAGC
301 AGCCGGGCGC  GTTTGGATAC  GCAGATTGTG  TTGGGGCTGA  TTGAGGTGGA
351 AAGCGGTTTC  CGCCAGTATG  CAATCAGTGC  TGTGCGGCGC  CGCGGCTTCA
401 TGCAGGTTAT  GCCGTTTGG  AAAAACTGCA  TCGGCAAAAC  GCGGCACAA
451 CTGTTTCGAC  TCCGCACCAA  CCGCGTTAC  GCGTGTACCA  TCTCGGCCA
501 TTACCGGAAT  CTTGAAAAAG  GCAACATCGT  CCGCGCACTC  GCCCGTTTTA
551 ACGGTAGCCT  CGGCAGCAAT  AAATATCCGA  ACGCCGTTT  GGGCGCGTGG
601 CGCAACCGCT  GGCAGTGGCG  TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.psp

1	<u>MKKPTD</u> <u>TLPV</u> <u>NLQRRRL</u> <u>CA</u> <u>AGALLS</u> <u>PLA</u> <u>QAGA</u> <u>QRE</u> <u>ETL</u> <u>ADDVAS</u> <u>VMRS</u>
51	SVGSINPRL VFNPKEGE WLSAMSARL RFVDEEERR RLLVNIQYES
101	SRAGLDIQIV LGLIEVESAF RQYAISGVA RGLMQVMPFW KNYTGKPAHN
151	LFDIRTLRY GCTILRHYN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201	RNRQWR*

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDDASVMRSSVGSVNPRL					
a907						
	10	20	30	40	50	60
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
a907						

1299

	70	80	90	100	110	120
	130	140	150	160	170	180
m907.pep	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
a907	RQYAISGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180
	190	200				
m907.pep	ARFNGSLGSNKYPNAVLGAWNRNRWQWRX					
a907	ARFNGSLGSNKYPNAVLGAWNRNRWQWRX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908.seq
1  ATGAG.AAAA GCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTGTGCGCA GGTGTAAGTG CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTACGATG ACTGATTTAT
151 CAAAACGTC CGCATTTAGA AATGTTTGAT GCGGAAGTAG AAGCAGATGA
201 AAGTTATTTT GCGGACAAC GCAAAGGCAA AC GCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 acaagtgaaa cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatT TTagcttcgc tgaaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908.pep
1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPNTQTAT LFPIIREQVK PDSIVYTDY RSYDVLDVSE FSHFSAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAGTG CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTTGGA AATGTTTGAT GCGGAAGTAG AAGCAGATGA
201 AAGTTATTTT GCGGACAAC GCAAAGGCAA AC GCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908.pep
1  MRKSRLSQYK QXKLIELFVT GVTARTAAEL VGVNKNNTAAY YFHRLRLLIY
51  QNSPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPNTQTAT LFPIIREQVK PDSIFYTDY RSYDVLDVRE FSHFSAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

```

g908/m908
10      20      30      40      50      60
g908.pep  MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAYDFHRLRLXLIYQNGPHLEMF

```


1300

m908	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAAYFHRRLRLLIYQNSPHLEMPD
	10 20 30 40 50 60
g908.pep	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
m908	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
	70 80 90 100 110 120
g908.pep	PDSIVYTDYRSYDVLDVREFSHFSFAETSFSYSQHTFCRTTKPYX
m908	PDSIFYTDCYRSYDVLDVREFSHFSFAETSFSYSQHTFCRTTKPYX
	130 140 150 160

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2739>:

a908.seq	1 ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAATAAAC TCATTGAGCT
	51 ATTTGTGCGCA GGTGTAACGT CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
	101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTACGATT ACTTATTTAT
	151 CAAAACAGTC CGCATTGGA AATGTTGAT GGCGAAGTAG AAGCAGATGA
	201 AAGTTATTTT GGCGGACAAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
	251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
	301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTTCTTA TTATCCGTGA
	351 ACAAGTGAAA CCTGACAGCA TTGTTTATAC GGATTGTTAT CGTAGCTATG
	401 ATGTATTAGA TGTGCGCGAA TTAGCCATT TTAGCTTCGC TGAAACTTCG
	451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
	501 A

This corresponds to the amino acid sequence <SEQ ID 2740; ORF 908.a>:

a908.pep	1 MRKSRLSQYK QNKLIELFVA GVTARTAAEL VGVNKNNTAA YFHRRLRLLIY
	51 QNSPHLEMPD GEVEADESYF GGQRKGKGRG GAAGKVAVFG LLKRNGKVYT
	101 VTPNTQTAT LFPPIIREQVK PDSIVYTDY RSYDVLDVRE FSHFSFAETS
	151 FSYQSQHTFC RTTKPY*

m908/a908 98.2% identity in 166 aa overlap

m908.pep	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAAYFHRRLRLLIYQNSPHLEMPD
a908	MRKSRLSQYKQXKLIELFVAGVTARTAAELVGVNKNNTAAAYFHRRLRLLIYQNSPHLEMPD
	10 20 30 40 50 60
m908.pep	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
a908	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
	70 80 90 100 110 120
m908.pep	PDSIFYTDCYRSYDVLDVREFSHFSFAETSFSYSQHTFCRTTKPYX
a908	PDSIVYTDYRSYDVLDVREFSHFSFAETSFSYSQHTFCRTTKPYX
	130 140 150 160

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2741>:

g909.seq (partial)	1 atgcgtaaaa ccgtacttat cCTgaccatc tccgcccggc tttgtcggg
	51 ctgcacatgG gaaacttatac aagacggcag cggcaaaacc gccgtccgtg
	101 caaaatgttc caccggcagc ccgctgtgtt ggcaagacgg gcgcggctcg

1301

151 aaaaaggtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg
 201 caaccaaaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga
 251 aaccgagttt ccgggcgagg gacggggggg ggcgggtgaa cagggcagaa
 301 acgggggagg ggaagcgatc ggcgagg..

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS
 51 KKVDCDEYGG ERRAVLNRQK RGKPATRRAA TLGKPSFRAR DGGGRVNRAE
 101 TGEKRSAR..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCCC TTTTGTGCGG
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTACCC
 201 CAATCAAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AACCAAAGTT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

1 MRKTFLEFLTA AAALLSGCAW ETYQDGNgKT AVRQKYPAGT PVYYQDGSYS
 51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDGNgKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		: :	: : : : : : :	: :	: :	: : : :
g909	MRKTVLILTI	SAALLSGCTW	ETYQDGSgKT	AVRAKSTGT	PLCWQDGRGS	KKVDCDEYGG
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVLPNQT	GNNADEEHRQ	HWQKPKFQNR			
	: : :	:	: :	: :		
g909	ERRAVLRNQK	RGKPATRRAA	TLGKPSFRAR	DGGGRVNRAE	TGEKRSAR	
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

1 ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCCC TTTTGTGCGG
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTACCC
 201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AGCCCAAATT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

1 MRKTFLEFLTA AAALLSGCAW ETYQDGNgKT AVRQKYPAGT PVYYQDGSYS
 51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDGNgKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		: :	: : : : : : :	: :	: :	: : : :
a909	MRKTFLEFLTA	AAALLSGCAW	ETYQDGNgKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
	10	20	30	40	50	60

1302

```

              70      80      90
m909.pep    ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX
             |||
a909        ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCTAAATG CCGCAACCGC
51 ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTGTT
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGAACAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910.pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51 VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCGC
51 ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTGTT
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATGCG GGTAAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910.pep
1  MKKLLLAADV SLAAAAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51 VYDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

```

g910/m910
              10      20      30      40      50      60
g910.pep    MKKLLLAADVSLNAATAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDYW
             |||
m910        MKKLLLAADVSLAAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDHW
              10      20      30      40      50      60

              70      80      90
g910.pep    GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
             |||
m910        GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
              70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTGAGTG CCGCAACCGC
51 ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTGTT
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGAACAGCG CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATGCG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

```

a910.pep

```

1303

1 MKKLLLVAVV SLAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
51 VHDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

m910/a910 95.7% identity in 94 aa overlap

	10	20	30	40	50	60
m910.pep	MKKLLLAADVSLSAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDDHW					
	: : : : : :					
a910	MKKLLLVAVVSLAATAFAGDSAERQIYGDYPYFEQNRTKAVKMLEQRGYQVHDVDADDDHW					
	10	20	30	40	50	60
	70	80	90			
m910.pep	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	: : : : :					
a910	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

g911.seq
1 ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCTTGATCGG
51 CGCGGCGGCG GTTGCCTTTC TCGCTTCCG CGTGGCGGGC GCGCGGCGGT
101 TCGGCGGTTC GGACAAACT TACGCCGTTT ATGCCGATTT CGGCGACATC
151 GCGCGTTTGA AGGTCAATGC CCCCGTCAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTTGATT GGACGGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG
351 CGGCGATACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAATT
401 CTGCAATGGT TCTGGAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC
451 GAGAAAAACG CTGAGGGCGG CAATGCGGAA AAAGCCGcag aAtaa

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

g911.pep
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNAEGGNAE KAAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

m911.seq
1 ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCCTGATTGG
51 CGCGGCGGCG GTTGCCTTTC TCGCTTCCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTC GGACAAACT TACGCCGTTT ATGCCGATTT CGGCGACATC
151 GCGCGTTTGA AGGTCAATGC CCCCGTCAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAATT
401 CTGCAATGGT TCTGGAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

m911.pep
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

10	20	30	40	50	60
----	----	----	----	----	----

1304

```

g911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAFVK
|||||
m911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAFVK
              10      20      30      40      50      60

              70      80      90      100     110     120
g911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
|||||
m911      SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              70      80      90      100     110     120

              130     140     150     160
g911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
|||||
m911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1  ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGA CTGTTTCG TCCTGATTGG
51 CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTC GGACAAACT TACGCCGTTT ATGCCGATT CGGCGACATC
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAGTT
401 CTGCAATGGT TCTGGAAAC CTTATCGGCA AATTCATGAC GAGTTTGGCC
451 GAGAAAAATG CCGACGGCGG CAATGCCGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAFFGGSDKT YAVYADFGDI
51 GGLKVNAFVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDDGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

m911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAFVK
|||||
a911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAFVK
              10      20      30      40      50      60

              70      80      90      100     110     120
m911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
|||||
a911      SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              70      80      90      100     110     120

              130     140     150     160
m911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
|||||
a911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1  gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51 CGGCATGGCA TTTGCCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

g912.pap

```

1  VKKSSFISAL GIGILSIGMA FASPADAVGQ IRQATQVLT ILKSGDAASA
51  RPKAEAYAVP YFDFQRM TAL AVGNPWR TAS DAQKQALAKE FQTL LIR TYS
101 GTMLKFKNAT VNVKDNPIVN KGGKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGTSLVTVYR NQFGEI I KAK GIDGLIAELK AKNGGK*

```

m912.seq

1	ATGAAAAAAT	CCTCCCTCAT	CAGCGCATTG	GGCATCGGTA	TTTGTAGCAT
51	CGGCATGGCA	TTTGCCGCCC	CTGCCGACGC	GGTAAGCCAA	ATCCGTCAAA
101	ACGCCACTCA	AGTATTGAGC	ATCTTAAAAA	ACGGCGATGC	CAACACCGCT
151	CGCCAAAAAG	CAGAAGCTTA	TGCGATTCCC	TATTTGATTT	TCCAACGTAT
201	GACCGCATTG	CGCGTCGGCA	ACCTTTGGCG	CACCGCGTCC	GACGCGCAAA
251	AACAAGCGTT	GGCCAAAGAA	TTTCAAACCC	TGCTGATCCG	CACCTATTCC
301	GGCACGATGC	TGAAATTAAA	AAACGCCAAC	GTCAACGTCA	AAGACAATCC
351	CATCGTCAAT	AAAGGCGGCA	AAGAAATCAT	CGTCCGCGCC	GAAGTCGGCG
401	TACCCGGGCA	AAAACCCGTC	AACATGGACT	TCACCACCTA	CCTAAGCGGC
451	GGTAAATACC	GTACCTACAA	CGTCGCCATT	GAAGGCGCGA	GCTTGGTTAC
501	CGTGTAACCG	AACCAATTCT	GCGAAATTAT	CAAAGCGAAA	GGCGTGGACG
551	GACTGATTGC	CGAGTTGAAA	GCCAAAAACG	CGGGCAAATA	A

m912.pcp

1 MKKSSLISAL GIGILSIGMA FAAPADAVSQ IRQATQVLS ILKNGDANTA
51 RQKAEAYAIP YFDFQRM TAL AVGNPWR TAS DAQKQALAKE FQTL LIR TYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVP GQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTVYR NOFGEI IKAK GVDGLIAELK AKNGGK*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

q912/m912

	10	20	30	40	50	60
g912.pep	VKKSSFISALGIGILSIGMAFASPADAVGQIRQATQVLTILKSGDAASARPKAEAYAVP					
	:	:	:	:	:	:
m912	MKKSSLISALGIGILSIGMAFAAPADAVSQIRQATQVLSILKNGDANTARQKAEAYAIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g912.pep	YFDFQRM TALAVGNPWR TASDAQKQALAKEFQTL LIR TYSGTMLKFNATVNVKONPIVN					
	:	:	:	:	:	:
m912	YFDFQRM TALAVGNPWR TASDAQKQALAKEFQTL LIR TYSGTMLKLNANVNVKONPIVN					
	70	80	90	100	110	120
	130	140	150	160	170	180
g912.pep	KGKKEIIVRAEVGIPGQKPVNMDFTTYQSGGKYRTYNVAIEGTSLVTVYRNQFGEI IKAK					
	:	:	:	:	:	:
m912	KGKKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTVYRNQFGEI IKAK					
	130	140	150	160	170	180
	190					
g912.pep	GIDGLIAELKAKNGGKX					

1306

```

      |:|||||
m912  GVDGLIAELKAKNGGKX
      190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

```

a912.seq
1   ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
51  CGGCATGGCA TTTGCCGCC CTGCCGACGC GGTAAACCAA ATCCGTCAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
151 CGCCAAAAAG CCGAAGCCTA TGCATTCCC TATTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTGGCG CACCGGTCC GACGCGCAA
251 AACAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAATTAAA AACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGCGGCA AAGAAATCAT CGTCCGCCG GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGATCCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGTGGACG
551 GACTGATTGC CGATTGAAG GCTAAAAACG GCAGCAAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

```

a912.pep
1   MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA
51  RQKAEAYAIP YDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTYR NQFGEI I KAK GVDGLIAELK AKNGSK*

```

m912/a912 98.0% identity in 196 aa overlap

```

m912.pep      10      20      30      40      50      60
MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP
|||||:|||||
a912          10      20      30      40      50      60
MKKSSFISALGIGILSIGMAFAAPADAVNQIRQNATQVLSILKSGDANTARQKAEAYAIP

m912.pep      70      80      90      100     110     120
YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNANVNVKDNPIVN
|||||:|||||
a912          70      80      90      100     110     120
YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNANVNVKDNPIVN

m912.pep     130     140     150     160     170     180
KGGKEIIVRAE VGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYR NQFGEI I KAK
|||||:|||||
a912         130     140     150     160     170     180
KGGKEIIVRAE VGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYR NQFGEI I KAK

m912.pep      190
GVDGLIAELKAKNGGKX
|||||:|||||
a912          190
GVDGLIAELKAKNGSKX
190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

```

g913.seq
1   atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTG GCAGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTACGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTAAACAACC TGC GCGACGT GGT CAGTTTC GGCAGCAATA
251 TCTTGC GTTT GGAc at CAAA cgcgCAAGcg aAGACctcgT CCGcgtcggc
301 atCAATACCA CCTTCGGTTT GGgcgGGCTC ATTGATATTG CCGGcgGgGg
351 cggcgttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
401 GctgGAAAAa cagcaATTAT TCGTgttgc CCGtcttagg cccgtccacc

```

1307

```

451 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
501 tatcggttttc catacccctg ccggacgctg GGgcacgact gCCGCTGCCG
551 CCGTcagtag gcgcgaagc ctcctcgatt tgaccgacag Tctggacgaa
601 gccgcatCG ACAAATACAG CTACACGCGc gacctctata tgAAAGTCCG
651 CGcacgGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
701 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
751 CCCGCCGTTC ACGAAGATTG CGTATCCGAA ACACAGGCAG AAGCAGCAGG
801 GGAAGCCGAA ACGCAACCTG GAACACAACC CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:

```

g913.pep
1  MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
51  AARGYRKVTP KPVVAGVSNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGVP DNKNTLGDTF ASGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYPPKNIVF HTPAGRWGTT AAAAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDIDEL VESAETGAAE
251 PAVHEDSVSE TQEAAGEAE TQPGTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

```

m913.seq
1  ATGAAAAAAA CCGCCTATGC CTCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTGCGCCCT
151 GCGCGCGCGG GCTACCGCAA AGTTGCGCGG AAACCCGTCC GCGCGGCGGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTGAGCTTC GGCAGCAATA
251 TCTTGCCTTT GGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGC
301 ATCAACACCA CTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCCTCGTGGG
401 GATGAAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCACGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGCTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

```

m913.pep
1  MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
51  AARGYRKVAP KPVVAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

g913/m913

```

          10      20      30      40      50      60
g913.pep  MKKTAYAILLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVTP
          |||||:|||||
m913      MKKTAYAFLLLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVAP
          |||||:|||||
          10      20      30      40      50      60

          70      80      90     100     110     120
g913.pep  KPVVAGVSNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGVP
          |||||:|||||
m913      KPVVAGVSNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGIP
          |||||:|||||
          70      80      90     100     110     120

```


1308

	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWN	SNYFVLPVLPSTVR	DALGTGITSVYPPKN	IVFHTPAGRWGTT		
m913	DNKNTLGDTFASWGWN	SNYFVLPVLPSTVR	DALGTGITSVYSPKN	IVFRTVPVGRWGTT		
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAVSTREGLLDLTD	SLDEAAIDKYSYTR	DLYMKVRRARQTGA	TPAEGTEDNIDIDEL		
m913	AVSAVSTREGLLDLTD	SLDEAAIDKYSYTR	DLYMKVRRARQTGA	TPAEGTEDNIDI--DEL		
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAETGAAEPAVHED	SVSETQAEAAEAE	TQPQTQPX			
m913	VESAETGAAETA	VQEDSVSETQAEAAE	TQPQTQPX			
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

a913.seq

1	ATGAAAAAA	CCGCCTATGC	CTTCCTCCTG	CTGATCGGGT	TCGCTCCGC
51	CCCTGCATTT	GCCGAAACCC	GCCCCGCCGA	CCCTTATGAA	GGCTACAACC
101	GCGCCGTTTT	CAAATTC AAC	GACCAAGCCG	ACCGCTACAT	TTTCGCCCTT
151	GCCGCGCGCG	GCTACCGCAA	AGTTGCGCCG	AAACCCGTCC	GCGCCGGCGT
201	GTCCAATTTT	TTTAAACAACC	TGTGCGACGT	GGTCAGCTTC	GGCAGCAATA
251	TCTTGCGCTT	AGACATCAAA	CGCGCAAGCG	AAGACCTTGT	CCGCGTCGGT
301	ATCAACACCA	CTTTCGGTTT	GGGCGGGGTT	ATCGACATCG	CCGGCGCGGG
351	CGGCATTCCC	GACAATAAAA	ACACCTTGGG	CGACACGTTT	GCTTCGTGGG
401	GATGGAAAAA	CAGCAATTAT	TTCGTGTTGC	CCGTCTTAGG	GCCGTCCACC
451	GTCCGCGACG	CGCTCGGCAC	GGGTATTACC	TCCGTTTATT	CGCCCAAGAA
501	TATCGTCTTC	CGCACCCCTG	TCGGACGCTG	GGGCACGACT	GCCGTATCCG
551	CCGTCAGTAC	GCGCGAAGGC	CTGCTCGATT	TGACCGACAG	TCTGGACGAA
601	GCCGCCATCG	ACAAATACAG	CTACACGCGC	GACCTCTATA	TGAAAGTCCG
651	TGCGCGGCAG	ACCGGTGCAA	CACCTGCCGA	AGGTACGGAA	GATAACATCG
701	ACATCGACGA	ATTGGTCGAA	AGTGCCGAAA	CCGGCGCGGC	GGAAACTGCC
751	GTTCAAGAAG	ATTCCGTATC	CGAAACACAG	GCAGAAGCAG	CAGGGGAAGC
801	CGAAACGCAA	CCTGGAACAC	AACCTGGAAC	ACAACCTTAA	

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

a913.pep

1	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVFKFN	DQADRYIFAP
51	AARGYRKVAP	KPVVRAGVSNF	FNNLCDVVSF	GSNILRLDIK	RASEDLVRVG
101	INTTFGLGGL	IDIAGAGGIP	DNKNTLGDTF	ASWGWN	FVLPVLPST
151	VRDALGTGIT	SVYSPKNIVF	RTPVGRWGTT	AVSAVSTREG	LLDLTDSLDE
201	AAIDKYSYTR	DLYMKVRRARQ	TGATPAEGTE	DNIDIDELVE	SAETGAAETA
251	VQEDSVSETQ	AEAAGEAETQ	PGTQPGTQP*		

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVFKFN	DQADRYIFAP	AARGYRKVAP
a913	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVFKFN	DQADRYIFAP	AARGYRKVAP
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPVVRAGVSNF	FNNLCDVVSF	GSNILRLDIK	RASEDLVRVG	INTTFGLGGL	IDIAGAGGIP
a913	KPVVRAGVSNF	FNNLCDVVSF	GSNILRLDIK	RASEDLVRVG	INTTFGLGGL	IDIAGAGGIP
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTFASWGWN	SNYFVLPVLPSTVR	DALGTGITSVYSPKN	IVFRTVPVGRWGTT		
a913	DNKNTLGDTFASWGWN	SNYFVLPVLPSTVR	DALGTGITSVYSPKN	IVFRTVPVGRWGTT		

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	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAEAEETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAEAEETQPGTQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacggttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCTG
451 taggctTCGA CGATTTTGTG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GGTGAAGGTA TGGAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAA TCCCATTG ATGTTTTTGG GCAGGTegaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTGTG TCGGGCGTGg tgTtttGcgC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAg cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPAFAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLV
201 SPVMTAFAPK PMVRNIFIC SGVVCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGTG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTTCGTAGG CTTTCGACGAT TTTTTCGACC AAAGGATGCC GGACAACGTC
501 TTGCGCGGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTTGATGT TTTTGGGCAG GTCGATTTGG
601 CTGGTGTGCG CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TCGGGGTCAG
651 GAACATTTTC ATTTGTTCCG GCGTGGTGTT TTGCGCTTCG TCGAGGATGA
701 TGTATGCGCC GTTGAGCGTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 IRCRKFDXCI GWTDKETDTE TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

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151 DSXASTIFCT KGCRTTSSPV KWKYSPSTL CSFSRASFPD LMFGRSIW
 201 LVSPVMTAFA PKPMRVRNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMP	AFADRISDLEARLAQ	LEHRVAVLES	GGNTVKIDLF	GSNSTMYVC	
m914	MKKCILGILTACAAMP	AFADRIGDLEARLAQ	LEHRVAVLES	GGNTVKIDLF	GSNSTMYVC	
	10	20	30	40	50	60
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDR	NEGVARQKVRQAC	NRETSAMFCGDEA	IRCRKFDXCIGW	TDKETDT-	
m914	SVTPFQKTFEASDR	NEGVARQKVRQAC	NRETSAMFCDEA	IRCRKFDXCIGW	TDKETDTD	
	70	80	90	100	110	120
	120	130	140	150	160	170
g914.pep	-ELGFRLCFSLPDF	PCIGFQTALE	CQSCSADS	XSASTIFCT	TRGCR	TSSPVKWKYSPATP
m914	TELGFRLCFSLPDF	PCIGFQTALE	CQSCSADS	XSASTIFCT	KGCR	TSSPVKWKYSPSTL
	130	140	150	160	170	180
	180	190	200	210	220	230
g914.pep	CSFSRASFPDLMFL	GRSIWLVSPVMTA	FAPKPMRVRNIF	ICSGVVFCASS	SRMMYAPLSV	
m914	CSFSRASFPDLMFL	GRSIWLVSPVMTA	FAPKPMRVRNIF	ICSGVVFCASS	SRMMYAPLSV	
	190	200	210	220	230	240
	240					
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCAGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGTG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGCGGTG CAACCGCGAA ACTTCGGCAA TGTTTTCGCA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTATCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAATGTC AGTCGTGTTT TGCCGATTTCG
451 TAGGCTTCGA CGATTTTTTG CACCAAAGGA TGCCGGACAA CGTCTTCGCC
501 GGTAAGGTG TGGAATACA GCCCTTCCAC GCCGTGCAGT TTCTCACGCG
551 CATCTTTTAA TCCCGATTG ATGTTTTTGG GCAGGTGCAT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCGCCGAAG CCGATGCGGG TCAGGAACAT
651 TTTCATTTGT TCGGGCGTGG TGTTTTGCGC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAG CGTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

```

1  MKKCILGILT ACAAMPADF RIGDLEARLA QLEHRVAVLE SGSNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCEDEA
101 IRCRKFD*CI GWTDKETDTE LGFRICFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTKG CRTTSSPVKV WKYSPSTPCS FSRASFPDLM FLGRSIWLV
201 SPVMTAFAPK PMRVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

m914/a914 98.4% identity in 244 aa overlap

	10	20	30	40	50	60
m914.pep	MKKCILGILTACAAMPADFADRIDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
a914	MKKCILGILTACAAMPADFADRIDLEARLAQLEHRVAVLESGSNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD					
a914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--					
	70	80	90	100	110	
	130	140	150	160	170	180
m914.pep	TELGRICFSLPDPFCIGFQTALEQCSCSADSXASTIFCTKGCRRTSSPVKWKYSPSTL					
a914	TELGRICFSLPDPFCIGFQTALEQCSCSADSXASTIFCTKGCRRTSSPVKWKYSPSTP					
	120	130	140	150	160	170
	190	200	210	220	230	240
m914.pep	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
a914	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	180	190	200	210	220	230
m914.pep	LPRIX					
a914	LPRIX					
	240					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915.seq

1	ATGAAGAAAA	CCCTGTTGGC	AATTGTTGCC	gtTTTCGCCT	TAAGTGCCTG
51	CCGGCaggcg	gaAGaggcac	cgccgCCTTT	ACCCCGGCAG	AtTAGCGacc
101	gttcggtcgg	aCACTAttgC	Agtatgaacc	tgaccgaaca	caacggcccc
151	aaagcccaga	tttttttgaa	cGGCAAACCC	GATCAGCCCG	TTTGGTTCTC
201	CACCGTcaag	cagatgttcg	GCTATACCAA	GCTGCCCGAA	GAGCCCAAAG
251	GCATCCGCGT	GATTACGTT	ACCGATATGG	GCAATGTTAC	CGATTGGACG
301	AATCCTAATG	CCGACACGGA	GTGGATAGAT	GCGAAAAAAG	CCTTTTACGT
351	CATCGACAGC	GGCTTTATCG	GCGGTATGGG	CGCGGAAGAC	GCGCTGCCGT
401	TCGGCAACAA	GGAGCAGGCT	GAAAAATTG	CAAAGGATAA	AGGCGGCAAG
451	GTCGTCGGTT	TTGACGATAT	GCCCGATGCT	TACATTTTCA	AGTAA

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

g915.pep

1	MKKTLLAIVA	VFALSACRQA	EEAPPPLPRQ	ISDRSVGHYC	SMNLTEHNGP
51	KAQIFLNGKP	DQPVWFSTVK	QMFGYTKLPE	EPKGIRVIYV	TDMGNVTDWT
101	NPNADTEWID	AKKAFYVIDS	GFIGGMAED	ALPFGNKEQA	EKFAKDKGGK
151	VVGFDMPDA	YIFK*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915.seq

1	ATGAAGAAAA	CCCTGTTGGC	AATTGTTGCC	GTTTCGCCT	TAAGTGC.tG
51	CCGGCAGGCG	GAAGAGGGAC	CGCCGCCTTT	ACCcCGGCAG	ATTAGCGACC
101	GTTCCGTCGG	AACTATTGTC	AGTATGAACC	TGACCGAACA	CAACGGCCCC
151	AAAGCCCAAG	TTTTCTTGAA	CGGCAAACCC	GATCAGCCCG	TtTGGTTCTC
201	CACCATCAAG	CAGATGTTTC	GCTATACCAA	GCTGCCCGAA	GAGCCTAAAG
251	GCATCCGCGT	GATTACGTT	ACCGATATGG	GCAATGTTAC	CGATTGGACG
301	AATCCCAATG	CCGACACGGA	GTGGATGGAT	GCGAAAAAAG	CCTTTTACGT
351	CATCGACAGC	GGCTTTATCG	GCGGTATGGG	TGCGGAAGAC	GCGCTGCCGT
401	TCGGCAACAA	AGAGCAGGCT	GAGAAATTG	CAAAGGATAA	AGGCGGTAAG

```

1  MKKTLILAIVA VSALSXCRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMGAED ALPFGNKEQA EKFAKDGGK
151 VVGFDMPDPT YIFK*

```

ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m915.pep	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	:					
g915	MKKTLLAIVAVFALSACRQAEAEPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFGYTKLPEEPKGIIRVIYVTDMGNVTDWTPNPADTEWMDAKKAFYVIDS					
	:					
g915	DQPVWFSTVKQMFGYTKLPEEPKGIIRVIYVTDMGNVTDWTPNPADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDGGKVVGFDDMPDYIIFKX					
	:					
g915	GFIGGMGAEDALPFGNKEQAEKFAKDGGKVVGFDDMPDAYIIFKX					
	130	140	150	160		

1	ATGAAAAAAA	CCCTGTTGGC	AATTGTTGCC	GTTTCGCCT	TAAGTGCCTG
51	CCGGCAGGCG	GAAGAGGGAC	CGCGCCTTT	ACCCCGGCAG	ATTAGCGACC
101	GTTCGGTCCG	ACACTATTGC	AGTATGAACC	TGACCGAACA	CAACGGCCCC
151	AAAGCCGACA	TTTTCTTGAA	CGCCAAACCC	GATCAGCCCG	TTTGCTTCTC
201	CACCATCAAG	CAGATGTTCC	GCTATACCAA	GCTGCCCGAA	GAGCCTAAG
251	GCATCCGCGT	GATTTACGTT	ACCGATATGG	GCAATGTTAC	CGATTGAGAC
301	AATCCCAATG	CCGACACGGA	GTGGATGGAT	GCGAAAAAAG	CCTTTTACGT
351	CATCGACAGC	GGCTTTATCG	CGGGTATGGG	TGCGGAAGAC	GCGCTGCCGT
401	TCGGACACAA	AGAGCAGGCT	GAGAAATTTG	CAAGGATAAA	AGGCGGTAA
451	GTTGTCGGTT	TCGACGATAT	CGCTGATACC	TATATTTTCA	AATAA

```

1  MKKTLIAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDGGGK
151 VVGFDMPDT YIEF*

```

```

              10      20      30      40      50      60
m915.pep      MKKTLLLAIVAVSALSXCRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
              |||||
a915           MKKTLLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
              10      20      30      40      50      60

              70      80      90      100     110     120
m915.pep      DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
              |||||
a915           DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS

```

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccact cgcCGTCctg actgctTtgc tgcttgccagc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaaa
101 accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTGCGCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAAATCCG
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCCT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGTACGGAC AAGCTGCCGG ACAACCAGTG
501 GGATTTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACAT
601 TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GGCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTTG ATGGAGGACG
1001 AATTTAaaaa CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCTAT CCGGCCGCG GCATTGAAGT TTATGGTGCG
1101 CCA GTGGCAG GATGTGAAG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKQNG IKVTYDVYDS DETLESKVL T GSKGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKALGTD KLPDQNDLV FNPEYTFKLK QCGISYLD SA AEIYPMVLNY
201 LKGNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDLNIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCTT GGCCGTCCTG ACTGCTTTGC TGCTTGCCAGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAAACGT ATTGAAAATT TACAACTGGT CGGAATATGT CGATCCGGAA
151 ACCGTGCGCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGTACGGAC AAGCTGCCGG ACAACCAGTG
501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC

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1314

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751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAAGTGCAG GATGTGAAGG CGGGGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

```

m917.pep
  1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
 51 TVADFEKKNG IKVTYDVYDS DETLESKVLTKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLDLS AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPKKEGVI IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAENQNVLKIYNWSEYVDPETVADFEKKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAENQNVLKIYNWSEYVDPETVADFEKKNG					
	10	20	30	40	50	60
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
g917	EMMRLMDGVDPDHEYAVPFYWGNTFAINTERVKKALGTDKLPDNQWDLVFNPEYTFKLK					
	130	140	150	160	170	180
m917.pep	190	200	210	220	230	240
	QCGISYLDLSAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFSSGFIDDLA					
g917	QCGISYLDLSAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	250	260	270	280	290	300
	RGDTCVTIGFGGDLNIAKRRRAEEAGGKEKIRVMPKKEGVIWVDSFVIPKDAKNVANAHK					
g917	RGDTCVTIGFGGDLNIAKRRRAEEAGGKEKIRVMPKKEGVIWVDSFVIPKDAKNVANAHK					
	250	260	270	280	290	300
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNFSFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARDLMEDEFKNDNTIFPSGEDLKNFSFIMVPIRPA					
	310	320	330	340	350	360

370

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m917.pep ALKFMVRQWQDVKAGKX
 |||||
g917 ALKFMVRQWQDVKAGKX
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

a917.seq
1 ATGACCAAAC ATCTGCCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGACAGC
51 GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA
101 ACCGAAACGT ATTGAAAATT TACAACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTAAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCTG
251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCG ACAAACAGTG
501 GGATTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCGG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

a917.pep
1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
51 TVADFEKKNG IKVTYDVYDS DETLESKVL T GSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDQWDLV FDPEYTSKLG QCGISYLD SA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNEFTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

m917/a917 99.7% identity in 376 aa overlap

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAEQNVLKIYNWSEYVDPETVADFEKKNG					
a917	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAEQNVLKIYNWSEYVDPETVADFEKKNG					
	10	20	30	40	50	60
m917.pep	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
a917	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLG					
a917	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLG					
	130	140	150	160	170	180
m917.pep	QCGISYLD SAAEYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
a917	QCGISYLD SAAEYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	QCGISYLD SAAEYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
a917	QCGISYLD SAAEYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					

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a917      QCGISYLDAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRTSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pep  RGDTTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKEGVGIWVDSFVI PKDAKNVANAHK
           |||||||
a917      RGDTTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKEGVGIWVDSFVI PKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFVITYAPSSKPAELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           |||||||
a917      YINDFLDPEVSAKNGNFVITYAPSSKPAELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360

           370
m917.pep  ALKFMVRQWQDVKAGKX
           |||||||
a917      ALKFMVRQWQDVKAGKX
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC ACCTGCTCCG CTCGCCCTCG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCCG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATT TGGCAAAAGC CTGCAATCCT
251 TCCGCTCCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGCCCCAAG CCTTTCAAAC CCCCGTGCA TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGC cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtacggt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGAc ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACGCCCG ACCTCTCCCG ATTCCCATC ACCGCGCGCA CAACGGcaat
651 caaaggCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCGgcgTT GACGGCAAag cccCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTTCATGCAC AtccaaggCT CGGGCCGCT
801 GAAAAACCCg tccggcaaat acatCCGCat cggTaagcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcac aaagcCTATA TGGCGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GCGGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

g919.pep

```

1  MKCHLLRSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAQQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTEARFFPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIRGR FEGRFLPYH TRNQINGGAL DGRAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGFPVGAIG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

This corresponds to the amino acid sequence <SEQ ID 2792; ORF 919>:

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N.gonorrhoeae*
ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF
919.ng) from *N. gonorrhoeae*:
m919/g919

	10	20	30	40	50	60
m919.pep	MKKYLFR	AALYGLIAAA	ILAACQSKSI	QTFFQPDTS	VSINGPDRP	VGIPDPAGTT
	:	:	:	:	:	:
g919	MKKHLLRS	ALYGLIAAA	ILAACQSR	SISQTFFQPD	TSVINGPDR	PAGIPDPAGTT
	:	:	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLS	PLPHWAAQD	FAKSLQSF	RLGCANLKN	RQGWQDVCA	QAFQTPVHSF
	:	:	:	:	:	:
g919	YTVVPHLS	MPHWAAQD	FAKSLQSF	RLGCANLKN	RQGWQDVCA	QAFQTPVHSF
	:	:	:	:	:	:
	70	80	90	100	110	120

```

a919.seq
1 ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGCATCG CGCGGCCAT
51 CCTCGCCGCT TGCCAAAGCA AGACATCCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC GCACCCGCCG
151 GGAACGACGG TCGGCGGCCG CGGGGCCGTT TATACCGTTG CTCGCGACCT
201 GTCCTGCCCC CTCTGGGCGG CGCAGGATT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGCGCCAAG CTTTTCAAAC CCCCGTCCAT TCGGTCAGG CAAAACAGTT
351 TTTTGAACGC TATTTACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTTC GGTATTCCCG ACGATTTTAT
501 CTCGCTCCCC CTGCTGCCG GTTTGCGGAG CGGAAAAGCC TTGTGCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCCA ATTCCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC CGCGTCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAG CCCGATACT ACCTTAGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAAACCCG TCCGCAAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCAT GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GACGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCTGAGAGCT TACCGGAAGC AGCAATACG GGCCTGTCGG CGCATGGGG
1051 ACGCGCTGTA TGGCGGAGTA CGCCGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAGG

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1319

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1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CCGGATATGT CTGGCAGCTT CTGCCCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```

      1 MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
      51 GTTVGGGGAV YTVVPHLSLP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
     101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
     151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
     201 HTADLSQFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
     251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
     301 KLGQTSMQGI KAYMQQNPR LAEVLGQNPS YIFFRELTS SNDGFPVGALG
     351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
     401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap
      10      20      30      40      50      60
m919.pep MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
      |||||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
      10      20      30      40      50      60

      70      80      90     100     110     120
m919.pep YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFOAKQFFER
      |||||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER
      70      80      90     100     110     120

      130     140     150     160     170     180
m919.pep YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
      |||||
a919      YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
      130     140     150     160     170     180

      190     200     210     220     230     240
m919.pep LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
      |||||
a919      LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m919.pep DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
      |||||
a919      DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
      250     260     270     280     290     300

      310     320     330     340     350     360
m919.pep KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELTS SNDGFPVGALGTPLMGEYAGA
      |||||
a919      KLGQTSMQGIKAYMQQNPRLAEVLGQNPSYIFFRELTS SNDGFPVGALGTPLMGEYAGA
      310     320     330     340     350     360

      370     380     390     400     410     420
m919.pep VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
      |||||
a919      VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
      370     380     390     400     410     420

      430     440
m919.pep QKTTGYVWQLLPNGMKPEYRPX
      |||||
a919      QKTTGYVWQLLPNGMKPEYRPX
      430     440

```

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
151 GGCTGGAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTCCGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCT GGAAATCGTC
301 CCGCTGGACA ATCccgcccga caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtgttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtaccAT
401 TTGacggctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT cGacaccac cgacggcgaa ggCGaagtgg acatcatCCC
501 CTTGCgccaa GGCTTttgga aAgcGAGTGT CGAATAcaaa gccgAttctc
551 CCGATcaaAG CCTGTGccga AAACAggcgA ACTACaCaac TTtaaccttc
601 caaatcgccc attctCacca tTaa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YQYRSNRPVK DGSYLVTAEY QPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIT KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCACGCC CACCGmGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTAAACC TTCCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKXK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
```

1321

201 SDRSKTHXXE AQAFSDSTDD KGEVDIIXLR QGFWKANVEH KTDFFDQSVK
 251 QKQANYSTLT FQIGHSHH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 920 shows 91.3% identity over a 207 aa overlap with a predicted ORF (ORF 920.ng) from *N. gonorrhoeae*:

g920/m920

				10	20	30
g920.pep				PMQLVTEKGKENMIQ	RGTYNYQYRSNR	FPVK
m920	GGEYLKADLGYGEFPELEPIAKDRLHIFSKPMQLVTEKGKENMIQ	RGTYNYQYRSNR	FPVK			
	40	50	60	70	80	90
g920.pep	DGSYLVTAEYQPTFRSKNKAGWKQAGIKEMP	DASYCEQTRMFGKNIVNVGHESADTAII	IT			
m920	DGSYLVTAEYQPTFRSKNKAGWKQAGIKEMP	DASYCEQTRMFGKNIVNVGHESADTAII	IT			
	100	110	120	130	140	150
g920.pep	KPVGQNL	IVPLDNPA	DIHVGRF	KVRVLF	FRGEPL	NATVTATFDGFDTS
m920	KPVGQNL	IVPLDNPA	DIHVGRF	KVRVLF	FRGEPL	NATVTATFDGFDTS
	160	170	180	190	200	210
g920.pep	QAFSDTTDGE	GEVDIIP	LRQGFWKASVEYKAD	FPDQSLCR	QKQANYTT	LTFTQIAHSHHX
m920	QAFSDTTDGE	GEVDIIP	LRQGFWKASVEYKAD	FPDQSLCR	QKQANYTT	LTFTQIAHSHHX
	220	230	240	250	260	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2799>:

a920.seq

1	TGAAAGAAAA	CATTGACACT	GCTCGCCGTT	TCCGCCCTAT	TTGCCGCATC
51	CGCCACGCC	CACCGCGTCT	GGGTGGAAC	CGCCACACG	CACGGCGGCG
101	AATACCTTAA	AGCCGACTTG	GGCTACGGCG	AATTCCCGA	ACTCGAACCC
151	ATCGCCAAAG	ACCGCCTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAAAAGGC	AAGGAAAACA	TGATTCAACG	CGGCACATAC	AACTACCACT
251	ACCGAAGCAA	CCGTCCCGTT	AAGGACGGCA	GTTACCTCGT	CATCGCCGAA
301	TATCAGCCTA	CTTTCTGGTC	AAAAAACAAA	GCAGGCTGGA	AACAGGCGGG
351	CATCAAAACA	ATGCCTGACG	CAAGCTATTG	CGAACAAACC	CGAATGTTCC
401	GCAAAAACAT	CGTCAACGTC	GGACACGAAA	GCGCGGACAC	CGCCATCATC
451	ACCAAACCGG	TCGGACAAAA	CTTGGAATC	GTCCCGCTGG	ACAATCCCGC
501	CAACATTCAC	GTAGGCGAAC	GCTTCAAAGT	CCGCGTTCTG	TTCCGTGGCG
551	AACCGCTGCC	CAATGCCACC	GTTACCGCCA	CCTTTGACGG	CTTCGACACC
601	AGCGACCGCA	GCAAAACGCA	CAAAACCGAA	GCACAGGCTT	TCTCCGACAG
651	CACAGACGAC	AAAGGCGAAG	TGGACATCAT	CCCCTGCGC	CAAGGCTTCT
701	GGAAGCCCAA	TGTCGAACAC	AAAGCCGACT	TCCCGGATCA	AAGCGTGTGC
751	CAAAAACAGG	CGAACTACTC	GACTTTAACC	TTCCAAATCG	GCCATTTCGA
801	CCATTAA				

This corresponds to the amino acid sequence <SEQ ID 2800; ORF 920.a>:

a920.pep

1	*KKTLLTLLAV	SALFAASAHA	HRVWVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKDLRHIFS	KPMQLVTEKG	KENMIQRTY	NYQYRSNRPV	KDGSYLVAIE
101	YQPTFWSKNK	AGWKQAGIKQ	MPDASYCEQT	RMFGKNIVNV	GHESADTAII
151	TKPVGQNL	IVPLDNPA	DIHVGRF	KVRVLF	FRGEPLNAT
201	SDRSKTHKTE	AQAFSDSTDD	KGEVDIIP	LRQGFWKANVEH	KADFFDQSVK
251	QKQANYSTLT	FQIGHSHH*			

m920/a920 97.0% identity in 267 aa overlap

1322

	10	20	30	40	50	60
m920.pep	MKKTLTLLSVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
a920	XKKTLLTLLAVSALFAASAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m920.pep	KPMQLVTEKGKENMIQRGTINYQYRSNRPVKDGSYLVIAEYQPTFWSKXKAGWKQAGIKE					
a920	KPMQLVTEKGKENMIQRGTINYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m920.pep	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
a920	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m920.pep	FRGEPLPNATVTATFDGFDTSDRSKTHXXEAQAFSDSTDGKGEVDIIXLRQGFWKANVEH					
a920	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDGKGEVDIIPLRQGFWKANVEH					
	190	200	210	220	230	240
	250	260	269			
m920.pep	KTDFFDQSVQCQKQANYSTLTFQIGHSHHX					
a920	KADFFDQSVQCQKQANYSTLTFQIGHSHHX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA  CATTGACACT  GCTCGCcggt  TcCGCACTAT  TTGCCACATc
51  cgCaCACCCC  CACCgCGTCT  GGGTCGAAAC  CgccCACAg  cAcgCGGCG
101 AATACCTTAA  AGCCGACTTG  GGCTACGGCG  AATTCCCCGA  ACTCGAACCC
151 ATCGccAAAG  ACCgccTGCA  CATCTTCAGC  AAACCGATGC  AGCTGGTTAC
201 CGAAAAAGGT  AAGGAAAACA  TGATTCAACG  CGGCACATAC  AACTACCAAT
251 ACCGCAGCAA  CCGTCCCCTC  AAAGACGGCA  GCTACCTCGT  TACCGCCGAA
301 TATCAGCCTA  CTTTCCGGTC  AAAAAACAAA  GCAGGCTGGA  AACAGGCTGG
351 CATCAAAGAA  ATGCCTGACG  CAAGCTATTG  CGAACAAACC  CGTATGTTTC
401 GTAAAAACAT  TGTCAACGTG  GGACACGAAA  GCGCGGACAC  CGCCATCATC
451 ACCAAACCGG  TCGGACAAAA  CTTGGAAATC  GTCCCGCTGG  ACAATCCCGC
501 CAACATTCAC  GTAGGCGAAC  GCTTCAAAGT  CCGCGTTCTG  TTCCGTGGCG
551 AACCGCTGCC  CAATGCCACC  GTTACCGCTA  CATTTGACGG  CTTTCGACAC
601 AGCGACCGCA  GCAAAACGCA  CAAAACCGAA  GCCCAAGCCT  TCTCCGACAC
651 CACCGACGGC  AAAGGCGAAG  TGGACATCAT  CCCCTTGC GC  CAAGGCTTTT
701 GGAAGCGGAG  TGTCGAATAC  AAAGCCGATT  TCCCCGATCA  AAGCCTGTGC
751 CAAAAACAGG  CGAACTACAC  AACTTTAACC  TTCCAATCG  GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLTLLAV  SALFATSAP  HRVWVETAHT  HGGEYLKADL  GYGEFPELEP
51  IAKDRLHIFS  KPMQLVTEK  KENMIQRGTY  NYQYRSNRPV  KDGSYLVTAE
101 YQPTFRSKNK  AGWKQAGIKE  MPDASYCEQT  RMFGKNIVNV  GHESADTAII
151 TKPVGQNLEI  VPLDNPAIH  VGERFKVRVL  FRGEPLPNAT  VTATFDGFDT
201 SDRSKTHKTE  AQAFSDTIDG  KGEVDIIPLR  QGFWKASVEY  KADFFDQSLC
251 QKQANYTTLT  FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA  CATTGACACT  GCTCGCCGTT  TCCGCCCTAT  TTGCCACATC
51  CGCCCACGCC  CACCGCGTCT  GGGTCGAAAC  CGCCACACG  CACGGCGGCG
101 AATACCTTAA  AGCCGACTTG  GGCTACGGCG  AATTCCCCGA  ACTCGAACCC
151 ATCGCCAAAG  ACCGCCTGCA  CATCTTCAGC  AAACCGATGC  AGCTGGTTAC
201 CGAAAAAGGC  AAGGAAAACA  TGATTCAACG  CGGCACATAC  AACTACCACT
251 ACCGAAGCAA  CCGTCCCCTT  AAGGACGGCA  GTTACCTCGT  CATCGCCGAA

```

1323

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGACACC
601 AGCGACCGCA GCAAAACGCA CAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTGGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAATCG GTCATTGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

```

m920-1.pep
1  MKKTLTLLAV SALFATSAAH HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAQFSDSTD KGEVDIIPLR QGFWKANVEH KTDFFDQSV
251 QKQANYSTLT FQIGHSHH*

m920-1/g920-1 96.3% identity in 268 aa overlap

          10      20      30      40      50      60
m920-1.pep MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
          |||
g920-1      MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
          10      20      30      40      50      60

          70      80      90      100     110     120
m920-1.pep KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE
          |||
g920-1      KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVIAEYQPTFRSKNKAGWKQAGIKE
          70      80      90      100     110     120

          130     140     150     160     170     180
m920-1.pep MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL
          |||
g920-1      MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL
          130     140     150     160     170     180

          190     200     210     220     230     240
m920-1.pep FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAQFSDSTD KGEVDIIPLRQGFWKANVEH
          |||
g920-1      FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAQFSDTD KGEVDIIPLRQGFWKASVEY
          190     200     210     220     230     240

          250     260     269
m920-1.pep KTDFFDQSVCKQKQANYSTLT FQIGHSHHX
          |||
g920-1      KADFFDQSLCQKQANYTTLT FQIGHSHHX
          250     260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

```

a920.seq
1  TGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51  CGCCCACGCC CACCGCTGCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGACACC
601 AGCGACCGCA GCAAAACGCA CAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTGGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAATCG GCCATTGCA
801 CCATTAA

```


This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

```

a920.pep
1  *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRTY NYQYRSNRPV KDGSYLIVIAE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TRPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSVK
251 QKQANYSTLT FQIGHSHH*

m920-1/a920 98.9% identity in 267 aa overlap

      10      20      30      40      50      60
m920-1.pep MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
a920      XXXKTLTLLAVSALFAASAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
      10      20      30      40      50      60

      70      80      90     100     110     120
m920-1.pep KPMQLVTEKGKENMIQRTYNYQYRSNRPVKDGSYLIVIAEYQPTFWSKNKAGWKQAGIKE
a920      KPMQLVTEKGKENMIQRTYNYQYRSNRPVKDGSYLIVIAEYQPTFWSKNKAGWKQAGIKQ
      70      80      90     100     110     120

      130     140     150     160     170     180
m920-1.pep MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLEIVPLDNPANIHVGERFKVRVL
a920      MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLEIVPLDNPANIHVGERFKVRVL
      130     140     150     160     170     180

      190     200     210     220     230     240
m920-1.pep FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
a920      FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
      190     200     210     220     230     240

      250     260     269
m920-1.pep KTDFFPDQSVKQKQANYSTLTFQIGHSHHX
a920      KADFPDQSVKQKQANYSTLTFQIGHSHHX
      250     260
  
```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

```

g921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51 Ccagtctatt tatGtgccca cattgacgga aatccccgTg aatcccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCCTCG
151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGCTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggAA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

```

g921.pep
1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51 HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAVD SQRGINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMKMQP LK*
  
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

```

m921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51 CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
  
```

1325

251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:

m921.pep

1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
 101 YEIYLRSID SQRGAINTAQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng) from *N. gonorrhoeae*:

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
g921	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLAPSHWADVAKISD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSIDSQRGAINTAQ					
	:					
g921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSIDVDSQRGEINTAQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	:					
g921	SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2811>:

a921.seq

1 ATGAAAAAT ACCTTATCCC TCTTCCATT GTGGCAGTTC TTTCCGGCTG
 51 CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
 101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTCCGCCT TGCCTCTTCG
 151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
 251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:

a921.pep

1 MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
 101 YEIYLRSID SQRGAINTAQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

m921/a921 99.4% identity in 162 aa overlap

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
a921	MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	10	20	30	40	50	60

1326

	70	80	90	100	110	120
m921 . pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921 . pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922 . seq

```

1   ATGGAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCCGC GTTTGACGCG
151 GCAGCCGTAC CGGTATCCGA CAGCGGTTT GCCGCCAATG CAAATGTCCG
201 CCGTTTGTG GACGATGAAG TCGGGAAGG GGATTTTTC CAGCGCGAAT
251 GGCAGGATT TTTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATt
301 ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGtgttcc gCacggGAAa
351 ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaAacc
401 gcgcggttat cgatgatgtg gcgCAAAAat acggcgtGCC TGCCGAGCTT
451 ATCGTGGCGA TTATCGGGAT TGAAACGAAT TACGGCAAAA ATACGGGCAG
501 TTTCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551 GCGCCGGTT TTTCCAAAAA GAATTGGTCG AGCTTTTAA GCTGGCAAAA
601 GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651 GGGTATGCCG CAATTTATGC CTTGAGCTA CCGGAAATGG GCGGTGATT
701 ATGAcgggga cggacatCGG GATATatggg GCAACGTcgg tgatgtegcg
751 gcatcggTTG CCAATTatata gaagCAGCAC GGTGGCGCA CgggcggTAA
801 AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CaggcAATCA
851 TTGGCGAAAA AACCGCCCTG ACGCGACGG TGGCGGATT GAaggCGTAc
901 ggcacatcc ccggggaaac GCTCGCAGAT GATGAAAAGg cgGTTTGTt
951 CAACTGGAA ACCGCACCCG GCGTGTTTGA ATATTATTG GGCTTGAACA
1001 ATTTTATAC GGTATGGCAG TACAACCACA GCCGATGTA TGTAAcgcg
1051 gtcaggGACA TTGCCAATTC GCTCGCGGC CCGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922 . pep

```

1   MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KESRPAFDA
51  AAVPVSDSGF AANANVRRFV DDEVGKDFS QAEWQDFFDK AAYKADIVKI
101 MHRPSTSRPW YVFR TGNSGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
151 IVAIIGIETN YGKNTGSFRV ADALATLGFY YPRRAGFFQK ELVELLKLAK
201 EEGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251 ASVANVMQKH GWR TGGMKLV SATLAPADV QAIIGEKTAL TRTVADLKAY
301 GIIPGETLAD DEKAVLFKLE TAPGVFEYYL GLNNFYTVWQ YNHSRMYVTA
351 VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922 . seq

```

1   ATGAAAAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACGCCCC TCCACATCG GTCCGTGGTA
351 TGTGTTCCGC ACGGGAAT CCGGCAAGGC GAAATTCGC GGCGCGGCC
401 GGTTTTATGC GGAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCTG CCGAACTTAT CGTGCGGTT ATCGGATTG AAACGAATTA
501 CCGCAAAAT ACGGGCAGT TCCGTGTGGC GGACGATTG GCGACCTTAG
551 GCTTTGATTA CCCCCCGC GCCGGTTTT TCAAAAAGA ATTGGTCGAG

```

m922.ppt

1	<u>MKKRKILPL</u>	<u>ICLAALSACT</u>	AMEARPPRAN	EAQAPRAVEM	KKESRPAFDA
51	AAVFDAAAVP	VSDSGFAANA	NVRRFVDDVE	GKGDFSRAEV	QDFFDKAAAYK
101	ADIVKIMHVR	STSRPWFYVR	TGNSGKAFER	GARRFYAENR	ALIDDDVAQYK
151	VGPAELIHAV	IGIETWYGNK	TGSRFVADAL	ATLGFDYPRR	AGFFQKELVE
201	LLKLAKEEGG	DVFAFKGSYA	GAMGMPQFMP	SSYRKWAVDY	DGDGHRDIWG
251	NVGDVAASVA	NYMKQHGWRV	GKKMLVSTATL	APGADVQAI	I GEXTALTRTV
301	ADLMYAGIIP	GEELLADDEKA	VLFKLETAPG	VFEYYLGLNN	FYTVQKYNHS
351	RRKYVTAVRDI	ANSLGGPGGL*			

Homology with a predicted ORF from *N. gonorrhoeae*

m922/g922

		10	20	30	40	50	60
m922.pep		MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKKESRPAFDAAAVFDAAAVP					
		:					
g922		MEKRKILPLAICLAALSACTAMEARTPRANEQAQAPRADEMKKESRPAFDAA-----AVP					
		10	20	30	40	50	
		70	80	90	100	110	120
m922.pep		VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
				:			
g922		VSDSGFAANANVRRFVDDEVGKGDFSQAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
		60	70	80	90	100	110
		130	140	150	160	170	180
m922.pep		TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL					
		: : :		:		:	
g922		TGNSGRAKFHGAARRFYAENRAVIDDVAQKYGVPAELIVAIIGIETNYGKNTGSFRVADAL					
		120	130	140	150	160	170
		190	200	210	220	230	240
m922.pep		ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
g922		ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
		180	190	200	210	220	230
		250	260	270	280	290	300
m922.pep		DGDGHRDIWGNVGDVAASVANYMKQHGWRGTGGKMLVSATLAPGADVQAIIGEKTALTRTV					
g922		DGDGHRDIWGNVGDVAASVANYMKQHGWRGTGGKMLVSATLAPGADVQAIIGEKTALTRTV					
		240	250	260	270	280	290
		310	320	330	340	350	360
m922.pep		ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSMYVTVAVRDI					
g922		ADLKAYGIIIPGETLADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSMYVTVAVRDI					

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	300	310	320	330	340	350
		370				
m922 . pep	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922.seq
1  ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCCGCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACCGC
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACGCCGCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAATTT CCGGCAAGGC GAAATTTTCG GCGCGCGGCC
401 GGTTTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCCTG CCGAATTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CCGCAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCCG GCCGGGTTT TCCAAAAAGA ATTGGTCGAG
601 CTTTAAAGC TGGCAAAAGA AGAAGGCGGC GATGTTTTCG CCTTAAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AATGTTGGCG ATGTCGCGGC ATCGATTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAAA TACTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GGCGAAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGTA AGGCGTACGG CATCATCCCC GGCGAAGAGC TTGCCGATGA
951 TGAAAAGGCG GTTTTGTTC AACTGGAAAC CGCACC CGGC GTGTTTGAAT
1001 ATTATTTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAATCACAGT
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTTCG TTGGCGGCCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922.pep
1  MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KKE SRPAFDA
51  AAVFDAAAVP VDSGFAANA NVRRFVDEV GKGD FSRAEW QDFFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPAELIVAV IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKEEGG DVFAFKG SYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHWRT GSKILVSATL APGADVQAI GEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922 . pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKKE SRPAFDAAVFDAAAVP					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEQAQAPRADEM KKE SRPAFDAAVFDAAAVP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m922 . pep	VDSGFAANANVRRFVDEVGKGD FSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
a922	VDSGFAANANVRRFVDEVGKGD FSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m922 . pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL					
a922	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL					
	130	140	150	160	170	180
	190	200	210	220	230	240

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```

m922.pep  ATLGFDPYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ATLGFDPYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          190      200      210      220      230      240

          250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGEKALTRTV
          ||||||||||||||||:||||||||||||||:||||||||||||||:||||||||||||||
a922      DGDGHRDIWGNVGDVAASIANYMKQHGWRTGGKILVSATLAPGADVQAIIGEKALTRTV
          250      260      270      280      290      300

          310      320      330      340      350      360
m922.pep  ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          310      320      330      340      350      360

          370
m922.pep  ANSLGGPGLX
          |||||||||
a922      ANSLGGPGLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCTGTC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCTG CTCCTGCCTG CCTTGTTCCG
201 CGGTTGGACG GCGGCATACT TGGGTAGTAG GATGTTTCCG CATAAAACGG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGAATGTTT GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTC GTTCCGCCCG AACTTTTTGT
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRAVR
51  GKRRIPHLRL LLPALFGGWT GAYLGSRMFR HKTAKKRFV LFRLTVSGNV
101 LATCILIDYF VPPELTVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GCGCGTATT TCGGCAGCAT GACATTCAA CATAAGACAG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGAATGTTT AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTAA ACCAGTACGG
351 CGTTGCCTCG CCTTGCCGTA CTATTGTGAC TGTCTGCGGC TTCGTCGCCT
401 TGTCTGATT TTTGTTAATC CACTATAT.T ATTTTGTCCC GCCTGAATTT
451 TTCGTAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCAR
51  GQRRIPHLRL LLPALLGGWV GAYFGSMTFK HKTAKKRFV LFRLTVSGNV
101 LATLILYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HYXYFVPEF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

	10	20	30	40	50	60
g923.pep	MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLYAFALYGIDKRRVARGKRRIP E HRL					
m923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLYAFALYGIDKRC A I R G Q R R I P E H R L					
	10	20	30	40	50	60
	70	80	90	100		
g923.pep	LLPALFGGWTGAYLGSRMFRHKTAKKRFVVLFR LTVSGNVLATC I L I D-----					
m923	LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFR LTVSGNVLATL I L I Y S G L N L N Q Y G V A S					
	70	80	90	100	110	120
			110	120		
g923.pep	-----YFVPPEL F V K L G Q H L X					
m923	P C R T I C T V C G F V A L S X F L L I H Y I Y F V P P E F F V K L G Q N T X					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923.seq

```

1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTCTCTGC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAACGCGG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CCTTGTTTCG
201 CCGTTGGGCG GCGGCATACT TGGGCAGCAG GATATTCAGG CATAAACCG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGA CTGTTTC GGGCAATGTC
301 CTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTA.GCTC AAAGAGAACG ATTCTCTAAG GTGCTGAAGC
401 ACCAAGTGAA TCGGTTCCGT ACTATTGTA CTGTCTGCGG CTCGTGCGC
451 TTGTCTGAT TTTTGTTAAT CCACTAT.AT TATTTTGTCC CGCCTGAATT
501 TTTCTGAAAA CTCGGGCAGA ATACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923.pep

```

1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRAVR
51  GKRRIP E HRL LLPALFGGWA GAYLGSRIFR HKTAKKRFV V LFR LTVSGNV
101 LATLIL I YSG LNLNQYGVAS PXAQRERFSK VLKHQVNRFR TICTVCGFVA
151 LS*FLLIHYX YFVPPEFFVK LGQNT*

```

m923/a923 84.6% identity in 175 aa overlap

	10	20	30	40	50	60
m923.pep	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLYAFALYGIDKRC A I R G Q R R I P E H R L					
a923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLYAFALYGIDKRRVARGKRRIP E HRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m923.pep	LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFR LTVSGNVLATL I L I Y S G L N L N Q Y G V A S					
a923	LLPALFGGWAGAYLGSRIFRHKTAKKRFVVLFR LTVSGNVLATL I L I Y S G L N L N Q Y G V A S					
	70	80	90	100	110	120
			130	140	150	159
m923.pep	P C-----R T I C T V C G F V A L S X F L L I H Y X Y F V P P E F F V K L G Q N T X					
a923	P X A Q R E R F S K V L K H Q V N R F T I C T V C G F V A L S X F L L I H Y X Y F V P P E F F V K L G Q N T X					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

g925.seq

```

1  ATGAAACAAA TGCTTTTGGC cgtcggcgtg ggcGCGGTGT TGGCGGGCTG
51  CGGCAaggat gcCGGCGGtt acgagggTtA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTttACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGGCG
351 ACAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

g925.pep

```

1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51  KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKGQTA QAYLDARNAL PSNQTYYQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

m925.seq (partial)

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAG AAAAAGGCAA TTACTTCCTT
.....

```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

m925.pep (partial)

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFL				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKGQT				
	60	70	80	90	100
	110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

g925-1.seq

```

1  ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTttACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGGCG
351 ACAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51 KINVFTGKEE SLLSEKDG LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

m925-1.seq

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51 CGGCAAGGAT GCCGCGGTT ACAGGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTGTCTGA
201 AAAAGACGGC GCGCTTTCGA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAG
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

m925-1.pep..

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL
51 NKIHVVTGKE ESLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAAAMKDKI IAHQKKCGQT AQAYRDARNA LPSNQTYQQH LAAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTGKE					
g925-1	MKQMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE					
	10	20	30	40	50	
	70	80	90	100	110	120
m925-1.pep	ESLLSEKDGALSINTGIGEIPKLSDDGKELYVERRQYVKTDAAAMKDKIIAHQKKCGQT					
g925-1	ESLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAAMKDKIIAHQKKCGQT					
	60	70	80	90	100	110
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYQQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX					
g925-1	AQAYLDARNALPSNQTYQQRQAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

a925-1.seq

```

1  AATAAAATCA ACGTGTTCAC AGGTAAGGAA GAATCTATGC TTTGTCTGA
51 AAAAGACGGC GCGCTTTCGA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAG
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTCAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

a925-1.pep

```

1  NKINVFTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51 KTDAAAMKDKI IAHQKKCGQT AQAYLDARNA LPSNQTYQQH QAAIEQLKRR
101 FEAEFDELEK EIKCNGKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

		10	20	30
a925-1.pep		NKINVFTGKEESMLLSEKDGALSINTGIGE		
m925-1		AGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTGKEESMLLSEKDGALSINTGIGE		
	30	40	50	60
	70	80		
	40	50	60	70
	80	90		

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```

a925-1.pep  IPIKLSDDGKELYVERROYVKTDAAMKDKIIAHQKKCGQTAQAYLDARNALPSNQTYQQH
|||||
m925-1      IPIKLSDDGKELYVERROYVKTDAAMKDKIIAHQKKCGQTAQAYRDARNALPSNQTYQQH
              90      100      110      120      130      140

              100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
|||||
m925-1      LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX
              150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTGC AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGacAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGCTCTATCA GGCAGAGGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GCGGGCGCGC CCTtaccGCA
401 TCCGTTTACA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgcCGACAGT GGGGGGCaag tccgaacgtt gcaactGaa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGWTIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTGC AGCAGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGCTCTATCA GCGGAAAGT
301 GCGGAAGAAAT TGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCGAGTG GCAGGCGTGT GCGGGCGCGC CCTTACC GCA
401 TCTGCCCCGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACC
451 CCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTCA CCGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCAGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 ABELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGWTVGRT
151 ADSSGQVRTL QLNNGNLNR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

              10      20      30      40      50      60
g926.pep      MKHTVSASVILLTACAQLPQNNENLWQPSSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
|||||
m926          MKHTVSASVILLTACAQLPQNNENLWQPSSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
              10      20      30      40      50      60

              70      80      90      100     110     120
g926.pep      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEQTEDLSRQLVGFKLPIQYLHI
|||||
m926          PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAELSRLVGFKLPIQYLHI
              70      80      90      100     110     120

              130     140     150     160
g926.pep      WAEGRRVAGAPYRIRSDGILEQYGWTIGQNCROWGASPNVATE

```

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m926
 WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
 130 140 150 160 170 180

a926.seq
 1 ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
 51 GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
 101 GCAGTTTCAC GCGGGAAGGG CCGTTGGCAG TGAAAGCGGA AGGGAAAGGT
 151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
 201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
 251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GCGGGAAGT
 301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
 351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GCGGGGCGCG CCTTACCACA
 401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CCGCAGAACC
 451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
 501 GAACATCAGG CTGGTTTCA CCGAGATTGG TATGCCGTCT GAAACCGAAA
 551 CCCAAGAACA ATGCGCGGCA CGCATAAGT AA

a926.pep
 1 MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEKGK
 51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
 101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
 151 ADSGGQVRTL QLNNGNLNR LVFTEIGMPS ETETQECAA RIQ*

m926/a926 96.9% identity in 191 aa overlap

	10	20	30	40	50	60
m926.pep	MKHTVSASVILLTACAQLPQNNENLWQPSSEHISFAAEGRLAVKAEKGKSYANFDWTYQ					
a926	MKHTVSASVILLTACAQLPQNNENLWQPSSEHTRSFTAEGRLAVKAEKGKSYANFDWTYQ					
	10	20	30	40	50	60
m926.pep	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQESAELSRQLVGFKLPIQYLHI					
a926	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQESAELSRQLVGFKLPIQYLHI					
	70	80	90	100	110	120
m926.pep	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQESAELSRQLVGFKLPIQYLHI					
a926	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQESAELSRQLVGFKLPIQYLHI					
	70	80	90	100	110	120
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
	130	140	150	160	170	180
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
	130	140	150	160	170	180
m926.pep	ETETPERCAARTRX					
a926	ETETQECAAARIQX					
	190					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

g927.seq
 1 atgaaaacct acGCACaggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
 51 CAGCCCCgca GCcgatTcaa accaTCCGTC CGGAcAaaAT GCCCCGGCCA
 101 ATACCGAATC cgacGgaaAA AACATtaccC TGctcaatgc cTegtacgat
 151 gtGACACGGT ATTTttacaa agaatacgac cacTtgtttg tcggaaCATA
 201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAA TCCCACGGCG
 251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
 301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
 351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCTACA

g927.pcp

1	MKTYAQALYI	AALLTACSPA	ADSNHPSGQN	APANTESDGK	NITLLNASYD
51	VTRYFYKEYD	HLFVGTYQSE	HPGTSVSIQQ	SHGGFSKQAL	SVANGLQADV
101	VTMNLSSDD	LLEKXGLVEK	GWOQALPDHA	APYTSTMVFL	VRKNNPKQIR
151	DWMDLAKDGV	NIVIAKTTSGN	GRYAFGLGAY	YGLKANNGNE	QEAQKLVASI
201	LKNTPVFENG	GRXPPPPPSH	NATASPTSSYL	LKTKPTTSNAK	N

m927.seq

1	ATGAAAACCT	ACGCACCGGC	ACTCTATACC	GCAGCCCTGC	TCACCGCCTG
51	CAGCCCGCGA	GCCGATTCAA	ACCATCCGTC	CGGACAAAAT	GCCCCGGCCA
101	ATACCGAATC	CGACGGAAAA	AACATTACCC	TGCTCAACGC	CTCATACGAT
151	GTGGCAGCGG	ATTTTTCACAA	AGAATAACA	CCCTTATTTA	TCAAAACATA
201	CCAATCCGAA	CACCCCGGCA	CATCCGTCAG	CATCCAAACAG	TCCCACGGCG
251	GCTCCAGCAA	AACGGCATT	TCCGTAGCCA	ACGGCCTTCA	AGCCGATGTC
301	GTAACCATGA	ACCAATCCTC	CGACATCGAC	CTGCTCGAAA	AAAAAGGACT
351	GGTAGAAAAA	GGCTGGCACT	AAGCCCTCCC	CGACCAACGCC	GCGCCCTACA
401	CCAGCACTAT	GGTTTTCCTT	GTCCGAAAA	ACAACCCCAA	ACAGATCCCG
451	GATTGGAACG	ACCTTGCCAA	AGACGGCGTT	AACATCGTCA	TGCCCAATCC
501	CAAAACCTCG	GGCAACGGAC	GCTACGCCTT	CCTCGGCGCA	TACGGTTACG
551	GTCTGAAAC	CACCAACGGC	AACGAACAGG	AAGCCCAAAA	ACTCGTCGCA
601	TCCATCCTCA	AAAACACCC	CGTTTTTGAA	AACGGCGGAC	GckCgCCACC
651	ACCACCTTCA	CACAACCGCA	CATCCGGCAG	GTACTCATCA	CTTTTGAAAA
701	CGAAGCCAAC	TACGTACAGC	AAAAACTGA		

m927.ppt

1	MKTYAPALYT	AALLTACSPA	ADSNHPSGQN	APANTESDGK	NITLLNASYD
51	VARDFYKEYN	PLFTKYQSE	HPGTSVSIQQ	SHGGSSKOAL	SVANGLQADV
101	VTMNQSSDD	LLEKKGLEVK	GWQOALPDHA	APYTSTVMFL	VRKNNPKQIR
151	DWLNDLAKGV	NIVIANPKTS	GNRGYAFGLA	YGGLKTTNG	NEQEAQKLVA
201	SILNKTPVFE	NGGRXPPPPS	HNATSATYSS	LKTKPTTSA	KN*

Homology with a predicted ORF from *N.gonorrhoeae*

q927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQA	LYTAALLTACSPAADSNH	PSGQNAPANTESD	GKNITLLNASYDV	TRYFYKEYD	
m927	MKTYAPAL	YTAALLTACSPAADSNH	PSGQNAPANTESD	GKNITLLNASYDV	ARDVDFYKEYN	
	10	20	30	40	50	60
	70	80	90	100	110	120
g927.pep	HLFVGTYQ	SEHPGTSVSIQQSHGGFS	KQALS	VANGLOADVVTM	NQSSDID	LLEKXGLVEK
	:					
m927	PLFIKTYQ	SEHPGTSVSIQQSHGGSS	KQALS	VANGLOADVVTM	NQSSDID	LLEKKGLVEK
	70	80	90	100	110	120
	130	140	150	160	170	
g927.pep	GWQQALPD	HAAPYTSTMVFLVRK	NNPKQIRDW	NDLAKDGVN	IIVIA--K	TSNGNGRYAFLGA
m927	GWQQALPD	HAAPYTSTMVFLVRK	NNPKQIRDW	NDLAKDGVN	IIVIANPKT	SGNGRYAFLGA
	130	140	150	160	170	180

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```

      180      190      200      210      220      230
g927.pep  YGYGLKANNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTS
          |||||:|||||||||||||||||||||||||||||||||||||||||
m927      YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPP-SHNATSATYSSLLKTKPTTS
          190      200      210      220      230

      240
g927.pep  AKNX
          ||||
m927      AKNX
          240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
1  ATGAAACCT ACGCACC GGC ACTCTATACC GCAGCCCTGC TCAGCGCCTG
51  CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGGCCA
101 ATACCGAATC CGACGGA AAA AACATTACCC TGCTCAACGC CTCATACGAT
151 GTGGCACGGG ATTTTACAA AGAATAACA CCCTTATTTA TCAAAACATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG
251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
401 CCAGCACTAT GGTTCCTT GTCCGAAAAA ACAACCCCAA ACAGATCCGC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
501 CAAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
551 GTCTGAAAAC CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA
601 TCCATCCTCA AAAACACCCC CGTTTTTGAA AACGGCGGAC GCGCGCCACC
651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTGA AAAA
701 CGAAGCCAAC TACGTCAGCA AAAA ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
1  MKTYAPALYT AALLSACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51  VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
101 VTMNQSSDID LLEKKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA
201 SILKNTPVFE NGGRAPPPPS HNATSATYSS LLKTKPTTSA KN*

```

m927/a927 99.2% identity in 242 aa overlap

```

      10      20      30      40      50      60
m927.pep  MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          |||||:|||||||||||||||||||||||||||||||||||||||||
a927      MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          10      20      30      40      50      60

      70      80      90      100     110     120
m927.pep  PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          |||||:|||||||||||||||||||||||||||||||||||||||||
a927      PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          70      80      90      100     110     120

      130     140     150     160     170     180
m927.pep  GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          |||||:|||||||||||||||||||||||||||||||||||||||||
a927      GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          130     140     150     160     170     180

      190     200     210     220     230     240
m927.pep  YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA
          |||||:|||||||||||||||||||||||||||||||||||||||||
a927      YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA
          190     200     210     220     230     240

```

m927.pep KNX
 |||
 a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACccga CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
 351 TATCGCCGTT TTTGGAAGAA AAACgctggg CATCGGTTAC AGTCTCGCTC
 401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
 451 GTCGGCAATTA TACATCcgAT TATGCagtcg attgCcgCA GttacggctC
 501 caatCCCGCA AAAGGCACag aaggcaagat gggtaAATAT TtggcTTtgg
 551 tcaattaTCA TTCcaatCCC atttcgctgg ctAtggctat taCTGcaact
 601 gCCCCcaaCC CTTAATcgt caacttgatt gccGaaaaTt taggcagtag
 651 tttccgtCTT Tcttgggggg cgTGGGcgtg ggcaaTGGCT Gttcccgcg
 701 ttatcgccctt TtctgTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT
 751 GAAATTAAAG AAACGCCCAA TGCTGttcAA TTTGCCAAAG ACCGTCGAG
 801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
 851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
 901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT
 951 GCTTTTGCTT TCCGGTGTAT TGAATTGGGA CGATGTTTTG AAAGAAAAAA
 1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
 1051 TTTTAAATA AActcggact gattaaatGG TTCTCCGAG TGTGGCGGA
 1101 AagtgtcggC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
 1151 TGCTTGccta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
 1201 ATTACCGCTA TGTTCCGGCG ATTTCTCGCT GCTGCCGTTT CACTGAATGC
 1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
 1301 TGACCCCTAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCGGCTCG
 1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
 1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTTGG TGGAAAGTTC
 1451 TGGGATATTG GTAA

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep
 1 MKLGFKPIPL AIAAVLCLV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
 51 VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
 101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTSPNTARG
 151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHSNP ISSAMAITAT
 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
 251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
 301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTHI WFGALIMMAA
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
 401 ITAMFGAFLA AAVSLNAPAM PTALMMAAS NIMMTLTHYA TGTSPVIFGS
 451 GYTTMGEWWK AGFIMSVVNF LIFSVIGSIW WKVLGYW*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GGCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
 351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
 401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

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```

451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTCGTCGG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTAATCGT CAACTTGATT GCCGAAATTT TAGGCAGTAG
651 TTTCGCTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCGTTATG CCTTTGATT TATATTTwyT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTC CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGA CTGTTGGA CGATGTTTGT AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGGCGGA
1101 AAGTGTCGGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGCG GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGGCG ATTTTTCGCT GCTGCCGTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCCGTTTCG
1351 GCCTACACCA CAATGGGAGA ATGGTGAAG GCGGGTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

```

m929.pep
1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTPSNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMASTTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

```

          10      20      30      40      50      60
g929.pep  MKLGFKPIPLAIAAVLCALVLALPVPDGVK PQAWTLLAMFVGVIAAIIGKVMPLGALSII
          |||||
m929      MKLGFKPIPLAIAAVLCALVLALPVPDGVK PQAWTLLAMFVGVIAAIIGKAMPLGALSII
          10      20      30      40      50      60

          70      80      90      100     110     120
g929.pep  AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV
          |||||
m929      AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV
          70      80      90      100     110     120

          130     140     150     160     170     180
g929.pep  FGRKTLGIGYSLALSELLAPVTPSNTARGGGIHPIMQSIAGSYGSNPAKGTEGKMGKY
          |||||
m929      FGRKTLGIGYSLALSELLAPVTPSNTARGGGIHPIMQSIAGSYGSNPAKGTEGKMGKY
          130     140     150     160     170     180

          190     200     210     220     230     240
g929.pep  LALVNYHNSPISSAMAITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM
          |||||
m929      LALVNYHNSPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM

```

1339

	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNVQFAKDRLSEMGKMSADEIIMAVIFGILLLLWADV PALITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFAAAVSLNAPAM					
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

a929.seq

```

1  ATGAAATTGG  GTTTCAAACC  GATACCCCTC  GCCATTGCCG  CAGTATTGTG
51  CGCCTTGTT  TTGGCACTGC  CCGTACCCGA  CGGGGTCAAG  CCTCAGGCTT
101  GGACGCTGCT  GGCCATGTTT  ATCGGTGTGA  TTGCCGCCAT  TATCGGCAAG
151  GCCATGCCGT  TGGGTGCGCT  GTCGATTATT  GCCGTGCGGT  TGGTCGCAGT
201  AACCGGCGTA  ACCGCCGACA  AACCGGGTGC  GCGCATGAGC  GATGCGTTGA
251  GTGCGTTCGC  CAATCCGTTG  ATTTGGCTGA  TTGCCATCGC  AGTTATGATT
301  TCGCGCGGTT  TGCTCAAAAC  AGGGCTGGGG  ATGCGTATCG  GATATTGTGT
351  TATCGCCGTT  TTTGGAAGAA  AAACGCTGGG  CATCGGTTAC  AGTCTCGCTC
401  TTTCCGAAC  TCTGCTGGCT  CCCGTTACCC  CTTCCAATAC  CGCGCGCGGC
451  GCGCGCATT  TACATCCGAT  TATGCAGTCG  ATTGCCGCGA  GTTACGGCTC
501  CAATCCCGCA  AAAGGCACAG  AAGGCAAGAT  GGGTAAATAT  TTGGCTTTGG
551  TCAACTATCA  TTCCAATCCC  ATTCGTCGG  CTATGTTTAT  TACTGCAACT
601  GCCCCCAACC  CTTTAATCGT  CAACTTGATT  GCCGAAAATT  TAGGCAGTAG
651  TTTCCGTCTT  TCTTGGGGGG  CGTGGGCGTG  GGCAATGGCT  GTTCCCGCGC
701  TTATCGCCTT  TTTCGTTATG  CCTTTGATTT  TATATTTTTT  GTATCCGCCT
751  GAAATTAAAG  AAACGCCCAA  TGCCGTTCAA  TTTGCCAAAG  ACCGCTGAG
801  GGAGATGGGT  AAAATGTCGG  CAGACGAAAT  CATTATGGCG  GTCATTTTCG
851  GTATCTTGTT  GCTGTTGTGG  GCAGATGTTT  CCGCCCTTAT  TACCGGCAAT
901  CACGCTTTTA  GTATCAACGC  CACCGCCACC  GCATTTATCG  GATTAAGCCT
951  GCTTTTGCTT  TCCGGTGTAT  TGACTTGGGA  CGATGTTTGT  AAAGAAAAAA
1001  GCGCGTGGA  TACGATTATT  TGGTTTGCG  CATTGATTAT  GATGGCCGCA
1051  TTTTAAATA  AACTCGGACT  GATTAAATGG  TTCTCCGGAG  TGTGGCGGA
1101  AAGTGTCGGC  GGTGTTGGCG  TTAGCGGCAC  GGCTGCGGGC  GTAATCCTCG
1151  TGCTTGCTTA  TATGTATGCG  CATTATATGT  TTGCCAGTAC  TACTGCACAT
1201  ATTACCGCTA  TGTTCCGGCG  ATTTTTCGCT  GCTGCCGTTT  CACTGAATGC
1251  CCCGGCGATG  CCGACCGCGC  TGATGATGGC  GGCCGCATCT  AACATTATGA
1301  TGACCTCAC  TCATTATGCG  ACCGGTACTT  CGCCTGTGAT  TTTCCGTTCC
1351  GGCTACACCA  CAATGGGAGA  ATGGTGAAG  GCGGGTTTTA  TCATGAGCGT
1401  AGTCAATTTT  CTGATTTTTT  TCGTTATCGG  CAGCATTTGG  TGGAAAGTTC
1451  TGGGGTATTG  GTAA

```


This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

```
a929.pep
  1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
 51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101  SRGLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTSPNTARG
151  GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201  APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251  EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301  HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351  FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
401  ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451  GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*
```

m929/a929 99.6% identity in 487 aa overlap

	10	20	30	40	50	60
m929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
a929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFIGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
m929.pep	70	80	90	100	110	120
	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
a929	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
m929.pep	130	140	150	160	170	180
	FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
a929	FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
m929.pep	190	200	210	220	230	240
	LALVNYHNSPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
a929	LALVNYHNSPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240
m929.pep	250	260	270	280	290	300
	PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
a929	PLILYFLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	250	260	270	280	290	300
m929.pep	310	320	330	340	350	360
	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
a929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
m929.pep	370	380	390	400	410	420
	FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFFAAAVSLNAPAM					
a929	FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFFAAAVSLNAPAM					
	370	380	390	400	410	420
m929.pep	430	440	450	460	470	480
	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
a929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
m929.pep	WKVLGYWX					

a929

WKVLGYWX

g930.seq not found yet

g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

m930.seq

```

1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAAC GAATGGGTGT TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

m930.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNPAEIRM QODIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWLVEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

g930-1.seq (partial)

```

1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTT GAATAGTGGC AAGCTTCAAT TAACCTGAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAGG
201 ACGTATTGCA GCATTCCAAA ACAAAATTCC CACCCGCTCG AACGATCTGT
251 TGAATCTGCG TGATTGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAGACCA
351 AAGTGATGTC GTGGTGCAAT GCGGTAACG TCTGCTGCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGACTGAGTG ATATGTCTTA
501 TGTAAATTAT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTC AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTCCGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701 GTTACAACAC TGATTTCGGC TTCAACCGCC TGTGTATCG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAACTGTGG ACAGGGGAAA CAAAAGTTA
801 CATTGATGAT GCCGAACGTA CTGTACAACG GCGTAAACCC ACAGGTGGT
851 TGGCAGAACT TTCCACAAA GGATATATCG GTCGCGATG GGCAGATTTT
901 AAGTTGAAAT ATAAACACGG CACCGGCATG AAAGATGCTC TGGCGCGGCC
951 TGAAGAGGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GCGGCAACGA TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTATCGGG CCAAACTCTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGTTATTC GTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

g930-1.pep (partial)

```

1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQTLMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKCLP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMNDS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSLGSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYLSVKLV TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FEGGTSRMKI WTASADVNTF FOIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLSW
401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGQ IKLGGNLHYD

```

451 IFTGRALKKP EYFQTKKWT GFQVGYSF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```
1 ATGAACTTC CTTTATCCTA TTGCGCTAAT ATTGCGTTTT TGTCTTGGTG
51 CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCCGTGTTT TGCCATTAAC GAAGTGGTGT TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTGA TACCGAGCTA
501 TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG AACAAATTTC CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTGGA ACAAGGACTG GAAAATCTCA AACGTCTCCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAAAC
701 AAGTGTATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAATAA TGGACGTTCC ATTGGCGGTA CGCCCGATGA GGAAAGTTTT
901 GACGCGCCATC GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
951 AGCCCTTTTC GGTAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGAAAAA
1051 AGTTACAATA CTGATTTCGG CTTCAACCGC CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAACTGTG GATGAGGGAA AAAAAAGTT
1151 ACATTGATGA TGCCGAACAG ACTGTACAAC GGCCTAAAAC TCGCGGTTGG
1201 TTGGCAGAAC TTTCCACAA AGAATATATC GGTGCGAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAACGCGC GCACCGGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAGC CTTTGGCGAA GGCACGTCAC GTATGAAAT TTGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTCAAATC GGTAACAGC TATTTGCCTA
1401 TGACCATCC GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
1451 ACAAACTGGC TATCGGCGGA CACCACACCG TACGTGGCTT CGACCGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTTAAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTCAGGACA ATCCGCCAAA TGTTATCGG GCCAACTCT AGTCGGCACA
1651 GCAATTGGGA TACGCGGGCA GATAAAGCTT GCGCGCAACC TGCAATTACGA
1701 TATATTTACC GGCCGCGCAT TGAAAAAGCC CGAATTTTTC CAATCAAGGA
1751 AATGGCAAG CGGTTTTCAG GTAGGCTATA CGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:

m930-1.pep

```
1 MKLPLSYLPN IRFLSWCCLL AGIAPATLL ASPNPAEIRM QQDIQQRQRE
51 EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFG NKFPTRSNDL
201 LNLRLDLEQL ENLKLRLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDSNGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DCHRRKEGGS NYAVHYSAPF GKWTWAFNHN GYRYHQAQVS LSEVYDYNKG
351 SYNTDFGFNR LLYRDAKRKT YLGVKLWMRE TKSYYIDAEI TVQRRKTAGW
401 LAELSHKEYI GRSTADFLK YKRGTMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTP TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWI WRNDLSWQFK PGHQLYLGA VGHVSGQSAK WLSGQTLVGT
551 AIGIRGOIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFG VGYTF*
```

m930-1/g930-1 95.4% identity in 478 aa overlap

	90	100	110	120	130	140
m930-1.pep	AINEVVLEGEHHARFQFALKRALRETGFQAGKCLHAGNINQIMSLAQNALIGRGYTTTRI					
g930-1.pep	GKCLHAGDINQIMSLAQNALIGRGYTTTRI					
				10	20	30
	150	160	170	180	190	200
m930-1.pep	LAAPQDLNSGKLQTLIPSYLRSIRIDRSNDDQTHAGRIAAFGNKFPTRSNDLLNLRDLE					
g930-1.pep	LAAPQDLNSGKLQTLMPGYLRSIRIDRSNDDQTHAGRIAAFGNKFPTRSNDLLNLRDLE					
	40	50	60	70	80	90
	210	220	230	240	250	260
m930-1.pep	QGLENLKRLPTAEADLQIVPVEGEPNQSDVVVQWRQRLPYRVSVGMDSNGSEATGKYQG					

1343

```

g930-1.pep  QGLENLKLPTAEADLQIVPVEREPNQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQG
              100      110      120      130      140      150

m930-1.pep  270      280      290      300      310      320
NITFSADNPLGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g930-1.pep  NITFSADNPFGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210

m930-1.pep  330      340      350      360      370      380
NHNGYRYHQAVSGLSEVVDYNGKSYNTDFGFNRLLYRDAKRKTYLGVKLWMRETKSYIDD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g930-1.pep  NHNGYRYHQAVSGLSEVVDYNGKSYNTDFGFNRLLYRDAKRKTYLSVKLWLTRETKSYIDD
              220      230      240      250      260      270

m930-1.pep  390      400      410      420      430      440
AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALARAPEEAFGEGTSRMKI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g930-1.pep  AELTVQRRKTGWLAEASHKGYIGRSTADFKLKYKHGTGMKDALARAPEEAFGEGTSRMKI
              280      290      300      310      320      330

m930-1.pep  450      460      470      480      490      500
WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSDQKLAIGGHHTVRGFDGEMSLSAER
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSDQKLAIGGHHTVRGFDGEMSLPAER
              340      350      360      370      380      390

m930-1.pep  510      520      530      540      550      560
GWYWRNDLSWQFKPGHQLYLGADVGHVSGSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g930-1.pep  GWYWRNDLSWQFKPGHQLYLGADVGHVSGSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
              400      410      420      430      440      450

m930-1.pep  570      580      590
IFTGRALKKPEFFQSRKWASGFQVGYTF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g930-1.pep  IFTGRALKKPEYFQTKKWVTGFQVGYSEFX
              460      470

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2857>:

```

g931.seq
1  ATGAAACCCA AATTCAAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCCT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301 AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCCGCC CAATTCTTTA TCAATCTGGC GGACAACGGT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TACACCGTTT TCGGCAGGT AGAAAGCGGA
451 ATGGACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
551 GGCAGTAACA CGCAGACAGA CGTTCAGACG GCCTCGCCCG TTTCCAAAA
601 AACGCCGTTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

```

g931.pep
1  MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKTVAN
51  FVRYARKGFY DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA QFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2859>:

```
m931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAC CGTTGCTAAT
151 TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
201 CGTTATCGAC GGTTTTGTTA TCCAGGGCGG TGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACACCG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACCA.kCT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACGCCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
551 GGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

```
m931.pep..
1  MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS OFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

g931/m931

g931.pep	10	20	30	40	50	60
	MKPKFKTVLTALLLAVSLPSMAATRVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
m931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
g931.pep	70	80	90	100	110	120
	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	130	140	150	160	170	180
	OFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNVVPVQPVKIRR					
m931	OFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
	130	140	150	160	170	180
g931.pep	VVVGQX					
m931	VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

```
a931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CACCCAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACAATACGA TTTTTCACCG
201 CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAAACACTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGT GGACAATGAT TCGCTCAACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
```

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451 ATGAACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
 501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep
 1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
a931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVPVQPVKIRR					
a931	QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVPVQPVKIRR					
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCCGTCA TTTTGGGAAT
 101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCATTGAC
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAAGG CTGGTGTCGT AAGGTTTCG ACCCTTATCC CGAAAACAAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep
 1 MKYIVSISLA MGLAACSFGG FKPNPWDAAS FWELKNYANP YPGSASAALD
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWR KGFDPYPENK
 101 KYEWPREEGK TK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTGC CACTCACCGC

1346

```

51 CTGCCAAGAC GACACGCAGG CGCGGCTCGA ACGGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCCAGG CGCAGGCAAA
201 CGGCAACAAC GGTGAGCCCG TTACCGGCAA .AGAcggGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGA TTGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGG
351 GCAACCAAGA CAGCCCGCTC GCGCGTCGCG CGCGTGCTGC CTACCATCAG
401 TCCGCACGCC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCGCGCCCGT CAAttaccgc catcgcgcta tgcGCGGTTT CGgcagAagg
551 cggtaaaCCC GGCGCGTCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTGT TAGGGGCATT GTTATGTTGC CGTTTGATT TCAGACGGCA
651 TTTTGTTC AAGCGTTGA TGTcggGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2866; ORF 934.ng>:

g934.pep

```

1 MKKIIASALI ATFALTACQD DTQARLERQQ KQIEALQQQL AQQADDTVYQ
51 LTPEAVKDTI PAQAQANGNN GQPVTKRRA AVYLRPIDRK LAAAKPDWRG
101 GRRVYRQAG KQIHTGGQPR QPRRPSRACC LPSVRTPOCA HOQGFHAQP
151 PCKTTGGAGA ALPPDNAPAR QLPPSRYARF RQKAVNPARQ CRLKGFQTAF
201 LYLLGALLCC RLIFRRHFVS KRLMSGWQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2867>:

m934.seq (partial)

```

1 ..CGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
51 ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAAG
101 ACACCATTCG TGCCGAAGCA CAGGCAAACG GCAACAACgG GCAACCCGTT
151 ACCGGTAA.A GACGGGCAGC AGTATATTTA CGACCAATCG ACAGGAAGCT
201 GGCTGCTGCA AAGCCTGGTC GGCGCGGCGG CAGGCGCGTT TATCGGCAAC
251 GCCTGGCAA ACAAATTCAC ACGGCAGGC AACCAGACA GTCCCGTCGC
301 CCGGCGCGCG CGTGCAGCCT ACCATCAGTC CGCAGCCCC AATGCGCGCA
351 yCAGCAGGGA TTTGAACACG CGCAGCCTCC GTGCAAAACA ACAGGCGGCG
401 CAkGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACGCGCG
451 CCCCCTATG CGCGGTTTCG GCAGGAGGCG GTAAACCCGG CGCGCCAATG
501 CCGTCTGAAG AGCTTTCAGA CGGCATTtT GCATTGTGA GGGACATTGT
551 TATGTTGCCG TTTGATTTTC AGACGGCATT TTGTTTCCAA GCGTTTGATG
601 TCGGGATGGC AATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2868; ORF 934>:

m934.pep (partial)

```

1 ..RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51 TGXRRAAVYL RPIDRKLAAA KPGRRGGRRV YRQRAGKQIH TGRQPRQSR
101 PARACSLPSV RTPQCAHQOG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151 PRYARFRQEA VNPARQCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/g934

```

m934.pep          10      20      30
                  RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
g934              10      20      30      40      50      60
                  MKKIIASALIATFALTACQDDTQARLERQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI

m934.pep          40      50      60      70      80      90
                  PAEAQANGNNGQPVTKGRRRAAVYLRPIDRKLAAAKPGRRGGRVYRQRAGKQIHTGROPR
g934              70      80      90     100     110     120
                  PAQAQANGNNGQPVTKGRRRAAVYLRPIDRKLAAAKPDWRGGRRVYRQRAGKQIHTGGQPR

                  100     110     120     130     140     150

```

m934 . pep QSRRPARACSLPSVRTPQCAHQQGFEHAQPCKTTGGAXAALPPDNAPXRQLPPPRYARF
| | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g934 QRRRPSRACCLPSVRTPQCAHQQGFEHAQPCKTTGGAGAALPPDNAPARQLPPSYARF
 130 140 150 160 170 180

 160 170 180 190 200
m934 . pep RQEAVNPARQCRLKSFQTAFXHLGLTLLCCRLIFRRHFVSKRLMSGWQFX
| : | | | | | : | | | : | | | : | | | : | | | | | | | | | | | | | |
g934 RQKAVNPARQCRLKGFQTAFLLGALLCCRLIFRRHFVSKRLMSGWQFX
 190 200 210 220 230

```

a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTGC CACTCGCCGC
51  CTGCCAAGAC GACGCGCAGG CGGGCTCGA ACAGCAGCAG AAACAGATTG
101 ATGCCCTGCA ACAGCAGCTC GCACAGCAGT CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCGAAG CACAGGCAAA
201 CGGCAACAAC GGGCAACCCG TTACCGG.TA AAGACGGGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGG TCGCGCGCGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAATTTC ACACGGGCAG
351 GCAACCAAGA CAGTCCCCTC GCCCGGCGCG CGCGTGCCTC CTACCATTAC
401 TCCGCACATC CCAATGCGCG CACCAGCAGG GATTGGAACA CCGCAGCCTT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCAGA CGGTTACCGC CGGACAACGC
501 GCCCGCCCGC CAATTACCGC CGCCCCGCCA TGCGCGGTTT CGGCAGAAGG
551 CGGTAAATCC GGCCTGCCAA TGCCGTGTGA AGGGCTTTCA GACGGCATT
601 TTGTATTGTG TAGGGACATT GTTATCTTGC CGTTTGATT TTAGACGGCA
651 TTTTGTTC AAGAGTTTGA TGTGGGATG CGAATTCCTG

```

a934.pep

1	<u>MKKIIASALI</u>	<u>ATFALAACQD</u>	DAQARLEQQQ	KQIEALQQQL	AQQADDTVYQ
51	LTPEAVKDTI	PAEAQANGNN	GQVPTX*RR	AVYLRPTDRK	LAAAKPGRRG
101	GRRVYRQRG	KQIHTRGRPR	QSRPARACR	LPSVRTSQCA	HQQGFHAQP
151	PCKTTGGAGA	ALPPDNAPAR	QLPMPRHARF	RQKAVNPACQ	CRLKGFQT <u>AF</u>
201	LYLLGTLLCC	RLIFRRHFVS	KSLMSPGWOF*		

```

m934.pep      10      20      30
               RLEQQQKQIEALQQQLAQQAADTVYQLTPEAVKDTI
               |||||
a934          MKKIIASALIATFALAACQDDAARLEQQQKQIEALQQQLAQQAADTVYQLTPEAVKDTI
               10      20      30      40      50      60

               40      50      60      70      80      90
m934.pep      PAEAQANGNNGQPVTGXRRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
               |||||
a934          PAEAQANGNNGQPVTXXRRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
               70      80      90      100     110     120

               100     110     120     130     140     150
m934.pep      QSRRPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXKRLPPPRYARF
               |||||
a934          QSRRPARACRLPSVRTSQCAHQQGFEHAQPPCKTTGGAGAALPPDNAPARQLPPPRHARF
               130     140     150     160     170     180

               160     170     180     190     200
m934.pep      RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
               ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a934          RQKAVNPACQCRLKGFQTAFLYLLGTLCCRLIFRRHFVSKSLMSGWQFX
               190     200     210     220     230

```

g935.seq not found yet

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCCGGGCGCA GGCTTGAATT
701 ATGAAATCGA GGCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAATC
801 AGCTTATGAC GACGGGTTTCG GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAACAAAA CGGGTAAACA ACCGCCGCTT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCCAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTTCG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCAGCGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTC ATGCCGGCTG
1251 GGCAGCGAG TGGCGGCGAG TGGCGGCTT GAACAGTCGG GTTTCGCGCT
1301 CTTATGCCCC CGCAACTAT AAGGGCGTTG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

```

a935.pep
1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRLKSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNIEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDAKTK RVNNRRLPPY MLAGHVGVL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNPVYA KRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

m935.pep	10	20	30	40	50	60
	MLYFRYGLVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
a935	MLYFRYGLVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
	10	20	30	40	50	60
m935.pep	70	80	90	100	110	120
	DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
a935	DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
	70	80	90	100	110	120
m935.pep	130	140	150	160	170	180
	AEAVARYRELHGENAADERILLDLAAAEFDDFRLKSAERHFAEAAKLDLPAPVLENVGRF					
a935	AEAVARYRELHGENAADERILLDLAAAEFDDFRLKSAERHFAEAAKLDLPAPVLENVGRF					
	130	140	150	160	170	180
m935.pep	190	200	210	220	230	240
	RKKTEGLTGWRFGGSGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNIEIEAEK					
a935	RKKAEGLTGWRFGGSGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNIEIEAEK					
	190	200	210	220	230	240
m935.pep	250	260	270	280	290	300
	LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1 ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51 TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTGCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTTCG CGACGCGCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGTG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTT CGGAAAAAAA
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCGGGCGGGA GCGGGCGGCA GGGTTGAATT
701 ATGAAATCGA GCGGAAAAAG CTGACGCCGT TGGCAGATAA TCATTATTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTC AGTAAAAATC
801 AGCTTATGAT GACGGGTTCG GCAGGGCGTA TTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCT
901 GGCAGCGACG GCTTTGATGC GAAAACAAA CGGGTAAACA ACCGCCGCTT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGCTG TCCCATACTT
1001 ACCGCCCAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CGGGTTTTAT GTTTCGTTCG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTT ATGCCGGTTG
1251 GGCGCAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTCCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCATTG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTT GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCT
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1 MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51 KVENDAPRV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRLLKSAERH FAEAAKLDLP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRONGRQI CSVSRAERAA GLNIEIEAEK LTPLADNHYL
251 LFRSNIGGTS YFYSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDAKTK RVNRRRLPPY MLAGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFEGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAQE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRRNSEVFSV
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1 ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51 TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTGCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTTCG CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGTG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCCGAGG CGGAAAAAAT
501 GGATTTGCCG GCGCCGTTT TGGAAAATGT GGGGCGTTT CGGAAAAAAG
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```

1350

	310	320	330	340	350	360
m935.pep	GSDGFDKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFDKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVSASYARRNYKGIAAFSTEQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVSASYARRNYKGVAAFSTEQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNPYAKRRNSEVFVSADWRFK					
a935	GRTESNPYAKRRNSEVFVSADWRFK					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGCGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGccgAACCA CCGgcgcgca AACCgATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACCTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCacegT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGT
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPPEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCgACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT LIAAIFSLAL SGCVS AVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTA...

```

1351

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng)

from *N. gonorrhoeae*:

m936/g936

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
	: : : : :					
g936	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAGAKSVIDRRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	: : : : :					
g936	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
	130					
m936.pep	VASLPRTAXXX					
g936	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

a936.seq

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTGCCG	CCGTCCTCAG
51	CCTTGCCCTC	GGCGGCTGCG	TCAGCGCAGT	CGTCGGCGGC	GCGGCGGTGCG
101	GCGCGAAATC	CGCCGTCGAC	CGCCGAACCA	CCGGCGCGCA	AACCGACGAC
151	AACGTAATGG	CGCTGCGTAT	CGAAACCACC	GCCGCTCCT	ATCTGCGCCA
201	AAACAACCAA	ACCAAAGGCT	ACACGCCCCA	AATCTCCGTT	GTCGGCTACA
251	ACCGCCACCT	GCTGCTGCTC	GGACAAGTCG	CCACCGAAGG	CGAGAAACAG
301	TTCGTCGGTC	AGATTGCACG	TTCCGAACAG	GCCGCCGAAG	GCGTGTACAA
351	CTACATTACC	GTGCGCTCCC	TGCCGCGCAC	TGCCGGCGAC	ATCGCCGGCG
401	ACACTTGGAA	CACATCCAAA	GTCCGCGCCA	CGCTGTTGGG	CATCAGCCCC
451	GCCACACAGG	CGCGCGTCAA	AATCGTTACC	TACGGCAACG	TAACCTACGT
501	TATGGGCATC	CTCACCCCCG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GCACCACCGT	CGGCGTACAA	AAAGTCATCA	CCCTCTACCA	AAACTACGTC
601	CAACGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2880; ORF 936.a>:

a936.pep

1	MKPKPHTVRT	LTAAVLSLAL	GGCVSAVVGG	AAVGAKSVD	RRTTGAQTDD
51	NVMALRIETT	ARSYLQNNQ	TKGYTPQISV	VGYNRHLLLL	GQVATEGEKQ
101	FVGQIARSEQ	AAEGVYNYIT	VASLPRTAGD	IAGDTWNTSK	VRATLLGISP
151	ATQARVKIVT	YGNVTYVMGI	LTPEEQAQIT	QKVSTTVGVQ	KVITLYQNYV
201	QR*				

m936/a936 95.3% identity in 128 aa overlap

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
	: : : : :					
a936	MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAGAKSAVDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	: : : : :					
a936	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
m936.pep	VASLPRTA					

1352

a936 |||||
 VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
 130 140 150 160 170 180

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

g936-1.seq

```

1  ATGAAACCCA  AACCACACAC  CGTCCGCACC  CTGATTGCCG  CCGTCCTCAG
51  CCTTGCCCTC  GCGCGCTGCT  TCAGCGCAGT  CGTCGGCGGG  GCCGCCGTCG
101 GCGCAAAATC  CGTCATCGAC  CGcgcAACCA  CCGgcgcgca  AACCGATGac
151 aACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ACCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCGGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGTATACAA
351 CTACATTACC  GTCGCCTCCC  TGCCGCGCAC  TCGGGCGGAC  ATCGCCGGCG
401 ACACCTGGAA  CACGTCCAAA  GTCCGCGCca  cgCTGCTGGG  CATCAGCCCC
451 GCTACACAGG  CGCGCGTCAA  AATCATTACC  TACGGCAATG  TAACCTACGT
501 TATGGGCATC  CTCACCCCG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCaccgT  CGGCGTACAA  AAAGTCATTA  CCCTCTACCA  AAACCTACGT
601 CAACGCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

g936-1.pep

```

1  MKPKPHTVRT  LIAAVLSLAL  GGCFSAVVGG  AAVGAKSVID  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GQVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIT  YGNVTYVMGI  LTFEEQAQIT  QKVSTTVGVQ  KVITLYQNYV
201 QR*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

m936-1.seq

```

1  ATGAAACCCA  AACCACACAC  CGTCCGCACC  CTGATTGCCG  CCATTTTCAG
51  CCTTGCCCTT  AGCGGCTGCG  TCAGCGCAGT  AATCGGAAGC  GCCGCCGTCG
101 GCGCGAAATC  CGCCGTCGAC  CGCCGAACCA  CCGCGCGCA  AACCGACGAC
151 AACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ATCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCGGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGTGTACAA
351 CTATATTACC  GTCGCCTCCC  TGCCGCGCAC  TCGGGCGGAC  ATCGCCGGCG
401 ACACCTGGAA  CACATCCAAA  GTCCGCGCCA  CGCTGTTGGG  CATCAGCCCC
451 GCCACACAGG  CGCGCGTCAA  AATCGTTACC  TACGGCAACG  TAACCTACGT
501 TATGGGCATC  CTCACCCCG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCACCGT  CGGCGTACAA  AAAGTCATCA  CCCTCTACCA  AAACCTACGT
601 CAACGCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

m936-1.pep

```

1  MKPKPHTVRT  LIAAIFSLAL  SGCVSAVIGS  AAVGAKSAVD  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GQVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIV  YGNVTYVMGI  LTFEEQAQIT  QKVSTTVGVQ  KVITLYQNYV
201 QR*
  
```

m936-1/g936-1 95.5% identity in 202 aa overlap

	10	20	30	40	50	60
m936-1.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSA	AAVGAKSAVD	RRTTGAQTDD	NVMALRIETT		
g936-1	MKPKPHTVRTLIAAVLSLALGGCFS	AVVGGAAVGAKSVID	RRTTGAQTDD	NVMALRIETT		
	10	20	30	40	50	60
	70	80	90	100	110	120
m936-1.pep	ARSYLRQNNQTKGYTPQISVVGYNRHLL	LLGQVATEGEKQFVGQIARSEQAAEGVNYIT				
g936-1	ARSYLRQNNQTKGYTPQISVVGYNRHLL	LLGQVATEGEKQFVGQIARSEQAAEGVNYIT				
	70	80	90	100	110	120
	130	140	150	160	170	180
m936-1.pep	VASLPRTAGDIAGDTWNTSKVRATLL	GISPATQARVKIVTYGNVTYVMGILTPEEQAQIT				

1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180

              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1   ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51  CCTGGCCCTC GCGGGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTGCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCACGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTT GTCGGGTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACCTGGAA CACATCCAAA GTCCGCGCCA CGTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCG AAGAACAGGC GCAGATTACC CAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAATACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1   MKPKPHTVRT LTA AVLSLAL GGC VSAVVG AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMI LTPEEQAQIT QKVSTTVGVQ KVTILYQNYV
201 QR*

```

a936-1/m936-1 97.0% identity in 202 aa overlap

```

              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAASAVDRRTTGAQTDDNVMALRIETT
              |||||
a936-1      MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAGVGAASAVDRRTTGAQTDDNVMALRIETT
              10      20      30      40      50      60

              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLLQGVATEGEKQFVGQIARSEQAEGVYNYIT
              |||||
a936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLLLQGVATEGEKQFVGQIARSEQAEGVYNYIT
              70      80      90      100     110     120

              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              |||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              130     140     150     160     170     180

              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1   atGAAAAATA TTCTCTTAgt ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51  CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAAT
101 GGAAactGGA AACTTccett acctacctgA acaGCGAAAAA cagCCGCGCC
151 GCACTTGCCT CACCGGTTTA CATTcAGACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGA CTGAccg GCAataccgA CATTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAAC TCGacg GCAACGGCAA

```

1354

```

351 AACCCGCAAC AAACGGATGT CCGACATATC CGCCGGCATC AGCCACACCT
401 TCCTtaAAGa cgGCAAAAAT CCCGCACTCA TCGCTTTCCT CGAAAGCACG
451 GTTTACGAAA AATCGCGCAA CAAAGCCTCG TCGGGAAAAT CGTGGCTCAT
501 CGCGCCACC ACCTACAAAG CCATAGATCC GATTGTCCTT TCCCTCACC
551 CCGCTACCG CATCAACGGC AGCAAAACCC TTTAGACGA CGTCAAATAC
601 AAAGCAGGCA ATTACTGGAT GCTGAATCCC AACATCTCAT TTGCCGCCAA
651 CGACAGAATC AGCCTGACCG GAGGCATCCA ATGGCTGGGC AAACAGCCCG
701 ACCGCATAGA CGGCAAAAAA GAATCCGCAA GAAACACATC CACCTACGCC
751 CATTTCGGCG CAGGTTTCGG TTTACCAAAA ACCCGGGCTT TAAACGCATC
801 CGCAGTTTC AACGTTTCAG GGCAAAGCAG TTCCGAACTG AAATTGGGCG
851 TACAGCATAC ATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2888; ORF 937.ng>:

g937.pep

```

1 MKNILLVFVS FVPLCVRTDL PLNIEDIMTD KGKWKLETS TYLNSENSRA
51 ALASPVYIQT GSASFIPVPT EIQENGSTND MLAGTLGLRY GLTGNTDIYG
101 SSGSYLWHEER KLDGNGKTRN KRMSDISAGI SHTFLKDGKN PALIAFLEST
151 VYEKSRNKAS SGKSWLIGAT TYKAIDPIVL SLTAAYRING SKTLSDDVKY
201 KAGNYWMLNP NISFAANDRI SLTGGIQWLG KQPDRIKGGK ESARNTSTYA
251 HFGAGFGFTK TAALNASARF NVSGQSSSEL KLGVOHTF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2889>:

m937.seq

```

1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATTCAA ACCGCGCGAA CCTCGTTTAT
201 CCCCATTCG ACCGAAATCC AAgAAAaCGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGGCG TACGGACTGA CCGGAATAC CGACATTAC
301 GCGACGCGGA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCTTAA AGACGACAAA AACCCGCCC TAATCAGCTT TCTTGAAGC
451 ACGGTTTACG AAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCTTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCACTACCT GCTGCTCAAC CCAACATCT CATTGCTGC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCCGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2890; ORF 937>:

m937.pep..

```

1 MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNRR
51 AELAAPVYIQ TGATSFIPIP TEIQENGSTND DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTLSDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVOHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 937 shows 86.9% identity over a 289 aa overlap with a predicted ORF (ORF 937.ng) from *N. gonorrhoeae*:

g937/m937

```

          10      20      30      40      50      59
g937.pep  MKNILL-VFVSFVPLCVRTDLPLNIEDIMTDKGKWKLETS LTYLNSENSRAALASPVYIQ
          || || : : : || : : ||||| : ||||| : ||||| : || : |||
m937      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETS LTYLNSENNRAELAAPVYIQ
          10      20      30      40      50      60
          60      70      80      90      100     110     119
g937.pep  TGSASFIPVPTTEIQENGSTNDMLAGTLGLRYGLTGNTDIYSGSGSYLWHEERKLDGNGKTR

```

```
a937.seq
1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC GTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GGAACCTTCC CTTACTTACC TGAACGCGCA AAACAACCGC
151 GCCGAACTTG CCGCACCGGT TTACATCCAA ACCGCGCGAA CCTCGTTTAT
201 CCCCATTCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGC GC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTCG ACGGCAACGG
351 CAAAACCGCA AACAAACGGA TGTCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCTCGCC TAATCAGCTT TCTTGAAGAG
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCATCGA CCCCCTCGTC CTCTCATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCTTTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCCATATAT CTTTCGCCG
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CGGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTG CGCGACGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGACGCT TTTCAAGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTG
851 GCGTACAGCA TACGTTTTAA
```

```
a937.pep
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNRR
51  AEELAAPVYIQ TGATSFPIPI TEIQENGSTN DMLVGTGLGR YGLTGTNDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAAYRIN GSKTLSNNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGG KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*
```

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	:					
a937	MKRIFLPALPAILPLSAYADPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m937.pep	TGATSFIPIPTEIQENGSTNDMLVGTGLGLRYGLTGNTDIYGSGSYLWHEERKLDGNSKTR					
	:					
a937	TGATSFIPIPTEIQENGSTNDMLVGTGLGLRYGLTGNTDIYGSGSYLWHEERKLDGNGKTR					
	70	80	90	100	110	120

1356

	130	140	150	160	170	180
m937.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a937	LSLTAAYRINGSKTLSSNTKYAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
a937	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

1  MKRLTLFAV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATCGG
201 CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CCGGTATGCC GGGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTGGGC GGTACGATC AGGCATATAT
501 TGTGAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGGAAGATAT TGCAAACCGT ATGTCTGAAG AAGATTGAA AGCGGTCGGC
601 AACTTTATCC AAGGTTGCG TTAA
```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

1  MKRLTLFAV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTHGSAV MKPVVMNLSQ QDILNVSAFY
101 AKQPKSGEA NPENPELGA KIYRGGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAYIVEQ MNAYKSGQRK NTIMEDIANR MSEDILKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLFAVLAAGAVSASP KADVEKGQVAATVCAACHAADGNSGIAMY PRLAAQHTAY					
a939	MKRLTLFAVLAAGAVSASP KADVEKGQVAATVCAACHAADGNSGIAMY PRLAAQHTAY					

1357

```

              10      20      30      40      50      60
              70
m939.pep      IYHQTIGIRDVNAP
              |||||
a939          IYHQTIGIRDGKRTHGSAAVMKPVVMNLSQDILNVSAFYAKQQPKSGEANPKENPELGA
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1  ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGCCGCCGGT GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGC GCGC CATCCAAATC TGCCGAAGGT TCGTGC GCGC CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.pep
1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGC GCGC CGGCTGCTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

```

              10      20      30      40      50
m950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----
              |||||
g950          MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGASKSAEGSCGASKSAEG
              10      20      30      40      50      60

              60      70      80      90      100
m950.pep      ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              |||||
g950          SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGC GCGC CGGCTGCTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

```

              10      20      30      40      50      60
a950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
              |||||
m950           MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
              10      20      30      40      50      60

              70      80      90      100
a950.pep      EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
              |||||
m950           EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90      100
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
1  ATGATTATGT TACCCGCCCG TTCACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGACAGGCGT ATGCTGCCGG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201 CAGGGTGTTT ACGCTGTGG GCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTTGAACG CACAAAATCC
301 CCCGAAGTCG CCGAACGCGC CTTGGAAATG GCCGTGTCGC TGAACGCGTT
351 TGAACAGGGC GAAATGATT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG GCGGGGTGGC TCGGGAACGT ATTGAGGGAA
451 GGGGGAATC AGCATCTGGA CGGGTTGGAA GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCAGGA TATTTTGCT GCTGGTGCAA GCGCCGTGC
551 AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGTTTCG CCGTGCAGCG
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CGGTGTTCGG
651 CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAAATA TTGCCCCCA CTTTAATGAC GTTGCTCTG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGCCG TCTGGCAGGA AATGGAATT ATGAATCTGG
851 TTTCCCTGCG TAAGCCGGAT GATGCCTATG CGCGTTTGA CGTGCTGTG
901 GAACACAACC CGAATGCAAA CCTGTATATT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAA GAAGGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101 AAAAGTGTCC GCGCCGGAAT ACCTGTTTGA CAAAGGCGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGCAGG AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACCTTC GCGCGCGGGA
1351 AGCACGGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTTACGA
1401 ACAGTTCGGC AAACGGGGAA AAATGATTGC CGACCTTGA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAATC AACC CGGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCCCGAAGT GCCGCCCAT TGGGCGAAGT
1701 GTTGTGGGCA TTGGGCGAAC GCGATCAGGC GGTGACGTA TGGACGAGG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GGGCGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
1  MIMLPARFTI LSVLAAALLA GQAYAAGAAD VELPKVEGVK LRKHRRYSEE
```

```

51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMIYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNQHL DGLE EVLAQSDDVQ KRRIFLLLVQ AAVQQGGVAQ KASKAVRRRAA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDTEI LPPTLMTLRL
251 TARKYPEILD GFFEQTDTQN LSAVWQEMEI MNLVSLRKP DAYARLNVLL
301 EHNPNANLYI QAAILAA NRK EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLK KVS APEYLF DKGV LAAAAAE LD GGRAALRQIG
401 RVRKLPEQQG RYFTADNLSK IQMLALS KLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQTAYQI NPDDTAVNDS IGWAYY LKGD AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

```

m951.seq
1  ATGATTATGT TACCTAACCG TTTCAAAATG TTAAGTGTGT TGACGGCAAC
51  CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCGGTGCG GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTTC AAGAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTTGCGGCAG TGGCGGAGCG
201 GGTAAATCAG ATATTTACGT TGCTGGGAGG GGAACCCGCC TTGCAAAAGG
251 GGCAGGCCGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AATATCCCGG AAGTCGCGA ACGGCCTTG GAAATGGCGG TGTCGCTGAA
351 CGCGTTTGAA CAGCGGAAA TGATTTATCA GAAATGGCGG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAGAG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
501 GCGCGGACGA GGACAGAACC GCAGGGTGT TTTATTGTTG GCACAAGCCG
551 CCGTGCAACA GGACGGGTTG GCGCAAAAG CATCGAAAGC GGTTCGCCGC
601 GCGGCGTTGA AATATGAACA TCTGCCGAA GCGGCGGTTG CCGATGTGGT
651 GTTCAGCGTA CAGGGACGCG AAAAGGAAA GGCATCGGA GCTTTCAGC
701 GTTTGGCGAA GCTCGATACG GAAATATTGC CCCCACCTT AATGACGTTG
751 CGTCTGACTG CACGCAATA TCCCGAATA CTCGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTT CGGCCGCTG GCAGGAAATG GAAATTATGA
851 ATCTGTTTC CCTGCACAG CTGGATGATG CCTATGCGG TTTGAACGTG
901 CTGTTGGAAC GCAATCCGAA TGCAGACCTG TATATTCAGG CAGCGATATT
951 GCGGCGAAAC GAAAAGAAG GTGCTTCCGT TATCGACGGC TACGCCGAAA
1001 AGGCATACCG CAGGGGACG GAGGAACAG GGAGCAGGGC GGCCTAACG
1051 GCGCGCATGA TGTATGCCGA CCGCAGGGAT TACGCCAAG TCAGGCAGTG
1101 GCTGAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CGGCTGCGGC GGCTGTCGAG TTGGACGCGC GCAGGGCGGC TTTGCGGCAG
1201 ATCGGCAGGG TGCGGAAACT TCCGAACAG CAGGGCGGCT ATTTACGGC
1251 AGACAATTG TCCAAAATAC AGATGCTCGC CCTGTCGAAG CTGCCCGATA
1301 AACGCGAGGC TTTGAGGGG TTGGACAAGA TTATCGAAA ACCGCTGCC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTCAAGTTG
1401 TTACGATCGG CTTGGCAAGC GGAATAAAT GATTTCAGAT CTTGAAAGGG
1451 CGTTCAGGCT TGCACCCGAT AACGCTCAGA TTATGAATA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCAA ACGTTTGAC GAAGGTTTCG CCCTGCTTCA
1551 GACGGCATA CAAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGGCGTA TTACCTGAAA GGCACGCGG AAAGCGCGCT GCCGTATCTG
1651 CGGTATTCTG TTGAAAACGA CCGGAGGCC GAAGTTGCCG CCCATTGGG
1701 CGAAGTGTG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 CGCAGGCGGC ACACCTTACG GGAGACAAGA AAATATGGCG GGAACGCTC
1801 AACGTCACG GCATCGCATT GCCCAACCT TCCGAAAAC CTCGGAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

```

m951.pep
1  MIMLPNRFKM LTVLTATLIA QVSAAGGGA GDMKQPEVG KVFRKQQRYS
51  EEEIKNERAR LAAVGERVNQ IFTLLGGETA LQKGQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIYQKWR QIEPIPKAQ KRAEWLRNVL
151 RERGNQHL DGL LEEVLAQADE QNRRVFLLL AQAQVQDGL AQKASKAVRR
201 AALKYEHLPE AAVADVFSV QGREKEAIG ALQRLAKLDT EILPPTLMTL
251 RL TARKYPEI LDGFFEQTDT QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAAILAA RKEGASVIDG YAEKAYGRGT EEQRSRAALT
351 AAMMYADRRD YAKVRQWLK VSAPEYLF DKGVLAAAAVE LDGGRAALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALS LKLPDKREALRG LDKIIEKPPA
451 GSNTLQAEA LVQRSVVYDR LGKRKMSD LERAFRLAPD NAQIMNNGY
501 SLTDSKRLD EGFALLQTAY QINPDDTAVN DSIWAYY LKGD AESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDQAV DVWTQAAHLT GDKKIWRETL
601 KRGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

m951.pep	10	20	30	40	50	60
	MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVGVFRKQRYSEEEIKNERAR					
g951	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGVLRKHRRYSEEEIKNERAR					
	10	20	30	40	50	
m951.pep	70	80	90	100	110	120
	LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
g951	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
	60	70	80	90	100	110
m951.pep	130	140	150	160	170	180
	QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLGLEEVLAQADEGNRRVFLLL					
g951	QAEMIQKWRQIEPIPGEAQKRAGWLRNVLRERGNQHLGLEEVLAQSDDVQKRRIFLLL					
	120	130	140	150	160	170
m951.pep	190	200	210	220	230	240
	AQAAVQODGLAQKASKAVRRAALKYEHLPAAVADVVSVOGREKEKAIGALQRLAKLDT					
g951	VQAAVQGGVQAQKASKAVRRAALKYEHLPAAVADVVSVOGREKEKAIEALQRLAKLDT					
	180	190	200	210	220	230
m951.pep	250	260	270	280	290	300
	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVQEMEIMNLVSLHRLDDAYARLNV					
g951	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVQEMEIMNLVSLRKPDDAYARLNV					
	240	250	260	270	280	290
m951.pep	310	320	330	340	350	360
	LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEEQSRRAALTAAMMYADRRD					
g951	LLEHNPANLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQGRRAAMTAAMIYADRRD					
	300	310	320	330	340	350
m951.pep	370	380	390	400	410	420
	YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRKLPEQQGRYFTADNL					
g951	YAKVRQWLKKVSAPEYLFDKGVLA AAAA AELDGGRAALRQIGRVRKLPEQQGRYFTADNL					
	360	370	380	390	400	410
m951.pep	430	440	450	460	470	480
	SKIQLALSCLPKREALRGLDKIIEKPPAGSNTLQAEALVQSRVVYDRLGKRRKMISD					
g951	SKIQLALSCLPKREALIGLNNIIAKLSAAGSTEPLAELAQRSIIYEQFGKRGKMIAD					
	420	430	440	450	460	470
m951.pep	490	500	510	520	530	540
	LERAFRLAPDNAQIMNNGYSLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	LETALKLTPDNAQIMNNGYSLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
	480	490	500	510	520	530
m951.pep	550	560	570	580	590	600
	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQA AHLTGDKKIWRETL					
g951	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQA AHLTGDKKIWRETL					
	540	550	560	570	580	590
m951.pep	610					
	KRHGIALPQPSRKPRK					
g951	KRYGIALPEPSRKPRKX					
	600	610				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:

```
a951.seq
1  ATGTTACCCG CCCGTTTCAC CATTTCATCT GTGCTCGCGG CAGCCCTGCT
51  TGCCGGGCGAG GCGTATGCCG CCGGCGCGGC GGATGCGAAG CCGCCGAAGG
101 AAGTCGGAAA GGTTCACAGA AAGCAGCAGC GTTACAGCGA GGAAGAAATC
151 AAAAAACGAAC GCGCACGGCT TCGCGCAGTG GCGCAGCGGG TTAATCAGAT
201 ATTTACGTTG CTGGGAGGGG AAACCGCCTT GCAAAAGGGG CAGGCGGGAA
251 CGGCTCTGGC AACCTATATG CTGATGTTGG AACGCACAAA ATCCCCCGAA
301 GTCGCCGAAC GCGCCTTGGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
351 GCGCGAAATG ATTTATCAGA AATGGCGGCA GATTGAGCCT ATACCGGGTA
401 AGGCGCAAAA ACGGGCGGGG TGGCTGCGGA ACGTGCTGAG GGAAGAGGGA
451 AATCAGCATC TAGACGGACT GGAAGAAGTG CTGGCTCAGG CGGACGAAGG
501 ACAGAACCCG AGGGTGTTTT TATTGTTGGC ACAAGCCGCC GTGCAACAGG
551 ACGGTTGGCG GCAAAAAGCA TCGAAAGCGG TTCGCCGCGC GGCCTTGAGA
601 TATGAACATC TGCCCGAAGC GGCGGTTGCC GATGTGGTGT TCAGCGTACA
651 GGGACGCGAA AAGGAAAAGG CAATCGGAGC TTTGCAGCGT TTGGCGAAGC
701 TCGATACGGA AATATTGCCC CCCACTTTAA TGACGTTGCG TCTGACTGCA
751 CGCAAATATC CCGAAATACT CGACGGCTTT TTCGAGCAGA CAGACACCCA
801 AAACCTTTTC GCCGTCTGGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
851 TGCACAGGCT GGATGATGCC TATGCGCGTT TGAACGTGCT GTTGAACGCG
901 AATCCGAATG CAGACCTGTA TATTCAGGCA GCGATATTGG CGGCAAAACCG
951 AAAAGAAGGT GCTTCCGTTA TCGACGGCTA CGCCGAAAAG GCATACGGCA
1001 GGGGACGGG GGAACAGCGG GGCAGGGCGG CAATGACGGC GGCATGATA
1051 TATGCCGACC GAAGGGATTA CACCAAAGTC AGGCAGTGGT TGAAGAAAGT
1101 GTCCGCGCCG GAATACCTGT TCGACAAAGG TGTGCTGGCG GCTGCGCGG
1151 CTGTCGAGTT GGACGGCGGC AGGGCGGCTT TGCGGCAGAT CCGCAGGGTG
1201 CGGAAACTTC CCGAACAGCA GGGGCGGTAT TTTACGGCAG ACAATTTGTC
1251 CAAATACAG ATGTTGCGCC TGTCGAAGCT GCCCGACAAA CGGGAGGCTT
1301 TGAGGGGGTT GGACAAGATT ATCGAAAAC CGCCTGCCCG CAGTAATACA
1351 GAGTTACAGG CAGAGGCATT GGTACAGCGG TCAGTTGTTT ACGATCGGCT
1401 TGGCAAGCGG AAAAAATGA TTTCAGATCT TGAAGGGCGG TTCAGGCTTG
1451 CACCCGATAA CGCTCAGATT ATGAATAATC TGGGCTACAG CCTGCTTTCC
1501 GATTCCAAAC GTTTGGACGA AGGCTTCGCC CTGCTTCAGA CGGCATACCA
1551 AATCAACCCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
1601 ACCTGAAAGG CGACGCGGAA AGCGCGCTGC CGTATCTGCG GTATTCTGTT
1651 GAAACGACCC CCGAGCCCGA AGTTGCCGCC CATTGGGCGG AAGTGTGTG
1701 GGCATTGGGC GAACGCGATC AGGCGGTTGA CGTATGGAGC CAGGCGGCAC
1751 ACCTTACGGG AGACAAGAAA ATATGGCGGG AACGCTCAAC ACGTCACGGC
1801 ATCGCATTGC CCCAACCTTC CCGAAACCT CGGAATAAA
```

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

```
a951.pep
1  MLPARFTILS VLAAALLAGQ AYAAGAADAK PPKEVGKVFR KQORYSEEEI
51  KNERARLAHV GERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSPE
101 VAERALEMAV SLNAFEQAEI IYQKWRQIEP IPGKAQKRAG WLRNVLRERG
151 NQHLDGLEEV LAQADEGQNR RVFLLLAQAA VQODGLAQKA SKAVRRAALR
201 YEHLPEAAVA DVVFSVQGRE KEKAIGALQR LAKLDEILP PTLMLRLRLTA
251 RKYPEILDGF FEQTDQNLN AVWQEMEIMN LVSLHRLDDA YARLNVLLER
301 NPNADLYIQA AILANRRKEG ASVIDGYAEK AYGRGTGEOR GRAAMTAAMI
351 YADRRDYTKV ROWLKKVSAP EYLFDKGVLA AAAAVELDGG RAALRQIGRV
401 RKLPEQQGRY FTADNLSKIQ MFALSKLPDK REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYSLLS
501 DSKRLDEGFA LLQATYQINP DDTAVNDSIG WAYYKLGDAE SALPYLRYSF
551 ENDEPEVEVA HLGEVLWALG ERDQAVDVWT QAAHLTGDKK IWRETLKRHG
600 IALPQPSRKP RK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*.

a951/m951 96.4% identity in 614 aa overlap

```

              10      20      30      40      50
a951.pep      MLPARFTILSVLAAALLAGQAYAG--AADAKPPKEVGKVFRKQORYSEEEIKNERAR
              ||| ||| :|||:|:|:|:| | | | | | | | | | | | | | | | | | | | | |
m951          MIMLPNRFKMLITVLTATLIAGQVSAAGGGAGDMKQPKVEVGKVFRKQORYSEEEIKNERAR
              10      20      30      40      50      60

              60      70      80      90     100     110
a951.pep      LAAVGERVNQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
```

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|||||
m951    LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
          70      80      90      100     110     120

          120     130     140     150     160     170
a951.pep QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
          120     130     140     150     160     170
m951    QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
          130     140     150     160     170     180

          180     190     200     210     220     230
a951.pep AQAAVQQDGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
          180     190     200     210     220     230
m951    AQAAVQQDGLAQKASKAVRRAALKYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
          190     200     210     220     230     240

          240     250     260     270     280     290
a951.pep EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLHRLDDAYARLNV
          240     250     260     270     280     290
m951    EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLHRLDDAYARLNV
          250     260     270     280     290     300

          300     310     320     330     340     350
a951.pep LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
          300     310     320     330     340     350
m951    LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTEEQRSRAALTAAMMYADRRD
          310     320     330     340     350     360

          360     370     380     390     400     410
a951.pep YTKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRKLPEQQGRYFTADNL
          360     370     380     390     400     410
m951    YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRKLPEQQGRYFTADNL
          370     380     390     400     410     420

          420     430     440     450     460     470
a951.pep SKIQMFALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKMKISD
          420     430     440     450     460     470
m951    SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKMKISD
          430     440     450     460     470     480

          480     490     500     510     520     530
a951.pep LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQATAYQINPDDTAVNDSIGWAYYLK
          480     490     500     510     520     530
m951    LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQATAYQINPDDTAVNDSIGWAYYLK
          490     500     510     520     530     540

          540     550     560     570     580     590
a951.pep GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
          540     550     560     570     580     590
m951    GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
          550     560     570     580     590     600

          600     610
a951.pep KRHGIALPQPSRKPRK
          600     610
m951    KRHGIALPQPSRKPRK
          610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

```

g952.seq (partial)
1  ..TTGCTTATC GTTGAATGC TGCACCGATG TTAAACGATA ATCCTGTGTG
51  TTACGGAAAA ATCAAATGCG AGAGTTGGAA AGCGCGGCGG GATTTCATA
101 TTGTAAAGCA GGATTGGAT TTTTCCTGCG GGGCGGCTTC GGTGGCGACG
151 CTTTTGAACA ATTTTACGG GCAAAAGCTG ACGGAAGAAG AAGTGTGGA
201 AAAACTGGGT AAGGAACAGA TCGCGCGGTC GTTTGAGGAT ATCGCGCGCA
251 TTATGCCCGA TTTGGGTTTT GAGGCGAAAG GCTATGCCCT GTCTTTCGAA
301 CAGCTCGCGC AGTTGAAAAT CCCCGTCATC GTGTATCTGA AATACCGCAA
351 AGACGACCAT TTTTCGGTAT TCGCGGGAGT GGATGGCAAT ACGGTTTTGC
401 TTGCCGACCC GTCGCCGGGT CATGTTTCGA TGAGCAGGGC CGAGTTTTTG
451 GAGGCTTGGC AAACCCGTGA GGGAAATTTG GCAGGCCAAA TTTTGGCGGT
501 CGTGCCGAAA AAAGCGGAGG CGATTTCAAA TAAATTGTTT TTCACACATC
551 ATCCCAAGCG GCAGACGGAG TTTGCAGTCG GACAGGTAAA ATGGTGGCGT

```

601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)
 1 ..LSYRLNAAPM FNDNPVVYVK IKLQSWKARR DFNIVKQDLD FSCGAASVAT
 51 LLNNFYGQKL TEEEVLEKLG KEQMRASFED MRRIMPDLGF EAKGYALSFE
 101 QLAQLKIPVI VYLKVRKDDH FSVLRGVDGN TVLLADPSPG HVMSMSRAQFL
 151 EAWQTREGNL AGKILAVVPK KAEAISNKL FTHHPKQTE FAVGQVKWWR
 201 AY*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq
 1 ATGATGAAGT TCAATATGT TTTCTGTTG GCGTGTGTTG TCGTTTCTTT
 51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
 101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG CGCGCGGGA TTTCAATATT
 151 GTAAAGCAGG ATTTGGATTT TTCCTGTGGG GCGGCTTCGG TGGCGACGCT
 201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
 251 AGCTGGATAA GGAGCAGATG CGCGCTCGT TTGAGGATAT GCGGCGCATT
 301 ATGCTGTATT TGGGTTTGA GCGGAAGGCG TATGCCCTGT CTTTCGAGCA
 351 GCTCGCGCAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
 401 ACGACCATT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
 451 GCCGACCCGT CGCTGGGGCA TGTTCATATG AGCAGGGCGC AGTTTTTGGA
 501 TGCTTGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCTGTCA
 551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
 601 CCAAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
 651 AGAGTAA

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep
 1 MMKFKEYVLL ACVVVLSYR LNAAPMFNDN PVVYVKIKVQ SWKARRDFNI
 51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKLDKEQM RASFEDMRR
 101 MPDLGF EAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
 151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTOH
 201 PKRQTEFTVG QIRQARAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952: 92.5% identity in 201 aa overlap

		10	20	30	40
g952.pep		LSYRLNAAPMFNDNPVVYVKIKLQSWKARRDFNIVKQDLDFSCG			
m952					
	10	20	30	40	50
	50	60	70	80	90
g952.pep	AASVATLLNNFYGQKLTEEEVLEKLGKEQMRASFEDMRRIMPDLGF EAKGYALSFEQLAQ				
m952					
	70	80	90	100	110
	110	120	130	140	150
g952.pep	LKIPVIVYLKVRKDDHFSVLRGVDGNTVLLADPSPGHVMSMSRAQFL EAWQTREGNLAGKI				
m952					
	130	140	150	160	170
	170	180	190	200	
g952.pep	LAVVPKKA E AISNKLFFTHHPKQTEFAVGQVKWWRAYX				
m952					
	190	200	210		
	LAVIPKKAETISNKLFFTOH PKRQTEFTVGQIRQARAE				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq
 1 ATGATGAAGT TCAATATGT TTTCTGTTG GCGTGTGTTG TCGTTTCTTT

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51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTGTGTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG AAAGCGGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATTT TTCCTGCGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATT CTGCGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGTCA TGTTTCAATG AGCAGGGCGC AGTTTNGGA
501 TGCTTGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCGGTCG
551 TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTT CACACATCAT
601 CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

a952.pep

```

1 MMKFYVFL ACVVVSLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLNKLDKEQM RASFEDMRRRI
101 MPDLGFCAK YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

a952/m952 97.7% identity in 218 aa overlap

	10	20	30	40	50	60
a952.pep	MMKFYVFLACVVVSLSYRLNAAPMFNDNPVVYGKIKVQSWKERRDFNIVKQDLDFSCG					
m952	MMKFYVFLACVVVSLSYRLNAAPMFNDNPVVYGKIKVQSWKARRDFNIVKQDLDFSCG					
	10	20	30	40	50	60
a952.pep	AASVATLLNNFYGQTLTEEEVLKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ					
m952	AASVATLLNNFYGQTLTEEEVLKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ					
	70	80	90	100	110	120
a952.pep	LKIPVIVYLKRYKDDHFSVLRGIDGNTVLLADPSLGHVSM SRAQFXDAWQTREGNLAGKI					
m952	LKIPVIVYLKRYKDDHFSVLRGIDGNTVLLADPSLGHVSM SRAQFLDAWQTREGNLAGKI					
	130	140	150	160	170	180
a952.pep	LAVVPKKAETISNKLFFTHHPKRQTEFAVGQIRQARAE					
m952	LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE					
	190	200	210	219		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

g953.seq

```

1 ATGAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51 CTCGCCACC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCTGACC
151 GGTTCGTCG AGTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCCGTC GCCAACCTGC AAAGCGGTTT GCAACCCCTT ACCGGCCACC
251 TGAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTTCACCA AATTCAACTT CAACGGCAAA AAAGTTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACCGCCCT CGTCAAACTC AAAGCCGAAA
401 AATTCAACTG CTACCAAGC CCGATGGCGG AAACCGAAGT TTGCGGCGGC
451 GACTTCAGCA CCACCATCGA CCGCACCAAA TGGGGCGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAACAATA A

```

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This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:

g953.pep
 1 MKKIIFAALA AAAGVTASAT YKVDEYHANV RFAIDHFNTS TNVGGFYGLT
 51 GSVVEFDQAKR DKGIDITIPV ANLQSGSQPF TGHLSADIF DAAQYPDIFR
 101 VSTKFNENGK KLVSVVDGNLT MRGKTAPVKL KAEKFNCYQS PMAETEVC GG
 151 DFSTTIDRTK WGVVDYLVNAG MTKNVRIDIQ IEAAKQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

m953.seq
 1 ATGAAAAAAA TCATCTTCGC CGCACTCGCA GCCGCCGCCA TCAGTACTGC
 51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCTG
 101 CCATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
 151 ACCGGTTCCG TCGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
 201 CACCATCCCC ATTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
 251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
 301 TTTGTTTCCA CCAAATTCOA CTTCAACGGC AAAAACTGG TTTCCGTTGA
 351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAA CTCAAAGCGG
 401 AAAAATTCAA CTGCTACCAA AGCCCGATGG AGAAACCGA AGTTTGTGGC
 451 GCGGACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
 501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
 551 CAGCCAAACA ATAA

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

m953.pep
 1 MKKIIFAALA AAAISTASAA TYKVDEYHAN ARFAIDHFNT STNVGGFYGL
 51 TGSVEFDQAK RDGKIDITIP IANLQSGSQH FTDHLKSADI FDAAQYPDIFR
 101 FVSTKFNENG KLVSVVDGNLT TMHGKTAPVK LKAEKFNCYQ SPMEKTEVCG
 151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

m953/g953 93.0% identity in 187 aa overlap

	10	20	30	40	50	60
m953.pep	MKKIIFAALAAAAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
g953	MKKIIFAALAAAAAVGTASA-TYKVDEYHANVRFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
	10	20	30	40	50	
m953.pep	RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIFVSTKFNENGKLVSVVDGNL					
g953	RDGKIDITIPVANLQSGSQPFTGHLKSADIFDAAQYPDIFVSTKFNENGKLVSVVDGNL					
	60	70	80	90	100	110
m953.pep	TMHGKTAPVKLKAKEFNQYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
g953	TMHGKTAPVKLKAKEFNQYQSPMAETEVC GGDFSTTIDRTKWGVVDYLVNAGMTKNVRIDI					
	120	130	140	150	160	170
m953.pep	QIEAAKQX					
g953	QIEAAKQX					
	180					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

a953.seq
 1 ATGAAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCACTGC
 51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCT
 101 CTATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
 151 ACCGGTTCCG TTGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
 201 CACCATCCCC GTTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
 251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
 301 TTTGTTTCCA CCAAATTCOA CTTCAACGGC AAAAACTGG TTTCCGTTGA

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```

351 CCGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGC GGC
451 GCGCACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
  1 MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
 51 TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYPDIR
101 FVSTKFNENG KKLVSVDGNL TMHGKTAPVK LKAEKFNCYQ SPMLKTEVCG
151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

```

a953/m953    97.3% identity in 187 aa overlap

          10      20      30      40      50      60
a953.pep    MKKIIIAALAAAIGTASAATYKVDEYHANARFSIDHFNTSTNVGGFYGLTGSVEFDQAK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m953         MKKIIIFAALAAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK
          10      20      30      40      50      60

          70      80      90     100     110     120
a953.pep    RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSDGNL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m953         RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSDGNL
          70      80      90     100     110     120

          130     140     150     160     170     180
a953.pep    TMHGKTAPVKLKAERFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m953         TMHGKTAPVKLKAERFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
          130     140     150     160     170     180

a953.pep    QIEAAKQX
          |||||
m953         QIEAAKQX

```

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
  1 ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
 51 GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
101 AATATCAATT TGCAGATGAG AACAGGCTT TTTATTTTGA ACGCGCCGCC
151 CGTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT
201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
251 TTACTCAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
301 TACCGCGTCT GCAAACAGGC TGCGCAAGAT GCAGAAATCC TGATGAAGAG
351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTTAGAT AAGGAAAGTT
401 ATCAAAATTA CCGAAAATCA ATGCAAGAAT GCCGTAAAC AATAACGGAA
451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
  1 MKKFYFVLLA LGLAACGQEQ SOKADAEQYF FANKYQFADE KOAFYFERAA
 51 RFRVLQQLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDP
101 YRVCKQAAQD AEILMKSMVT SGGGGTTDL D KESYQNYRKS MQECRKTITE
151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

```
g957.seq (partial)
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCTGTGCA GTCGGAGAAG GATTATCTCG CGCTCGTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGTTGTTT TGGCAACCGG
551 ACGGTTTCGG ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATCGGGGAAT TGATGCCCGG GGGGatgaag gcgaacagtc ttgtggtcgg
801 ctatgatgcg gacggtCtgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaacc ccaaagtgtc gaattattatt tgaaaaacgg aaatcttttt
901 attgccaat cttcgacggt aaccttgaac acggatggcg taacggcgga
951 tatgcaaac tatcatgctc aacaaacgtt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

```
g957.pep (partial)
1  MFKKFKPVL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNFAV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFVSU VYGGTAHGEN YETTGEYRVV WQPDGVSFDA AGRGKIGEDV
201 YENCLGCMQ AOVYLAKYRD VANDEQKQWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGM ANSLVGYDA DGLFPKQVYS VDNGKKPQSV EYLYKNGNLF
301 IAQSSTVTLK TDGVTADMQT YHAQOTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

```
m957.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCTT TGCCGGAACT GTGGATGACG
251 GTCCTGTGCA GTCGGAGAAG GATTATCTCG CGCTCGTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGTTGTTT TGGCAACCGA
551 ACGGTTTCGG ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGGAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAGC CCAGAGTTTC GAATATTATT TGAATAACGG AAATCTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGATG GGCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGGAATTT TGGAAAAGA GGTGCGCGGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTGCGGC GGCAGGCGCG ACCTTTCTCA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

```
m957.pep
1  MFKKFKPVL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPKNPFAV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFVSU VYGGTVHGEN YETTGEYRVV WQPDGVSFDA AGRGKIGEDV
201 YENCLGCMQ AOVYLAKYRD VANDEQKQWD FRKESNRIAS DSRNSVFYQN
```

1368

251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
 301 IAQSSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
 351 LENLEKEVRR YAEAAARRSG GRRDLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

	10	20	30	40	50	60
g957.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNFAVAKLARLFRNA					
m957	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNFAVAKLARLFRNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
g957.pep	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLAIRLSRLKEKAKWFHVTEQEHGEEV					
m957	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLAIRLSRLKEKAKWFHVTEQEHGKEV					
	70	80	90	100	110	120
	130	140	150	160	170	180
g957.pep	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFVSVNVYGGTAHGENYETTGEYRVV					
m957	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFVSVNVYGGTVHGENYETTGEYRVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
g957.pep	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKQVWDFREESNRIAS					
m957	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKQVWDFRKESNRIAS					
	190	200	210	220	230	240
	250	260	270	280	290	300
g957.pep	DSRDYVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSVDNGKKPQSVEYYLKNGNLF					
m957	DSRNVVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
	250	260	270	280	290	300
	310	320	330			
g957.pep	IAQSSSTVTLKTDGVTADMOTYHAQQTLYLDG					
m957	IAQSSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
m957	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

1	ATGTTTAAAA	AATTCAAACC	GGTACTGTTG	TCATTTTTTG	CAC TTGTATT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAATCCGA	ATGCTTTTGT	GGCGAAACTT
151	GCCCGCCTGT	TCCGAAATGC	CGACAGGGCG	GTTGTCATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TTGCCGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCGGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAAACG	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTTGATGC	GTCGGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCTCGGGT	GTTATCAGAT	GGCCAGGTA	TATTTGGCGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGACTCGCGC	GATTCTGTGT	TTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAAACAGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAAT	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC

951 CTATCATGCG CAACAGACGT GGTATTAGA TGGCGGGCGG ATTGTCCGCG
 1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
 1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCGGG
 1101 CGGCAGGCGC GACCTTCTC ACTGA

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

a957.pep
 1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
 51 ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
 101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLRYN
 151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
 201 CLGICYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
 251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
 301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
 351 LEKEVSRVYE AAARRSGGRR DLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

a957.pep	10	20	30	40	50	
m957	10	20	30	40	50	
a957.pep	60	70	80	90	100	110
m957	60	70	80	90	100	110
a957.pep	120	130	140	150	160	170
m957	120	130	140	150	160	170
a957.pep	180	190	200	210	220	230
m957	180	190	200	210	220	230
a957.pep	240	250	260	270	280	290
m957	240	250	260	270	280	290
a957.pep	300	310	320	330	340	350
m957	300	310	320	330	340	350
a957.pep	360	370				
m957	360	370				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

g958.oaeg
 1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
 51 TTTCCGGCAG CATTGCGCCG CCGATACCGT TCGGCGGAA GAGCGGACG

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101 GGCCTGTCTCG AGAAGGCGGT GCGCAGGCGC CGTCCGAATC CGCACAAGCT
151 TCCGATTTGA CCTTCGGTTC GACCTGCCTG TTTTGCAGTA ACGAAAGCGG
201 CAGCCCCGAG AGAACCGAAG CCGCCGTCCTA AGGCAGCGGC GAAGCATCCG
251 TCCCCGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TCGCGCGCGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTCCGC CTCCAACAGG ACGGTACGCT GATTCTGGGG
451 GAAACCTGTA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACTG
501 CCGTATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAAGC GTCAGCCGCA
551 CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCAATTC
601 AACACCTGTT CCGCCGAGAG TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
651 CGAAGCCGAT CCGGGAAAAG GCATAGGCGT TGCCAAACAC GCGCCTTCG
701 TGTTCCGGCG CGTTCCTCTT TTCTATACGC CTTGGGCGGA CTTCCCGCTT
751 GACGGCAACG GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCCGGTTC
801 GGACGGCGTT TCCCTTTCCG TCCCTTATTA TTTCAACCTT GCCCCAACT
851 TCGATGCCAC TTTCCGCCCC GGCATTATCG GCGAACGCGG CGCGACGTTT
901 GACGGACAAA TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCACGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GCGGGGTGTC
1051 GATTTCAACC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAAGAAATC GCCGGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
1151 ATGGCGGCGA GCGGGCGGGA GGCAGCCTGA ATGCCGCGCT TTCGGTTCAG
1201 AAATACCAGA CGCTGGCAAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCCGCCAA
1351 GACGGGAGCC GACTGGTCGT GTATCCCGGT ATCAATGGG ATTTCAGCAA
1401 CAGCTGGGGC TACGTCGCGC CAAACTCGG GCTGCACGCC ACTTATTACA
1451 GCCTTCGACG TTTCCGGCGG AAAGCATCCC GCAGCGTCGG GCGCGTTTG
1501 CCCGTTGTCA ATATCGACGG CGGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCCGCGCCTG TTCTACAACT
1601 ATATTCTTGC CAAATCTCAA AACGACCTGC CCAATTTCTG TTCGTCGGAA
1651 AGCAGGTTCT GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACGCCGCCA ACAGCCTTTC CACCGCGGTG CAGAGCCGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTCAG
1801 AAATTTCTAT TCAAGGATGA TCGGCTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCCGTTCCG ACTGGGTGGC ATTGCGCTCC GCGGCGATAG
1901 GCGGGCGGTT CACCTCTGAC AGCAGCATCC ACTACACCA AAACGACAAA
1951 CCGCGCGAAC ATTACGCCGT CCGCGCAGGC TACCGCCCCG CCCCCGAAA
2001 AGTGTGTAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGGCGGACGG TTCCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAAATGG CGCTGACGCG CAACCTGTCT GCCGTCTGTC GCTACAACTA
2151 CGGTTTTGAA GCCAAAAAAC CGATAGAAAT GCTTGCCGGT GCAGAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGGGGCG TGTACGCCCA ACGCTACGTT
2251 ACCGGCGAAA ACACCTACAA AAACGCGGTC TTTTTCAC TTCAGTTGAA
2301 AGACCTCAGC AGCGTCGGCA GAAACCCCGC AGGCAGGATG GATGTCGCGC
2351 TTCCCGGCTA CATCCCGGCC CACTCTCTTT CCGCCGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

```

g958.pep
1  LARLFLSKPL VLALGFCEGT HCAADTVAAE EADGRVAEGG AQGASESAQA
51  SDLTLLGSTCL FCSNESGSPE RTEAAVQSGS EASVPEDYTR IVADRMEGQS
101 KVKVRAEGSV IIERDGAVLN TDWADYDQSG DTVTVGDRFA LQQDGTILRG
151 ETLYNLDDQ TGEAHNVME TEQGGRRLOS VSRTEMLGE GRYKLTETQF
201 NTCSAGDAGW YVKAASVEAD RGKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLRLP YSGQDGLTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSLNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSDGRQ
451 DGSRLVVYPG IKWDFSNSWG YVRPKLGLHA TYYSLDSFGG KASRSVGRVL
501 PVVNIDGGTT FERNTLFGG GVVQTIETPL FYNYPKASQ NDLPNFDSSSE
551 SSFGYQQLFR ENLYYGNDR I NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSGVGNPR SRSDWAFAS GGIIGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLDADGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAGRYV
751 TGENTYKNAV FFSLQLKDL S SVGRNPAGRM DVAVPGYIPA HSLSAGRNRK
801 P*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

```

m958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCCTCTG
51  CTTCCGACAG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA CGGTGTCCGA ACCCATACAG

```

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTGCA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCAGAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAACCG
351 GACGACCCTC AATACCGATT GGGCGGATTA CGACCAGTCG GCGGACACCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGGGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGCATG GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGTCGAAGCC GATCGGGAAG AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGCGA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCCGCCGG
801 TTCGACGGGC GTTTCCTTTT CCGTTCCTTA TTATTTC AAC CTGCCCCCA
851 ATCTCGATGC CACGTTTCGG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGGCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCAGC ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTC ACAAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACCTCAACCT CAACCGCGGT GTATGGCTGG
1151 ATTTATGGCG CAGGCGGGCG GCGGCGAGCC TGAATGCCGG CTTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAAACGTA
1251 TGCCCTCATG CCGCGCCTTT CGGTGCGAGTG GCGTAAAAAC ACCGCGAGGG
1301 CGCAATCCG CGTGTCCGCA CAATTTACCC GATTACGCCA CGACAGCCGC
1351 CAAGACGGCA GCGCCTGGT CGTCTATCCC GACATCAAT GGGATTTCAG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAC CTGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATTT TCAACATCGA CAGCGGCGCA ACTTTTGAGC GGAATACGCG
1551 GATGTTGCGC GGAGAAGTCC TGCAAACCTT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAACGACC TGCCCAATTT CGATTGCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAAGCC
1751 GTATTTTGA CCGCGCGACG GGGGAAGAGC GTTTCGCGC CGGCATCGGT
1801 CAGAAATTCT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTTGCC TCCGGCAGCA
1901 TCGGCAGCCG CTTTATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAAGTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGTCTG AACGCCCGCT ACAATAACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCAACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGCTG TCCGTTACAA
2151 CTACGGTTT GAAGCCAAA AACCAGATGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGTGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTCT GCAGAAACCC CGCAGACAGG ATGGATGTCTG
2351 CCGTTCGCGG CTATATCACC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CGACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

```

m958.pep
1  LARLFSKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51  PLSLSLSTG LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMGQ
101 SQVQVRAEGN VVVERNRTTL NTDWADYDQS GDTVTAGDRF ALQQDGLIR
151 GETLTYNLEQ QTGEAHNVRM EIEQGGRLQ SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKIGVAK HAAFFVGVPV IFYTPWADFP
251 LDGNNRKSGLL VPSLSAGSDG VSLSPYYFN LAPNLDATEFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QTRFSDSR
451 ODGSRLLVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSR
501 LPIVNIDSGA TFERNTRMFG GEVLQTLFPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGSGVKKP RNRSDWVAFS SGSIGSRFIL DSIHYNQND
651 KRAENYAVGA SYRPAQGVKL NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVLG GAELYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNN
801  RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

m958/g958 89.3% identity in 802 aa overlap

	10	20	30	40	50	60
m958.pep	LARLFS	LKPLVL	ALGLCF	GTGTHCAA	ADAVAAE	ETDNPTAG
g958	LARLFS	LKPLVL	ALGLCF	GTGTHCAA	-DTVAEE	ADGRVAEG
	10	20	30	40	50	
	70	80	90	100	110	120
m958.pep	LFCSNE	SGSPER	TEAAVQ	SGSEAS	IPEDYTR	IVADRM
g958	LFCSNE	SGSPER	TEAAVQ	SGSEAS	VPEDYTR	IVADRM
	60	70	80	90	100	110
	130	140	150	160	170	180
m958.pep	NTDWAD	YDQSGD	TVTAGD	RFALQQ	DGTLIR	GETLTYN
g958	NTDWAD	YDQSGD	TVTAGD	RFALQQ	DGTLIR	GETLTYN
	120	130	140	150	160	170
	190	200	210	220	230	240
m958.pep	SVSRTA	EMLGEG	HYKLT	TETQFN	TCSAGD	AGWYVKA
g958	SVSRTA	EMLGEG	RYKLT	TETQFN	TCSAGD	AGWYVKA
	180	190	200	210	220	230
	250	260	270	280	290	300
m958.pep	IFYTPW	ADFP	LDGNRK	SGLLV	PSLSAG	SDGVSL
g958	IFYTPW	ADFP	LDGNRK	SGLLV	PSLSAG	SDGVSL
	240	250	260	270	280	290
	310	320	330	340	350	360
m958.pep	FDGQVR	YLRPD	YAGQSD	LTWLP	HDKSGR	NNRYQAK
g958	FDGQVR	YLRPD	YAGQSD	LTWLP	HDKSGR	NNRYQAK
	300	310	320	330	340	350
	370	380	390	400	410	420
m958.pep	YYRDFY	GNKEI	AGNVNL	NRVWLD	YGGRAG	GSNLAG
g958	YYRDFY	GNKEI	AGNVNL	NRVWLD	YGGRAG	GSNLAG
	360	370	380	390	400	410
	430	440	450	460	470	480
m958.pep	PRLSVE	WRKNT	GRAQIG	VSAQFT	RFSHDS	RQDGSRL
g958	PRLSAD	WHKN	AGRAQI	GVSAQF	TRFSDG	RQDGSRL
	420	430	440	450	460	470
	490	500	510	520	530	540
m958.pep	ATYYSL	NRFGS	QEARRV	SRTLPI	VNIDSG	ATFERN
g958	ATYYSL	NRFGS	QEARRV	SRTLPI	VNIDSG	ATFERN
	480	490	500	510	520	530
	550	560	570	580	590	600
m958.pep	QNDLPN	FDSS	ESSFGY	QGLFRE	NLYYGN	DRINTAN
g958	QNDLPN	FDSS	ESSFGY	QGLFRE	NLYYGN	DRINAAN
	540	550	560	570	580	590
	610	620	630	640	650	660
m958.pep	QKFYFK	DDAV	MLDGS	VGKPNR	SDWVAF	ASGSIG
g958	QKFYFK	DDAV	MLDGS	VGKPNR	SDWVAF	ASGGIG
	600	610	620	630	640	650
	670	680	690	700	710	720
m958.pep	SYRPAQ	GKVLN	ARYKYG	RNEKIY	LKSDGS	YFYDKL
g958	GYRPAQ	GKVLN	ARYKYG	RNEKIY	LQADGS	YFYDKL
	660	670	680	690	700	710

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	730	740	750	760	770	780
m958.pep	EAKKPIEVLAGEYKSSCGCWAGVYAQRVYTGENTYKNAVFFSLQLKDLSSVGRNPADR					
g958	EAKKPIEVLAGEYKSSCGCWAGVYAQRVYTGENTYKNAVFFSLQLKDLSSVGRNPAGR					
	720	730	740	750	760	770
	790	800				
m958.pep	MDVAVPGYITAHSLSAGRNRKP					
g958	MDVAVPGYIPAHSLSAGRNRKPX					
	780	790	800			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

a958.seq

```

1   TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCCGGCAGC CATTGCGCCG CCGCCGATGC CGTTGCGCGC GAGGAAACGG
101 ACATATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCCGA ACCCATACAG
151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTGTGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAATCG
351 GACGACCTTC AATGCCGATT GGGCGGATTA CGACCACTCG GGCGACACCG
401 TTACCCGAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTCGG
451 GGCGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGTATG GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCGTGTTCGG CGGCGTTCCT ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTC GTTCCCTCAC TGTCCGCCGG
801 TTCGGACGGC GTTTCCTTTT CCGTTCCTTA TTATTTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTTCGG CCCGGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGTATC
1001 AGGCGAAATG GCAGCACCGG CACGACATT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTC AACAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGCTGG
1151 ATTATGGCGG CAGGCGCGCG GCGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAACCCGTA
1251 TGCCCTGATG CCGCGCCTTT CCGCCGATTG GCGCAAAAC ACCGCGAGGG
1301 CGCAATCGG CGTGTCCGCC CAATTACCC GCTTCAGCCA CGACAGCCGC
1351 CAAGACGGCA GCCGCCTCGT CGTCTATCCC GACATCAAT GGGATTTCAG
1401 CAACAGCTGG GGTACGTCC GTCCAAACT CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGCG
1551 GATGTTCCGG GCGCGAGTCC TGCAAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTGCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTTTT CTGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAGGCC
1751 GTATTTTGGG CGGCGCGACG GGGGAAGAGC GTTTCGCGC CGGCATCGGG
1801 CAGAAATCTT ACTTCAAAAA CGACGCAGTC ATGCTTGACG GCAGTGTCCG
1851 CAAAAAACCG CGCAGCCGTT CCGACTGGGT GGCATTCCGC TCCAGCGGCA
1901 TCGGCGAGCA CTTTATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAATACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGTG AACGCCCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GCGCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGGTGACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTGC
2351 CCGTTCGCG CTATATCCCC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CCGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

a958.pep

```

1   LARLFSLKPL VLALGFCEFGT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PTLSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMERG
101 SQQVVRAGEN VVVERNRTTL NADWADYDQS GDTVTAGDRF ALQQDGLTLR
151 GELTYNLEQ QTGEAHNVRM ETEHGRRRLQ SVSRTEMLG EGHYKLTETO
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFFVGGVP IFYTPWADFP

```

```

251 LDGNRKSGLL VPSLSAGSDG VSLSVPPYYFN LAPNLDATFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QFTRFSHDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLTLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDV MLDGSGVKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GA EYKSSCGC WGAGVYAQRV
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

	10	20	30	40	50	60
a958.pep	LARLFSLKPLVLALGFCGTHCAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC					
m958	LARLFSLKPLVLALGFCGTHCAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC					
	10	20	30	40	50	60
	70	80	90	100	110	120
a958.pep	LFCSNESGSPERTEAAVQSGSEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL					
m958	LFCSNESGSPERTEAAVQSGSEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a958.pep	NADWADYDQSGDVTAGDRFALQQDGLIRGETLTYNLEQQTGEAHNVRETEHGGRRLO					
m958	NTDWADYDQSGDVTAGDRFALQQDGLIRGETLTYNLEQQTGEAHNVREIEQGGRRLO					
	130	140	150	160	170	180
	190	200	210	220	230	240
a958.pep	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKIGVAKHAAFFVGGVP					
m958	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKIGVAKHAAFFVGGVP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a958.pep	IFYTPWADFFLDGNRKSGLLVPSLSAGSDGVSLSVPPYYFNLAPNLDATFAPGVIGERGAV					
m958	IFYTPWADFFLDGNRKSGLLVPSLSAGSDGVSLSVPPYYFNLAPNLDATFAPSVIGERGAV					
	250	260	270	280	290	300
	310	320	330	340	350	360
a958.pep	FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG					
m958	FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG					
	310	320	330	340	350	360
	370	380	390	400	410	420
a958.pep	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
m958	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
	370	380	390	400	410	420
	430	440	450	460	470	480
a958.pep	PRLSADWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH					
m958	PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH					
	430	440	450	460	470	480
	490	500	510	520	530	540
a958.pep	ATYYSLNRFSGQEARRVSRTLPIVNIDSGMTFERNTRMFGGVLQTLERLFFNYIPAKS					
m958	ATYYSLNRFSGQEARRVSRTLPIVNIDSGMTFERNTRMFGGEVLQTLERLFFNYIPAKS					

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	490	500	510	520	530	540
	550	560	570	580	590	600
a958.pep	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRIANTANSLSAVQSRILDGATGEERFRAGIG					
m958	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRIANTANSLSAVQSRILDGATGEERFRAGIG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a958.pep	QKFYFKNDVMDGSGVGGKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
m958	QKFYFKNDVMDGSGVGGKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
	610	620	630	640	650	660
	670	680	690	700	710	720
a958.pep	SYRPAQGVKNLARYKYGRNEKIYKSDGSYFYDKLSQLDLQAQWPLTRNLSAVVRNYGFG					
m958	SYRPAQGVKNLARYKYGRNEKIYKSDGSYFYDKLSQLDLQAQWPLTRNLSAVVRNYGFG					
	670	680	690	700	710	720
	730	740	750	760	770	780
a958.pep	EAKKPIEVLGAIEYKSSCGCWGAGVYAQRVVTGENTYKNAVFFSLQKDLSSVGRNPADR					
m958	EAKKPIEVLGAIEYKSSCGCWGAGVYAQRVVTGENTYKNAVFFSLQKDLSSVGRNPADR					
	730	740	750	760	770	780
	790	800				
a958.pep	MDVAVPGYIIPAHSLSAGRNRKRP					
m958	MDVAVPGYIIPAHSLSAGRNRKRP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

g959.pep

```

1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAARAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGGCGGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

m959.pep

```

1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

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m959/g959 95.4% identity in 108 aa overlap

	10	20	30	40	50	60
m959.pep	MN	IK	HL	LL	TS	AA
g959	MN	IK	HL	LL	TS	AA

	70	80	90	100	109
m959.pep	VGG	KIT	DID	LE	HD
g959	VGG	KIT	DID	LE	HD

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

```

1  ATGAACCTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51  CATTTCGGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCGGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

a959.pep

```

1  MNFKRLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51  AQAEEAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a959.pep	MN	FK	RL	LL	TA	AA
m959	MN	IK	HL	LL	TS	AA

	70	80	90	100	109
a959.pep	VGG	KIT	DID	LE	HD
m959	VGG	KIT	DID	LE	HD

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

```

1  ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT
51  TAAGCCCCCC TTGTTTGAAG CTCGCGGGCT CCGCGGAGC TTCACCGACC
101 CCGTGTGCCC CAAGCTCTCT GCTCCGGCGG GCTACATTGT CGACATCCCC
151 AAAGGCAATC TGAAGACCGA AATCGAAAAG CTGGCCAAAC AGCCCCAGTA
201 TGCCTATCTG AAACAGCTCC AAGTAGCGAA AAACGTCAAC TGGAAACAGC
251 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGG CTTAACCAGA
301 GCCGGTGCAG CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGGCGC
351 GGGAGTCGGA GCCGCACTAG GCTTAAACGG CGCAGCCGCA GCAGCGGCCG
401 ATGCCGCCTT TGCCTCACTC GCTTCTCAGG CTTCCGTATC GCTCATCAAC
451 AATAAAGCGC ATGTCGGCAA AACCTGAAG GAACTGGGCA GAAGCCGCAC
501 GGTAAAAAAT CTGTTGTAG CGGCGGCAAC GGCAGGCGTA TCCAACAAAC

```

```

551 TCGGTGCCTC TTCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAAACAAC
601 CTCAACGTTA ACCTGGCCAA TGGGGGCGAGT GCCGCGCTGA TCAACACCGC
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAT ATCCTGGCGG
701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCC CAAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGTGTCAGCG GCGAATAAGG GCAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTGCGG GAGGCTTTGG TTAAAAATAC CGATTTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCCTA
951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTGC ACAAACCGCA CAAAACGCGG TAGAAAAATA TCGGTTTAAA
1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATTT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTTATTCTGA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTATG
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGAAAA CAGCTGGCTC AAATTCAGA
1401 AAAGACAACG CTTCCGACG AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAATA ACCGGTGATA GGTTTTATTT AGATGGCCAA
1501 CATAAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAAT TTAAGTTTGT
1551 TCTAAATATG GATGGTTCGC TTAACCAAA GAAACTGGG GCAGCAAAAG
1601 GTCGTAAATT AAACCTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

m960.pep

```

1 MQVNIQIPCM LYRRGSVKPP LFEAPRLIPS FTDPVVPKLS APGGYIVDIP
51 KGNLKTIEK LAKQPEYAYL KQLQVAKNVN WNOVQLAYDK WDKQEGLTR
101 AGAAIIALAV TVVTAGAGVG AALGLNGAAA AAADAFAASL ASQASVSLIN
151 NKGDVVGKTLK ELGRSRTVKV LVVAAATAGV SNKLGASSLA TWSETPWVNN
201 LNVNLANAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GEAASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKKGKQDGA IGAAVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVVY KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTTLFDETL
401 DWNDAKAVID IVVGTELNRA NKGEAAQVKV EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPFGK QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TKDRFYLDGQ
501 HKNHLEVFDEK NGNEKFVILNM DGSLNQMKTG AAKGRKLNK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

m961.seq

```

1 ATGAGCATGA AACACTTTCC AGCCAAAAGTA CTGACCACAG CCATCCTTGC
51 CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGTGCCTT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTTA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGACTA ACCTGACCAA AACCGTCAAT
301 GAAAAACAAC AAAACGTCGA TGCCAAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTTGCTGA AGAGACTAAG ACAATATCG TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CCGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAAAAC
651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAGCCG
701 AAGCTGCGGC TGGCAGAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCTGTGTCG AACCTTACAA CGTGGGTCGG TCAATGTAA CGGCTGAGT
951 CGGCGGTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTTCCTCCG CAGCCTACCA TGTGCGCGTC AATTACGAGT GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

m961.pep

```

1 MSMKHFPKAV LTTAILATFC SGALAATSDD DVKKAATVAI VAAYNNGQEI

```

```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEA FN DIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV D AKV KAAETAA GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPYNVGR FNVTAAVGGY KSESAVAIGT GFRFTENFAA KAGVAVGTS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet

a961.pep not found yet

g972.seq not found yet

g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

m972.seq

```

1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTCG GAGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTGTGATG GAGAGTACAC GCCGGATCAG CGGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTGT TCGTGTATAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAAA AGCAAATGGG TAAGGTTCCA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCA
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTGA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

m972.pep

```

1  LTNRRGAKLK TXSKSSERMS EVEYFSHFIS DGKGLLEIP QRRGKQDGVF
51  VDWSIFTFHE DTLLKVS GCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFQXQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSIRT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNRPKSE
201 TIGTAWRNED GSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIPLD ILINQGSYFC GAFFICRKFK NMPVPERFDQ RKKKLNLTFF
301 HKLHYAKNAV GKLNVFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKQYEYLS KVVHQNVDYD YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

a972.seq

```

1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTCG GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGCGG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAAAT CTCGTTTGT TCGTGTATTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAAATGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTCTGT GGAGCTTTTC CAATTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAAATATG TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTC GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

a972.pep

```

1  LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGKGKLEIP QRRGKQDGVF
51  VDWISFTFHE DTLLKVS GCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFGGQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE DSGKTFYVGR KNSRFRVRY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICKKFK NMPVPERFDQ RKKTLLNLTFE
301 HKLHYAKNAV GKLNVNFIEM GFDNSEIVES LKADSGFEPK LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVVHQNVDYD YF*

```

m972/a972 99.3% identity in 422 aa overlap

	10	20	30	40	50	60
m972.pep	LTNRGGAKLKTXSKSSERMSEVEYFSHFISDGKGKLEIPQRRGKQDGVFVDWISFTFHE					
a972	LTNRGGAKLKTNKSSERMSEVEYFSHFISDGKGKLEIPQRRGKQDGVFVDWISFTFHE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m972.pep	DTLLKVS GCP LFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE					
a972	DTLLKVS GCP LFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m972.pep	VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALDFFDGEYTPDQ					
a972	VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALDFFDGEYTPDQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m972.pep	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDSGKTFYVGRKNSRFRVRYEKGRQLGDKE					
a972	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDSGKTFYVGRKNSRFRVRYEKGRQLGDKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m972.pep	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICKKFKNMPVPERFDQ RKKKLLNLTFE					
a972	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICKKFKNMPVPERFDQ RKKKLLNLTFE					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m972.pep	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
a972	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPTYDVEKERKYQEYLSKVYHQNVVDYD					
a972	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPTYDVEKERKYQEYLSKVYHQNVVDYD					
	370	380	390	400	410	420
m972.pep	YFX					
a972	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

g973.seq

```

1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CCTGCCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCAAC TTTGAAGACA TCATCGAGCa aatcgtcggt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCACTC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTCCGTACG GAatacggca gcgaagaagc cgacaccatc ggcggtTGG
701 TCATTcAGGA ATTGGGACAC CTGCCCCTGC GCGGCGAAAA AGTCCTTAtc
751 ggcgGTTTGC agttcaccgt CGCCCGCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgcccgttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

g973.pep

```

1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLLE
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQPHLKSIVL PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGSLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFFGT EYGSEADTI GGLVIQELGH LPVRGEKVLI
251 GGLQFTVARA DNRRLLHTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

m973.seq

```

1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCG
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTCCGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTAAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCAAC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTcm
601 GaACGcTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT

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651 CTTCCGGCAGC GAATACAGCA kCGAAGAAGC CGACACCATT GCGCGCCTGG
 701 TCATTCAAGA GTTGGGACAT CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
 751 GCGCGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973.pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLRLE
 51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGGLVT FEDIIEQIVG EIEDEFDEDD SADNIHAVSS
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVL
 251 GGLQFTVARA DNRRLHTLMA TRVK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLRLEKVLDFSDLEV					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLRLEKVLDFAELEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973.pep	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
g973	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIIEQIVG					
g973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIIEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
	:					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAFFGTEYGSSEADTIGGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973.seq

1 ATGGACGGCG CACAACCGAA AACAAATTT TTTGAACGCC TGATTGCCCG
 51 ACTCGCCCGC GAACCGGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA
 151 AAAGTCCTCG ATTTTCTGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
 201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAA CGCATCACC
 251 CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCCGTCAT CGGTGAAGAC
 301 AAAGACGAAG TTTGGGTAT TTTGCACGCC AAAGACCTGC TCAAATATAT
 351 GTTCAACCCC GAGCAGTTCC ACCTCAAATC GATATTGCGC CTGCGCGTCT
 401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTGGG
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGCG GACATCGAAG
 551 ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCC

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601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCGGCACG GAATACAGCA GCGAAGAAGC CGACACCATC GCGCGCCTGG
701 TCATTACAGG ATTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
751 GCGCGTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
  1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLRLLE
  51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGSLVT FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
 201 ERWRIHAATE IEDINAFSGT EYSSEADTI GGLVIQELGH LPVRGEKVL
 251 GGLQFTVARA DNRRHLTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAR	EPDSAEDVLTLLRQAHEQEV	FDADTLRLLEKVLDFSDLEV			
a973	MDGAQPKTNFFERLIARLAR	EPDSAEDVLTLLRQAHEQEV	FDADTLRLLEKVLDFSDLEV			
	10	20	30	40	50	60
	70	80	90	100	110	120
m973.pep	RDAMITSRMNVLKENDSIE	RITAYVIDTAHSRFPVIGED	KDEVLGILHAKDLLKYMFP			
a973	RDAMITSRMNVLKENDSIE	RITAYVIDTAHSRFPVIGED	KDEVLGILHAKDLLKYMFP			
	70	80	90	100	110	120
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSL	TALLKEFREQRNHMAIVIDE	YGGTSGSLVTFEDIIEQIVG			
a973	EQFHLKSILRPAVFVPEGKSL	TALLKEFREQRNHMAIVIDE	YGGTSGSLVTFEDIIEQIVG			
	130	140	150	160	170	180
	190	200	210	220	230	240
m973.pep	EIEDEFDEDDSDADNIHAV	SSERWRIHAATEIEDINTFF	GTSEYSXEEADTIGGLVIQELGH			
a973	DIEDEFDEDESADNIHAV	SAERWRIHAATEIEDINAF	SGTEYSSEADTIGGLVIQELGH			
	190	200	210	220	230	240
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVAR	ADNRRHLTLMATRVKX				
a973	LPVRGEKVLIGGLQFTVAR	ADNRRHLTLMATRVKX				
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCCAC TCGCGCTGTC
  51 TGCCTGCGGC GGTCAGGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
 101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
 151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
 201 GATGGCGAAG GCGGGCAATT TTAAATCGA ATTCAAACAC CAGCCGTGGG
 251 ACAGCCTTTT CCCCGCCTTG AACAAACGCG ATGCGGACGT TGTGATGTCG
 301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
 351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
 401 CTTCTTCCGA AGATTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
 451 CACACGGGCG ATTTCTCCGT TTCCAACTC TTGGGCAACG ACAATCCGAA
 501 AATCGCGCGC TTCGAAAACG TCCCCGTGAT TATCAAAGAA CTGGAACACG
 551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTACATCG CAATTATGTG
 601 AAAAAACAAC CGGCCAAAGG AATGGACTTC GTTACCTGCG CCGACTTCAC
 651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
 701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
 751 AAGATCTACG CCAAATATTT TGCCAAAGAG GCGGACAGG CTGCGAATA
 801 A

```

1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

```

g981.pep
1  MKKWIAAALA CSALALSACG GQKDAAPA ANPGKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK KMNKGVVVTG
151 HTGDFSUSKL LGNDNPKIAR FENVPLIIE LENGGLDSVV SDSAVIANVY
201 KNNPAKGMDF VTLDPFTTEH YGIAVRKGE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE GGQAAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

```

m981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGTGTCT
51  TGCCTGCGGC GGTACGGGCA AAGATACCGC CGCGCCTGCC GCCAACCCCG
101 ACAAGTGTGA CCGCGTGGCT TCCAACGCGC AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTTTA AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GCGCTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCGGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTGAAAAACG TTCCCTGAT TATCAAAGAA CTGAAAAACG
551 GCGGCTTGGT TTCCGTGGTC AGCGACAGCG CGGTCATCGC CAATTATGTG
601 AAAAAACATC CGGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATTACG CCAATATTTT TGCAAAGAA GACGGACAGG CCGCAAATA
801 A

```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

```

m981.pep
1  MKKWIAAALA CSALALSACG GQKDTAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK NMNKGVVVTG
151 YTGDFSUSKL LGNDNPKIAR FENVPLIIE LENGGLDSVV SDSAVIANVY
201 KNNPAKGMDF VTLDPFTTEH YGIAVRKGE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE DGQAAK*

```

m981/g981 98.1% identity in 266 aa overlap

	10	20	30	40	50	60
981.pep	MKKWIAAALACSALALSACGGQKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
g981	MKKWIAAALACSALALSACGGQKDAAPAANPGKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE					
g981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE					
	70	80	90	100	110	120
981.pep	ITQVVLVPKGKKVSSSEDLKMNKGVVVTGYTGDFSUSKLLGNDNPKIARFENVPLIIE					
g981	ITQVVLVPKGKKVSSSEDLKMNKGVVVTGHTGDFSUSKLLGNDNPKIARFENVPLIIE					
	130	140	150	160	170	180
981.pep	LENGGLDSVSDSAVIANVYKNNPAKGMDFVTLDPFTTEHYGIAVRKGEATVKMLNDAL					
g981	LENGGLDSVSDSAVIANVYKNNPAKGMDFVTLDPFTTEHYGIAVRKGEATVKMLNDAL					
	190	200	210	220	230	240
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
1   ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAAGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTTAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTTGG AACACGGCG ATGCGGACGT TGTGATGTCG
301 GCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGA CTAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAATAT
401 CTTCTTCCGA AGATTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAACAATC CGACCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAAATATTT TGCAAAGAA GACGGACAGG CCGCAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
1   MKKWIAAALA CSALALSACG GQGKDAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVM
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKISSSEDLK NMNKVGVTG
151 YTGDFSLSKL LGNDNPKIAR FENVPLIIE LENGGLDSV SDSAVIANV
201 KNNPTKGMDF VTLPDFTEH YGIAVRKGE ATVKMLNDAL KKVRESGEYD
251 KIIYAKYFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

m981.pep	10	20	30	40	50	60
	MKKWIAAALACSALALSACGGQGKDTAAPANPDKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALACSALALSACGGQGKDAAPANPDKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
m981.pep	70	80	90	100	110	120
	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMMSGVTITDDRKQSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMMSGVTITDDRKQSMDFSDPYFE					
	70	80	90	100	110	120
m981.pep	130	140	150	160	170	180
	ITQVVLVPKGKVVSSSEDLKNMNKVGVTGYTGDFSLSKLLGNDNPKIARFENVPLIIE					
a981	ITQVVLVPKGKIISSSEDLKNMNKVGVTGYTGDFSLSKLLGNDNPKIARFENVPLIIE					
	130	140	150	160	170	180
m981.pep	190	200	210	220	230	240
	LENGGLDSVVSDDSAVIANVVKNNPAKGMDFVTLPDFTEHYGIAVRKGEATVKMLNDAL					
a981	LENGGLDSVVSDDSAVIANVVKNNPTKGMDFVTLPDFTEHYGIAVRKGEATVKMLNDAL					
	190	200	210	220	230	240
m981.pep	250	260				
	EKVRESGEYDKIYAKYFAKEDGQAAKX					
a981	KKVRESGEYDKIYAKYFAKEDGQAAKX					
	250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

g982.seq

```

1 atcgcatcgc aaaaccttcg attcgacaat cgattcctcc aaaaaatggt
51 caacggcgTg aatattttgc cggccgcCga ttgggtagcC ttgGGcgCca
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAAGTAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAGT CGCGTCCAAA ACCAAcgaCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAAggca TGAAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGccg ttgCCGCTtt ggttgAAGAg cTGAAAAACA
401 TCGCCAAACC TTGCGATACT TCCAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCCTTACT TTATCAACGA CGCGGAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGTT TTGCTGTTTC ACAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCCGTGTG GGAACAAGTG GCGAAAGCCA GCCGCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTTC TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
851 GCCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATttccGAAG Aagtcggcct GTCTTTGGA AAAgcgactT TGgacgaCTT
951 Gggtcaaacc aaACGcatCG AAATCGGtga agaaaaact ACCGTCATcg
1001 acgGCTTCGG CGACGcagc CAAatcgaag cgCGTGTGC CGAAATCCGC
1051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAAGTGGCAG GAGGCGTGGC AGTGATCAAA GTCGGCGCGG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAG ACCGCGTGA AGACCGCGTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGCGGT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGGCG
1451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCTGC CAAAGTAACC
1501 GTTTCGCGC TGCAACACGC CGCGTCTAtC GCCGGTCTGA TCGTGACGAC
1551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCGATA
1601 TGGGGGAAT GGGCGGTATG GCGGCATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

g982.pep

```

1 IASQNLRFDN RFLQKMNvG NILPAADWVA LGAKGRNVV DRAFGGPHIT
51 KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIv
101 AEGMKYVTAG MNPTDLKRGi DKAAALVEE LKNIAPCDT SKEIAQVGSi
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KsLENELDVV EGMQFDRGyL
201 SPYFINDAEK QIAGLDNPFV LFDKKISNI RDLLPVLEQV AKASRPllLI
251 AEDVEGEALA TLVVNNIRGI LKTVAVKAPG FGDRRKAMlQ DIAIlTGGVv
301 ISEEVGLSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKkDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALENLH TGNADQDAGV QIVLRavesP
451 LRQIVANAGG EPSVVVNKVL EGKGNyGYNA GSGEYGDmIG MGVLDPakVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGM GGMm*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

m982.seq

```

1 ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51 AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAAGTAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAGAAGT TCGGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAA CAAATCGCTG CTTTGGACAA

```

651	TCCGTTTGTGA	TTGTTGTTCTG	ACAAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCCTGTTTT	GGAACAAGTG	GCAAAAAGCCA	GCCGTCCGCT	GTTGATTATC
751	GCTGAAGACG	TAGAAGGCGA	AGCCTTGGCG	ACTTTGGTCG	TGAACAACAT
801	CCGAGGCATC	CTGAAACCG	TGTCGCTCAA	AGCCCTGGC	CTCGGCACCC
851	GCCGCAAAAG	GATGTTGCAA	GATGATGCCA	TCTGACCCG	GTCGGTGGTG
901	ATTTCCGAAG	AAGTCGGTCT	GTCTTTGGAA	AAAGCGACTT	TGGACGACTT
951	GGGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAAACC	ACCATCATCG
1001	ACGGCTTTG	CGACGCGAGC	CAAATCGAAG	CGCGTGTTC	CGAAATCCGC
1051	CAACAAATCG	AAATCGCAAC	CAGCGATTAC	GACAAAGAAA	AATCGCAAGA
1101	GCGCGTGGCT	AAATTGCGAG	GCGCGCTGGC	AGTCATCAAA	GTCGGTGCCG
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAG	ACCGCGTGGA	AGACGCGCTG
1201	CACGCTACCC	GCGCAGCCGT	TGAAGAAGGC	GTGGTTCGAG	GCGGCGGCGT
1251	AGCCCTGTTG	CGTGCCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAGA	CGCAGCGGTA	CAATCTGTCT	TGCGCGCGGT	TGAGTCTCCG
1351	CTGCGCGCAA	TCGTTGCCAA	CGCAGGCGCG	GAACCCAGCT	TGGTTTGCGA
1401	CAAAGTATTG	GAAGGCAAG	GCAACTACGG	TTACAACGCT	GGCAGCGGCG
1451	AATACGCGGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCGT	TGCAACACGC	CGCATCTATC	GCCGCGTTGA	TGCTGACCAC
1551	TGATTTCGATG	ATCGCTGAAA	TCCCCGAAGA	CAACCCGGCT	GTGCTGATA
1601	TGGGCGGCAT	GGGTGGTATG	GCGGCGATGA	TGTAA	

m982.seq

Homology with a predicted ORF from *N. gonorrhoeae*

10 20 30 40 50 60
 m982.pep MAAKDVFQFNEVRQKQMVNGVNILANAVRVTLGPKGRNVVVVDRAFGGPHITKDGVTVAKEI
 :::::|: ||||| | :|: |||||

1387

g982	IASQNLRFDNRFLQKMVNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
m982.pep	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
g982	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
g982	DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
m982.pep	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
g982	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGVV
	250 260 270 280 290 300
g982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGVV
	250 260 270 280 290 300
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
g982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
g982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
m982.pep	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLGKNGYGYNA
	430 440 450 460 470 480
g982	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLGKNGYGYNA
	430 440 450 460 470 480
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQAAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM
	490 500 510 520 530 540
g982	GSGEYGDMIEMGVLDPAKVTRSAHQAAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM
	490 500 510 520 530 540
m982.pep	GGMMX
g982	GGMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

```

a982.seq
1  ATGGCAGCAA AAGACGTACA ATTCGGCAAT GAAGTCGCC AAAAAATGGT
51  AAACGGCGTG AACATTTTGG CAAACGCCGT GCGCGTAACC TTGGGTCCCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCC GCACATACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT CGCGTCCAAA ACCAACGACG
251 TGGCGGGCGA CGGTACGACT ACCGCCACCG TATTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATACGT TACCGCCGGT ATGAACCCGA CCGACCTGAA
351 ACGCGGTATC GACAAAGCCG TCGCCGCTT GGTGAAGAG CTGAAAAACA

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1388

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401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGCGAAAAA CAAATCGCCG GCTTGGACAA
651 TCCGTTTGTG TTGCTGTTTCG ACAAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTGCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAACCTGGCAG GCGCGGTGGC AGTAATCAAA GTCCGTGCCG
1151 CGACCGAAGT GGAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGCGCT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGCGC
1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCGCGC TGCAACACGC CGCGTCTATC GCCGCGCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCATGA TGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

a982.pep

```

1  MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAVALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGDTV
301 ISEEVGLSLE KATLDDLQGA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSSEYGMIE MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGM GGM*

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m982/a982 99.3% identity in 544 aa overlap

```

          10      20      30      40      50      60
m982.pep  MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHITKDGVTVAKEI
          |||
a982      MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHITKDGVTVAKEI
          10      20      30      40      50      60

          70      80      90     100     110     120
m982.pep  ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSI VAEGMKYVTAGMNPTDLKRG I
          |||
a982      ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSI VAEGMKYVTAGMNPTDLKRG I
          70      80      90     100     110     120

          130     140     150     160     170     180
m982.pep  DKAVALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
          |||
a982      DKAVALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
          130     140     150     160     170     180

          190     200     210     220     230     240
m982.pep  KLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFV LFDKKISNIRDLLPVLEQV
          |||
a982      KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFV LFDKKISNIRDLLPVLEQV
          190     200     210     220     230     240

```

1389

	250	260	270	280	290	300
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQIETATSDY					
a982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQIETATSDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m982.pep	RARAALNLTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKNGYGYNA					
a982	RARAALNLTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKNGYGYNA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPMGGMGMGM					
a982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPMGGMGMGM					
	490	500	510	520	530	540
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCTTT
51	GCTGGCAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCCGACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAGGCAG	CCCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTTC	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCAGGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTC
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCTG	CAAAATCGGC	AATCCCAAAA	ATTTGAAACC	GGGCGAATGG
601	GTCGCTGCCA	TGCGCGCGCC	CTTCGGCTTT	GACAAAGCGG	TGACCCCGCG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCCT
701	TCATCCAAAC	CGACGTTGCC	ATCAATCCGG	GCAATTCCGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgTCGGCATC	AATTCGCAAA	TATACAGCCG
801	CAGCGcgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTGCG	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTCAGGA	AGTATCCTAC	GGTTTGCGAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGCGCTG	CAGGCGGGCG	ACATCGTCTT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TCGGCGCCAT
1101	TACGCCGGGA	AAAGAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	cggagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAGcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgctcgtacgg	gtttccgacg	cggcagaacg	cGCAGGCTTA

1390

1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
 1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
 1451 TGGTCAtgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

g986.pep

1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
 101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILTN THVVAGMGS
 151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVG I NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
 301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHGTAS
 401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVND EAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

m986.seq

1 GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
 51 GCTGGCAGGC TGCACAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
 101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
 151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCGGGC
 201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCG
 251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCCGTTCTAC
 301 GAATTTTTC AACGCCTCGT CCCGAATATG CCCGAAATCC CCAAGAAGA
 351 AGCAGATGAC GCGCGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
 401 ACGGCTACAT CCTGACCAAT ACCACGTCG TTACCGGCAT GGGCAGTATC
 451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
 501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
 551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
 601 GTCGCCGCCA TCGGCGCGCC CTTGCGCTTC GACAACAGCG TGACCCCGCG
 651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCTC
 701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
 751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
 801 CAGCGGCGGA TTCATGGGCA TTCTCTTCGC CATCCCGATT GACGTTGCCA
 851 TGAATGTCGC CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
 901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTGTGGCAC AATCGTTCGG
 951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
 1001 CCGCAGAACG TGCCGGCCTG CAGGCGGGCG ACATCGTCTT CAGCCTCGAC
 1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
 1101 TACGCGGGA AAGAAGTCA GCCTCGCGT ATGGCGCAA GCGGAAGAAA
 1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
 1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
 1251 GGTCAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
 1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAAGC CGCAGGCTTG
 1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
 1401 AGCCGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
 1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

m986.pep..

1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
 101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILTN THVVAGMGS
 151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVG I NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
 301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVND EAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

Computer analysis of this amino acid sequence gave the following results:

1391

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALAAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	: :					
g986	VFKKYQYFALAAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
	: : : : : :					
g986	VQSEGPVVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	: : : : : :					
g986	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	: : : : : :					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	: : : : : :					
g986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

1392

	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	LGVIIQEVSYGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
g986	AGITLQTHTDSSGKHLVVVRVSDAAERAGLRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1   GTGTTCAAAA AATACCAATA CCTCGCTTGT GCAGCACTGT GTGCCGCTTC
51  GCTGGCAGGC TGCACAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACGT GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCA
251 GCAATGCCGA AACCATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTCA AACGCCTCGT CCCGAACATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GNGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGTATAT TCTGACCAAT ACGCAGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTT
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGCGGGA TTCATGGGCA TTTCCTTCGC CATCCGATT GACGTTGCCA
851 TGAATGTCGC CGAACAGCTG AAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCTTAC GGTTCGCGC AATCGTTCGG
951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CGGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTATGG TCGGCGCCAT
1101 TACGCCGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GGCGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGAAC ACGCTGTTTA TCGCATTAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1   VFKKYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPVVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIQEEADD GGLNFGSGFI ISKDGYILT NTHVVTMGSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ

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1393

301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGHLLVVVR VSDAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGN VPLLIMRRGN TLFIALNLQ*

m986/a986 98.2% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
a986	VFKKYQYLALALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVAVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD					
a986	VQSEGPVAVNIQAAPAPRTQNGSSNAETSDPLADSDPFYEFFKRLVPNMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGIVSAKGRSLPNESYTPFIQTDA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGXVSAKGRSLPNESYTPFIQTDA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLLVVVRVSDAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGN					
a986	AGITLQTHTDSSGGHLLVVVRVSDAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

g987.seq
 1 ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCCTCCTTC TCTGTTCATG

1394

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51  TTCTTCATGG TTGCCCCAC TGGAAGAAGC GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCCCTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCCACGA
201 AGCCTTTGCC GCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTC
301 AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTt
351 ggacgacaAC AACAcgcgcg gcttgacga tctcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCCTGTTCA ACCCCTtcgt CCTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCCGAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGACGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCTT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCG
901 CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAAATG GTGACGAGC GCATAGACGT TACCGTCTCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACCTC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATGTGTGAcg gCAAACGCAT
1251 CTTATCGGC TCATTCAACC TCACCCCCG TTCCGCACGG CTCAATACCG
1301 AAATGGCGT CGTCATCGAA AGCCCCAAA TCGCAGAAAC GATGGAGCGC
1351 AccctCGCG AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG

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This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

g987.pep

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1  MKTRSLISLL CLLCSCSSW LPPLERTES RHNTSKPVL LDNILQIRHT
51  PHNNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAERF VVRVLLDDN NTRGLDDLL ALDHPNI*v RLFNPFVLRK
151 WRALGYLTF PRNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPY QKIQTGRIDW QSVQTRLISD SPAGLDRDR
301 RKPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKLGTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHPATRK TYPNEPEAKL WKRIAAILLS
501 LLPIEGLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

m987.seq

```

1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCAC TGGAAGAAGC GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CTCATACCA ACGGGCTATC CGATATCTAT CTGTGAAAG ACCCCCACGA
201 AGCCTTTGCC GCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCCGAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GATTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGACGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCTT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC

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1395

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTTCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCTT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTCATCGGT TCGTTCAACC TCGACCCCG TTCCGCGCGT CTCAACACCG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGCG ACATCCCGC CACCCGAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1  MKTRSLISLL CLLLCSSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VVRLLDDN NTRGLDDLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALRY RETVEQSPY QKIQTGCIDW QSVTRLISD DPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIAANKLS
501 LPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
g987	MKTRSLISLLCLLLCSSSWLPPLEERTESRHFNTSKPVLLDNILQIRHTPHNGLSDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLDDN					
	:					
g987	LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAERGVRVRLDDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m987.pep	NTRGLDDLLALDSHPNIEVRLFNPFVLRKWRALGYLDFPRLNRRMHNKSFTADNRATI					
g987	NTRGLDDLLALDSHPNIXVRLFNPFVLRKWRALGYLDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFRYWASHSAHNATRIIRSGDIG					
g987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m987.pep	KGLQALGYNDETSRHALRYRETVEQSPYQKIQTGCIDWQSVTRLISDDPAKGLDRDR					
g987	KGLQALGYNDETSRHALRYRETVEQSPYQKIQTGRIDWQSVQTRLISDPAKGLDRDR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m987.pep	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNSLQATDVA					

1396

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|||||
g987      RKPFIAGR LQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pep  AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS LHAKTFIVDGKRIFIG
          |||||
g987      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS LHAKTFIVDGKRIFIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pep  SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNRLQWHD PATRK
          |||||
g987      SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHD PATRK
          430      440      450      460      470      480

          490      500      509
m987.pep  TYPNEPEAKLWKRIA AAKILSLLPIEGLLX
          |||||
g987      TYPNEPEAKLWKRIA AAKILSLLPIEGLLX
          490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

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a987.seq
1   ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAC TGGAGAAGAC GACGGAAAGC CGTCATTTC A
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTCCGGCCCG ACTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCGCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCCGC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTCGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCGG GCGGCTGCAA GACGCGCTCA AACAGCCGGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAAACCA TGCCGTCCTT GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTCATCGGC TCATTCAACC TCGACCCCGG TTCCGCACGG CTCAATACTG
1301 AAATGGGCGT TGTTATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCGCG CACCCGAAAA ACCTACCCGA
1451 ACGAACC CGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCC TAGAAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pep
1   MKTRSLISLL CLLLCSSSW LPPLEERTES RHFNSTKPV R LDNILQIRHT
51  PHTNGLSDIY LNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAAERG VVRLLDDDN NTRGLDDLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPFIAGR LQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL

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1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
 451 TLADTSPEYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIAAILKLS
 501 LLPIESLL*

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTPSKPVRLDNILQIRHTPHTNGLSDIY					
a987	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTPSKPVRLDNILQIRHTPHTNGLSDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLNLVYLAAERGVRVRLLLDDN					
a987	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLNLVYLAAERGVRVRLLLDDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m987.pep	NTRGLDDLLLALDHPNIEVRLFPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI					
a987	NTRGLDDLLLALDHPNIEVRLFPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
a987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVTRRLISDDPAKGLDRDR					
a987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRRLISDDPAKGLDRDR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m987.pep	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNTSLQATDVA					
a987	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNTSLQATDVA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m987.pep	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
a987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m987.pep	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNRQLQWHDPATRK					
a987	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDRHNRQLQWHDPATRK					
	430	440	450	460	470	480
	490	500	509			
m987.pep	TYPNEPEAKLWKRIAAILKLSLLPIEGLLX					
a987	TYPNEPEAKLWKRIAAILKLSLLPIESLLX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

q988.seq
 1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

1398

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTCGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTTAATCAAC CGCCgagggc
251 CagtTTGCGc gGCggacaag ctgGATTtGG TCAAATGccg Cgtcgagggc
301 catAAgGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTCGTT TTATACGAAC GCCAgatgcg tggTgtcatG CAcggcgaca
401 ccgttACCGT CCGTCCTGCG ggtatggaCC GCAGGGGccg ccgcGAAggg
451 acgtttctGG ATATTGTCGA ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGGCGTGG CGATTtTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTtGGAA CCGGACGGCG TGGCGCGTtT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATtGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTTt GGGCGATTAT GCCGACAGCG
701 GGATGGAAt cGAAATtGCC GTGCGCAAGC ATCATTtGCC GCaccgaTTC
751 AGTGAagcgt gtGcCAAAATC CGcgaAAAA ATtcccgacc ATGTACGCAA
801 AAGCGATTtG AAAGGCCGCG TCGATTtGTG CGACCTtCCT TTGGTAACGA
851 TAGACGGCGA AACGGCGCGC GATTtCGACG ACGCGGTtGT TGCCGAAAAA
901 GTCGGACGCA ATTACCGCCT GGTCTGtGGC ATTGCGGATG TCAGCCATTA
951 TGTCGCCCTT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 GCGTGTATtT CCCGCGCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGTCAA TCCCGATGTC GAGCGTtGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
1151 CCGCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGA
1201 TGGCTtTCAG ACGGCATCGG GAATCCGCAC AAAGCCCAAA TCGACACGCT
1251 TTACAAGCTG TTTAAAtTT TGCAGAAAAA ACGTCTGGCG CGCGGGGCGG
1301 TGGAGTTtGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAA TTGTCCCGT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGCGCA ATGTTtGCGC GGCGGATtTT CTGTTGAAAA
1451 ACAACATAC GGCTtTGtTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGCGCG
1551 CGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGGCAGGCC GGATGCCGAA TGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGCGCG TTTACGAACC GCATTGCGAA GGGCATtTCG GTTTGGCTTA
1701 TGAAGCATAC GCCCACTtTA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGGAAAAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTtT GGGCGTGCAT ACTTCGTTTt GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGGAaaa CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTCGGTGAA ATATTtGAAG GcaaaatCtc ccgggggtgtg
1951 gcaaaTtttg gaATATTtGT CACTTTGGAC GATATccata tcgacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgcccccAAA
2051 TCATGGCAAT CGAAGGCGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTtGCCG TCCGGGTGCG GCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCCGGAG AAAGCGGCAG GCGGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGGCGGCGG GGAAAGGGAA ATCGAAAAAC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGGCGT
2301 GCCTGCCGTT GCCGAATCGG GGAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

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This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

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1  MNKNIKSLNL REKDPFLSRE KORYEHPLPS REWIIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFGEFVP LMPMDEGDFV LYERQMRGVM HGDTVTVRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILPEPD KRLNQSIVLE PDGVARFKPE
201 SGQVIVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHRF
251 SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLTKL FKILQKKRLA RGAVEFESVE TQMIFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQQLG LGLQLGGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSWQALGVH TSFCERRADD AGRDVENWLK TYMYRDKVGE IFEGKISRGV
651 ANFGIFVTLT DIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPAV AESGKKAKKP VPIKVKKRKG KS*

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1399

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```
m988.seq (partial)
1  ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51  CTATATGGAT AGGGGCGTGG CGATTTTGGG GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAAGC TCGCAAAAAA ATCCCGTCC ATGTACGCAG
351 AAGCGATTTG AAAGGCCGCG TCGATTGCG CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
451 GTCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
501 TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATT TCTCGTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
651 CGATATGGTC GTTACCTATG CCGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCGCGCTGA CCTACAACCA AGTTTGGA
751 TGGATTTGAG ACGGCATCGA CCATCCGTAC AAAGCCCAA TCGACACCTT
801 TTACAACTC TTCAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAAA TCGTCCCGCT TGTCCGCAAC GATGCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTC CTGTTGAAAA
1001 ACAAGCATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201 CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCGTA
1251 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1301 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1351 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1451 TGCGCGATAA GGTGCGCGAA GTATTGGAAG GTAAAATCTC CGGCATGACC
1501 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATG ACGGCTTGGT
1551 GCATATCAGC GATTGTTGGC AAGACTATTT CAACTTCCGC CCCGAAATCA
1601 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTCAACAT GGGGGACAGG
1651 GTTGCCGTCC GGGTCGCCCC TGCCGATTG GATGACGGAA AAATCGATTT
1701 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
1751 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAAACCGCC
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1400

1801 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
 1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)
 1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
 51 SGQVIVGEIE VYPEQNRPAV AKIEVLGDY ADGMEIEIA VRKHHLPHQF
 101 SEACAKAAK IPVHVRKSDL KGRVDLRDL LVTIDGETAR DFDDAVFAEK
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFRR VIPMLPENLS
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMFDDNGK
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPDAE LLQVMMLRSM
 401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
 451 KKSQWALGVH TSFCERRADD ASRDVENWLK TTYMRDKVGE VFEGKISGMT
 501 SFGIFVTLTG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRENMGDR
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGPKPTA
 601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGVMHGDTVTVRPAGMDRRRREGTF	LDIVERAQSKVVGRFYMDRGVAILEPED				
	130	140	150	160	170	180
m988.pep	40	50	60	70	80	90
	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA					
g988	KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA					
	190	200	210	220	230	240
m988.pep	100	110	120	130	140	150
	VRKHHLPHQFSEACAKAAKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK					
g988	VRKHHLPHRFSEACAKSAKKIPDHVRKSDLKGRVDLCDLPLVTIDGETARDFDDAVFAEK					
	250	260	270	280	290	300
m988.pep	160	170	180	190	200	210
	VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFRRVIPMLPENLSNGICSLNPDV					
g988	VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFRRMIPMLPENLSNGICSLNPDV					
	310	320	330	340	350	360
m988.pep	220	230	240	250	260	270
	ERLCMVCDMVVTYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL					
g988	ERLCMVCDMVVTYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSDGIGNPHKAQIDTLYKL					
	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
g988	FKILQKKRLARGAVEFESVETQMFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE					
g988	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALAEQFKGRPDAE					

1401

	490	500	510	520	530	540
m988 . pep	400	410	420	430	440	450
	LLQVMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
g988	LLQVMLRSMQQAVYEPHCEGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNKRKTYTP					
	550	560	570	580	590	600
m988 . pep	460	470	480	490	500	509
	KKSWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKIS-GMTSFGIFVTLD					
g988	NKSWQALGVHTSFCERRADDAGRVDENWLKTYMRDKVGEIFEGKISRGVANFGIFVTLD					
	610	620	630	640	650	660
m988 . pep	510	520	530	540	550	569
	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
g988	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
m988 . pep	570	580	590	600	610	629
	IAGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKKTARGGKVRGRGASAAAESRKKAKKP					
g988	IAGESGRRRKVKLSASAKPAGAAGKGSKTTAEKKKTARCGKVRGRGVPVAESGKKAKKP					
	730	740	750	760	770	780
m988 . pep	630	640				
	VPIKVKRRKGKXS					
g988	VPIKVKRRKGKXS					
	790					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

```

a988 . seq
1  ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT
51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTGCCCCAGT CGGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
151 GTACGCGAAT TGTCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGCGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
251 CGGTTTGCGC GGCGGACAAA TTGGATTGG TCAAATGCCG TGCAAGGCG
301 CACAAAGACC GCTTCGGTTT CGCCGTGCGG CTCACGCCCG CCAAAGACGG
351 TGATTTTGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCACTGT TCGTCCTGCC GGCATGGACG GTAGGGGGCG CCGCGAAGGG
451 ACGGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGA GCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
601 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
701 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATTCCCGACC ATGTACGCAA
801 AAGCGATTTG AAAGGCCGCG TCGATTTGCG CGACCTGCCT TTGGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCCGAGAAA
901 ATCGGACGCA ATTACCGTCT GGTCGTGGCG ATTGCCGATG TCAGCCATTA
951 TGTCCGCCCC GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGCACCA
1001 GTGTTTACTT CCCGCGCCGC GTGATTCCCA TGTGCGCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGTTCTACC
1151 CCGCCGTGAT GCGCTCTCAT GCCGCGCTGA CCTACAACCA AGTTTGAAAA
1201 TGGCTTTCAG GCGGCATCGA GCATCCGTTT AAAACCCAAA TCGACACGCT
1251 TTACAACTC TTCAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGGGCGG
1301 TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACA AGCTGATTGA
1401 AGAATGTATG TTGGCGGCAA ACGTTTGCGC AGCGGATTTT CTGTTGAAAA
1451 ACAAGCATAC CGCATTGTTC CGCAACCATT TGGGGCCAC GCCCGAAAAA
1501 CTCGCCGCTT TCGCGAGCA GTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGGCGAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

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1402

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1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAACAGGCGG TTTACGAACC GCATGCGGAC GGACACTTTG GTCTTGCCCTA
1701 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1801 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1851 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1901 TGCCGCGATAA GGTGCGCGAA GTATTCGAAG GTAAAATCTC CGGCATGACC
1951 AGTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
2001 GCATATCAGC GATTGGGCG AAGACTATTT CAACTCCGC CCCGAAATCA
2051 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTCAACAT GGGGACAGG
2101 GTTGCCGTCC GGGTCGCCCG TGCCGATTG GATGACGGAA AAATCGATTT
2151 TGTCTGATT GCCGGGGGA GCGGCAGGG GCGGAAAGT AAATCATCCG
2201 CGTCTGCCAA ACCGCGAGG ACGGCGGGG AAGGGAAGCC GAAAACCGCC
2251 GCCGAGAAAA AAACAGCCCG AGGCGGCAA GTAAGGGGA GGGGCGCGTC
2301 TGCCGCCGCA GAATCGAGGA AAAAGGCAA GAAACCGTT CCGATTAAGG
2351 TAAAAAACG GAAAGGCAA TCATAA

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This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

a988.pep

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1 MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIIELLER KGVPSKIEAL
51 VRELSIKEEE YEFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVKA
101 HKDRFGFAVP LTPAKDGFV LYERQMRGIM HGDIVTVRPA GMDGRGRREG
151 TVLDIVERAQ SKVVGFRFXMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
201 SGQVIVGEIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHQF
251 SEACAKAAKK IPDHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK
301 IGRNYRLVVA IADVSHYVRP DDAIDTDAQE RSTSVYFRR VIPMLPENLS
351 NGICSLNPHV ERLCVCDMV ITYAGNIKEY RFYPVMRSH ARLTYNQVWK
401 WLSGGIEHPF KTQIDTLYKL FKILQKKRFE RGAVEFDSIE TQMLFDDNGK
451 IEKIVPVVRN DAHLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LAALREQLGL LGLQLGGGDN PSPKDYAALA GQFKGRPD AE LLQVMLRSM
551 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
601 KKSQWALGVH TSFCERRADD ASRDVENWLK TTYMRDKVGE VFEGKISGMT
651 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
701 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGPKPTA
751 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S*

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m988/a988 97.0% identity in 641 aa overlap

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                                10      20      30
m988.pep                                TVLDIVERAQSKVVGFRFYMDRGVAILEPED
a988                                LYERQMRGIMHGDIVTVRPA GMDGRGRREGTVLDIVERAQSKVVGFRFXMDRGVAILEPED
                                130      140      150      160      170      180

                                40      50      60      70      80      90
m988.pep                                KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
a988                                KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
                                190      200      210      220      230      240

                                100      110      120      130      140      150
m988.pep                                VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLP LVTIDGETARDFDDAVFAEK
a988                                VRKHHLPHQFSEACAKAAKKIPDHVRKSDLKGRVDLRDLP LVTIDGETARDFDDAVFAEK
                                250      260      270      280      290      300

                                160      170      180      190      200      210
m988.pep                                VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFRRVIPMLPENLSNGICSLNPDV
a988                                IGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFRRVIPMLPENLSNGICSLNPHV
                                310      320      330      340      350      360

                                220      230      240      250      260      270
m988.pep                                ERLCMVCDMVITYAGNIKEYRFYPVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL
a988                                ERLCVCDMVITYAGNIKEYRFYPVMRSHARLTYNQVWKWLSGGIEHPFKTQIDTLYKL

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1403

	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988	FKILQKKRFERGAVEFDSIETQMLFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGFTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE					
a988	LLKNKHTALFRNHLGFTPEKLAALREQLGLLGLQLGGGDNPSPKDYAALAGQFKGRPDAE					
	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLQVMMLRSMQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
a988	LLQVMMLRSMQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	510
	KKSQWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
a988	KKSQWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
	610	620	630	640	650	660
m988.pep	520	530	540	550	560	570
	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
	670	680	690	700	710	720
m988.pep	580	590	600	610	620	630
	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKAKKPV					
a988	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKAKKPV					
	730	740	750	760	770	780
m988.pep	640					
	PIKVKKRKGSX					
a988	PIKVKKRKGSX					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989.seq

1	ATGACCCCTT	TCACACTGAA	AAAAACCGTC	CTGCTGCTCG	GCACTGCCTT
51	TGCCGCGCA	TCTGTCCACG	CATCCGGCTA	CCACTTCGGC	ACACAGTCGG
101	TCAACGCGCA	AAGCACGGCA	AATGCCGCGG	ACGCGTCGAC	CATCTTCTAC
151	AATCCCGCCG	GCCTGACCAA	ACTCGACAGC	AGCCAGATT	CCGTCAACGC
201	CAACATCGTG	CTGCCAGCA	TTCATTATGA	AGCAGATTCC	GCCACCGACT
251	TTACCGGGCT	TCCCGTCCAA	GGTCTAAAA	ACGGCAAAAT	CACCAAAACC
301	ACGGTCGCAC	CCCACATTTA	CGGCGCATAC	AAAGTCAACG	ACAATCTGAC
351	CGTGGGCTTG	GGCGTGTACG	TCCCCTTCGG	CTCTGCCACC	GAATACGAAA
401	AAGATTCCGT	GTTGCGCCAC	AACATCAACA	AACTCGGTCT	GACCAGCATC
451	GCCGTGGAAC	CTGTCGCCGC	GTGGAACATC	AACGAACGCC	ATTCCTTCGG
501	CGCAGGCATC	ATCGCCCAAC	ATAATTCCGC	CGAACTGCGC	AAATATGCCG
551	ACTGAGGAAT	CCCAAAAAAA	GCGCAAATGC	TGCAAGCAAC	ACCTTCTAAT
601	CCTACTGCCG	CTGCTCAAAT	CAAGGCCGAC	GGACACGCCG	ATGTCAAAGG
651	CAGCGATTGG	GGCGTCGGCT	ACCAACTGGC	GTGGATGTGG	GACATCAACG
701	ACCGCGCGCG	CGTGGGCGTG	AACTACCGTT	CCAAAGTTTC	ACACACGCTC
751	AAAGCGGATG	CCGAATGGGC	GGCAGACGGC	GCGGCGGCGA	AACAACAGTG
801	GAATGACAA	ATGCTCACAC	CGCTCGTTTA	CACGGCGAAT	GAAAAAGCCA
851	GTGTCAAAAT	CGTAACGCCT	GAGTCTTTGT	CCGTACACGG	CATGTACAAA

1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAAC TTGGA CGCGCCACAG
951 CCGCTTCAAT AAGCGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAACTG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCCGCAAC GCCGACTacc
1151 GCATGAACAG CCTGCCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TCGGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```

g989.pep
1 MTPFTLKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNDNLTVGL GVVYVFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAAAIKAD GHADVKGS DW GVG YQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAKQQWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGM YK
301 VSDKADLFGD VTWTRHSR FN KAELFFEKEK NIANGKKS DR TTITPNWR NT
351 YKVGLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSA GM
401 KYHIGHKNHV DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQYTKFK *

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

```

m989.seq
1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51 TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCGG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATTTCAT TATGAGGCGG
251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGTTC GAAAAGCGGC
301 AAAATCACCA AAACCACGGT CGCGCCCGAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAGGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTCAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAAC TAC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACGGCGAA TGAAAAGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCCGCCA
951 CGTAACTTGG ACGCGCCACA GCGCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAAAGAAA AACCGTCGTC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCCG
1151 TCCGCAACCG CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGTTCTCCG CCGGTATGAA ATACCATATC GGTAAAAACC ACGTCGTCGA
1251 TGCCGCCTAC ACCCACATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAAACACG CCGACATCAT CCGTCTGCAA TACACCTACA AATTCAAATA
1401 A

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This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```

m989.pep
1 MTPSALKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEK DSVLRHNINKL
151 GLTSIAVEPV AAWKLND R HS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKPPKPN GVA EAAKIQADGH ADVKGS DWGF GYQLAWMW DI NDRARVGV NY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESIL
301 SVHGM YKVS D KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

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1405

351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI
 401 WFSAGMKYHI GKNHVVDAAI THIHINDTSY RTAKASGNDV DSKGASSARF
 451 KNHADIIGLQ YTYKFK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

	10	20	30	40	50
g989.pep	MTPFTLKKT	VLLLGTAFAAASVHASGYHFGTQSVNAQSTANAA	-----DASTIFYNPAGL		
m989	MTPSALKKT	VLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL			
	10	20	30	40	50
	60	70	80	90	100
g989.pep	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN				
m989	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN				
	70	80	90	100	110
	120	130	140	150	160
g989.pep	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERSFGAGIIAQHN				
m989	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT				
	130	140	150	160	170
	180	190	200	210	220
g989.pep	SAELRKYADXGIPKKAQMLQATPSNPTA	---AAQIKADGHADVKGSDWGVGYQLAWMWDI			
m989	SAELRKYADWGIKSKAEILTAKPPKNGVAEAAKIQADGHADVKGSDWGFYQLAWMWDI				
	190	200	210	220	230
	240	250	260	270	280
g989.pep	NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKQQWNDNMLTPLGYTANEKASVKIVTPES				
m989	NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANEKARVKIVTPES				
	250	260	270	280	290
	300	310	320	330	340
g989.pep	LSVHGMYSKADLFGDVTWTRHSRDNKAELFFEKEKNIANGGKSDRTTITPNWRNTYK				
m989	LSVHGMYSKADLFGDVTWTRHSRDNKAELVFEKEKTVVKGK-SDRTTITPNWRNTYK				
	300	310	320	330	340
	360	370	380	390	400
g989.pep	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
m989	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
	360	370	380	390	400
	420	430	440	450	460
g989.pep	AYTHIHINDTSYRTAKASGNDVDSKGASCFKNHADIIGLQYTYKFKX				
m989	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX				
	420	430	440	450	460

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989.seq

1	ATGACCCCTT	CGGCACTGAA	AAAAACCGTC	CTACTGCTCG	GCACTGCCTT
51	TGCCGCGCA	TCCGCACAAG	CCTCCGGCTA	CCACTTCGGC	ACACAGTCGG
101	TCAACGCGCA	AAGCACGGCA	AATGCCGCGG	CCGCAGAAGC	CGCCGACGCA
151	TCGACCATCT	TCTACAACCC	TGCCGGCCTG	ACCAAACCTG	ACAGCAGCCA
201	GATTTCCGTC	AACGCCAACA	TCGTGCTGCC	CAGCATTCAT	TATGAGGCGG
251	ATTCGCCAC	CGACTTTACC	GGGCTTCCCG	TCCAAGGTTC	GAAAAGCGGC

1406

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301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TGCGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAAC TA CCGTTCCAAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GCGGAAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTTC GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCAAC
1051 TGGCGCAACA CCTACAAAGT CCGCTTCGGC GGTTCCTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCGCA
1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCG ACGGCAACCG CATCTGGTTC
1201 TCCGCCGGCA TGAAATACCA TATCGGCAAA AACCACGTCG TCGATGCCGC
1251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCAGC GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGCGCGT CTTCCGCACG TTTCAAAAAC
1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

```

a989.pep
1  MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGS DWFGYQ LAWMDINDR ARVGVNYRSK
251 VSHTLKGDAE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMYKVSDKA DLFGDVTWTR HSRFDKAE LV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIGK NHVVDAAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN
451 HADIIGLQYT YKFK*

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m989/a989 93.1% identity in 467 aa overlap

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          10      20      30      40      50      60
m989.pep  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
          |||
a989      MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
          10      20      30      40      50      60

          70      80      90     100     110     120
m989.pep  TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          |||
a989      TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          70      80      90     100     110     120

          130     140     150     160     170     180
m989.pep  LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT
          |||
a989      LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHT
          130     140     150     160     170     180

          190     200     210     220     230     240
m989.pep  SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIADGHADVKGSDWFGYQLAWMWDI
          |||
a989      SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIADGHADVKGSDWFGYQLAWMWDI
          190     200     210     220     230

          250     260     270     280     290     299
m989.pep  NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTAN EKARVKIVTPES
          |||
a989      NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTAN EKARVKIVTPES

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1407

	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMKVSDKADLFGDVTWTRHSRFDKAEVFEKEKTVVKGKSDRTTITPNWRNTYKV					
a989	300	310	320	330	340	350
	LSVHGMKVSDKADLFGDVTWTRHSRFDKAEVFEKEKTVVKGKSDRTTITPNWRNTYKV					
m989.pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
m989.pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1  ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCAT
101 ATTTTTCAG CCGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGGC GGTAAAAAGT CAATTACAGG ATTTATACAA AACAAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTAGTA CGCTCAAACA GACGATGCCG GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACAGTCA AAATCGAAAA
501 CAAATCCCAC GTCGCCGGAC AGGTGTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCTT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAACTGAC
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CAAAACGGC GGATTCCGGT TCGTTTGGT
851 TTAAACAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCAAC AGGCTTATGC GGCATAACT TTGTTTGGG
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAATTGT GGCTGCGCTT CATCGCGGCG CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CGGCGTGATG
1201 GGCGGCAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGTATGGT ATGGCGGGGG TGTTTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCRAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTCCGAAAA GGCAATAATG TGCGGTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGCGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
1601 GCATTGCGGC AAAAACCCTT TTTGCTTTC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

1408

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLKQOC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGWRKGVQ IGGEVFRQON EGSRLAIGVM
401 GGRAGQHASV NGKGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLOP
501 QAQFTYLGVN GGFTDSEGTA VGLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

```

a990.seq
1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGCG ACTTCCCATT
101 ATTTTTCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AACTACAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCG GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTTATACAA AACAAGACCC
301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGAACA
351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTC AATCGAAAA
501 CAAATCCAC GTCCGCCGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGCGG TGGTTTGGG ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGCGGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTCCGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAAATTGT GGCTGCGCTT CATCGCGCGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GCGGCGGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CGGCGTGATG
1201 GCGGCGAGGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGGTT ATGGCGGGGG TGTTTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCGT TGTGCGAAAA GGCAATAATG TGCGGTTTTA CCTGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAAGTGCAA AGCCGCGCCG
1601 GCATTGCGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTGACACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCGGCAT TGAAGCCGGT TGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

```

a990.pep
1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITDLY GDNLKDAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEDKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLKQOC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGRRKGVQ IGGEVFRQON EGSRLAIGVM

```

1409

401 GGRAGQHASV NGKGGAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY
 451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGVVGK GNNVRFYLQP
 501 QAQFTYLGVN GGFTDSEGTA VLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
 551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
 601 YGKRTDGDKE AALSLKWL*

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQQKNYN					
a990	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQQKNYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m990.pep	SGILAVDNMPVVKYITEKYGADLKQAVKSQLQDLYKTRPEAWAENKKRTEEAYIAQFGT					
a990	SGILAVDNMPVVKYITDTYGDNLKDAVKKQLQDLYKTRPEAWAENKKRTEEAYIEQLGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m990.pep	KFSTLKQTMPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
a990	KFSILKQKNPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m990.pep	MTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP					
a990	MTLKDSLWEPRRHSDIHMLETSDNARIRLNTKDEKLTVHKAYQGADFLFGYDVRESDEP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m990.pep	ALTFEDKVSGQSGVVLERRPENLKTLDGRKLIAAKTADSGSFQKQNYRQGLYELLKQC					
a990	ALTFEEKVSGQSGVVLERRPENLKTLDGRKLIAAEKADSNSFQKQNYRQGLYELLKQC					
	250	260	270	280	290	300
	310	320	330	340	350	360
m990.pep	EGGFCLGVQRLAIPAEAVLYAQAYAAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
a990	EGGFCLGVQRLAIPAEAVLYAQAYAAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m990.pep	RSHQNIRGGAAADGWRKGVQIGGEVFVRQNEGSRLAIGVMGGRAGQHASVNGKGGAGSD					
a990	RSHQNIRGGAAADGRRKGVQIGGEVFVRQNEGSRLAIGVMGGRAGQHASVNGKGGAGSY					
	370	380	390	400	410	420
	430	440	450	460	470	480
m990.pep	LYGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
a990	LHGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
	430	440	450	460	470	480
	490	500	510	520	530	540
m990.pep	ALVAEGIVGKGNVRFYLQQAQFTYLGVNGGFTDSEGTA VGLLGSGQWQSRAGIRAKTR					
a990	ALVAEGVVGKGNVRFYLQQAQFTYLGVNGGFTDSEGTA VGLLGSGQWQSRAGIRAKTR					
	490	500	510	520	530	540
	550	560	570	580	590	600
m990.pep	FALRNGVNLQPFPAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					
a990	FALRNGVNLQPFPAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					

1410

	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLF	X				
a990	YGKRTDGDKEAALSLKWLF	X				
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

```

g992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGCGCGTTG  GGTATACGG
101 GATATGACAG  TGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGCACGTGAG  GGGACGTGGG  TTTCGACGCG  CCCGTCGCCC  GACGGGCATC
201 GGGGAAATCC  GGCCACAGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGATACCCT  TCACGTCATC  GACGGCGACG  GCGCGAAACA  TAAAATTCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GTACACGTTT
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAGGG  TAGGAAAGTC  AGTGTACGTG
401 TGTTTGAAAC  CGACCGCTAT  CAGCGCGAAG  TGGCGCAGGT  ATCCGCCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATTG
501 TAAAAGTTAT  GCTAAGAAGC  AGCAGGATAA  GCGCGATTTT  GCCGACTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAAATCCG  AAGCGCCGTG  GCGGTACCGC  CGGCGAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATCCGTGGG  CGAATGGTTG  GGCATTTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

```

g992.pep
1  MFRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GTAGDVGFDA  PVRRRASAKS  GHSYTGTVSK  VYDGDTLHVI  DGDGAKHKIR
101 MAYIDAFEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDVGEWL  GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

```

m992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGTGCCTTG  GGTATACGG
101 GTTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGGCGGGCAG  GGGACGGCGG  TTCCGACGCG  CCCGCCCGCC  GCCGAGCATC
201 GGGGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCT  TCACGTTATC  GACGGCGACG  GCGCGAAACA  CAAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTGCGCG
401 TGTTCGATAC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATTG
501 TAAAAGTTAT  GCTAAGAAGC  AGCAGGATAA  GCGCGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAAATCCG  AAGCGCCGTG  GCGGTACCGC  CGAGCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATCCGTGGG  CGAATGGTTG  GGCATTTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

```

m992.pep
1  MFRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGDTLHVI  DGDGAKHKIR
101 MAYIDAFEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDVGEWL  GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

1411

	10	20	30	40	50	60
m992.pep	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDV LGAAGDAGSDA					
g992	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDV LGTAGDVGFDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
g992	PVRRRASAKSGHSYTGTVSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVSVRVFD TDRYQREVAQVSVGKTDLNLMQVQDGA AWHYKSYAKEQQDKADF					
g992	LRAAAEGRKVSVRVFETDRYQREVAQVSGKTDLNLMQVQDGA AWHYKSYAKEQQDKADF					
	130	140	150	160	170	180
	190	200	210	220	230	
m992.pep	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DAVGEWLG IWX					
g992	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DSVGEWLG IWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

a992.seq

1	ATG	TTC	CAG	CAC	GGC	ATC	GGCA	TTT	GAAAA	AAT	ATG	CAG	ATTA	AAAAA	AAT	CAT
51	GAA	ATG	GCTT	CCC	GTC	GCCT	TGTC	GCCTTT	GGG	TGCG	TTG	GGT	TAT	ACGG		
101	GGT	ACG	GCAG	CGA	GGC	GGTG	CGG	ACG	CGCG	TTG	CCGT	ACT	CGA	CGT	ACTC	
151	GGC	GCG	GCAG	GGG	ACG	CGGG	TTCC	GAC	CGC	CCC	CCCC	GCC	GAG	CATC		
201	GGC	GAA	TCC	GGC	ACC	GCT	ACAC	AGG	CAC	GGT	GTCC	AAA	GTCT	TAT	GACG	
251	GCG	ACAC	CCT	TCAC	GTT	ATC	GAC	GGC	GACG	GCG	GAA	ACA	CAAA	TCC	CGG	
301	ATG	GCG	TATA	TCG	ACG	CGCC	GGAG	ATG	AAA	CAGG	CTT	ACG	GCAC	GCG	TTC	
351	GCG	GACA	CAAC	CTG	CGC	CGCG	CGG	CGGA	AGG	CAGG	AAA	AGTC	AGCG	TCC	CGG	
401	TGT	TCC	GAC	AC	CGCT	TAC	CAG	CGC	GAA	TGG	CGC	AGGT	TTCT	GTC	CGG	
451	AAA	ACCG	GATT	TGA	ACCT	GAT	GCAG	GTG	CAG	GAC	GGG	CGG	CGT	GGC	ATTA	
501	TAAA	AGTT	TAT	GCT	AAAG	AAC	AGC	AGG	ATA	GGC	GAT	TTT	GCC	GAT	TATG	
551	CCG	ACG	CTCA	AAT	TCA	GGCG	GAA	AGG	GAAC	GCAA	AGG	ATT	GTG	GAA	AGCT	
601	AAAA	TCCG	C	AAG	CGC	CTG	GGC	GTAC	CCG	CGG	CAGG	CA	GGAG	CGG	CGG	
651	GGG	CAATA	AAG	GATT	GGAT	G	ATG	CCG	TGGG	CGA	ATG	GTG	GGC	ATT	TGGT	
701	AA															

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

a992.pep

1	MFR	RHRL	KN	MQIK	KIM	KWL	PVAL	SLL	GAL	GYT	GYG	SEAV	RTAV	AVLD	V
51	GA	AGD	AGS	DA	PARR	RA	SAK	S	GHRY	TGT	VSK	VYD	GD	TL	HVI
101	MAY	ID	AP	EMK	QAYG	TR	SRDN	LRAA	EGR	KV	SVR	VFD	TD	RY	QRE
151	KT	DLN	LMQ	VQ	DGA	A	WHY	KSY	AKE	Q	QD	KADF	ADY	AD	AI
201	KNP	QAP	WAY	R	RAG	R	SGG	GNK	DWM	D	AV	GE	W	L	GIW

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992.pep	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDV LGAAGDAGSDA					
m992	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDV LGAAGDAGSDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
m992	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180

1412

```

a992.pep  LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
          |||
m992      LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
          |||
          130      140      150      160      170      180

          190      200      210      220      230
a992.pep  ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGNGKDWMDAVGEWLGIX
          |||
m992      ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGNGKDWMDAVGEWLGIX
          |||
          190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1  CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATCCG ATGGTGGAAA
101 TTACCGGGCA GTATCTGCAC TATATTGCC AAATGGAAGC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCGCTCTGC TTGCCTACGA GCAAATGAAA
301 CTGGCGGCGC AGGGTTTGA GCGCTGCCG CGTGGCGGAC GGGATTTGCG
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCAGAG
401 TTTACATCGC CGATTGATG CAGGCATGGT TGGGCATCTT TTCTCGGGCA
451 AACATACGCG GCAGCCACGA AGTAATCCAA GAAACCCTTT CCGTGCAGCG
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCGGC ACACGGGGCG GCGCGGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1  LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVEITGOYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTAEVD EADPRAELV RLLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLSVRAQMT AILRRLNEHG ICRFHALFNP EQGAAYVIVN
201 FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1  TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTACT GGATATCCG ATGGTGAAGA
101 TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCGCCTGC TGGCTTACGA ACAGATGAAG
301 CTGGCGGCGC AGGGTTTGA GCGCTGCCG CGAGCCGGAC GGGATTTGCG
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAGG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCAAA GAAACCATCT CCGTGCAGCG
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCTGCAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCGGC ACACGAGGCG GCGCGGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1  LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVKITEOYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RLLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNGHG ICRFHDLFNP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

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m993/g993 93.1% identity in 248 aa overlap

m993.pep	10	20	30	40	50	60
	LKVVLSFGQPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQI	ETYQFDLAAEYLLMA			
g993	LKVVLSFGQPLDLLLYLIRKQNI	DVLDIPMVEITGQYLHYIAQME	AYQFDLAAEYLLMA			
	10	20	30	40	50	60
m993.pep	70	80	90	100	110	120
	AMLIEIKSRLLLPRTETVEDEE	ADPRAELVRRLLAYEQMKLAA	QGLDALPRAGRDFAWAY			
g993	AMLIEIKSRLLLPRTETVEDEE	ADPRAELVRRLLAYEQMKLAA	QGLDALPRAGRDFAWAY			
	70	80	90	100	110	120
m993.pep	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQ	AWLGILSRKHTRSHEVIKETIS	SVRAQMTAILRLNKGH			
g993	LPLEIAAETKLPEVYIADLMQ	AWLGILSRKHTRSHEVIQETLS	SVRAQMTAILRLNKGH			
	130	140	150	160	170	180
m993.pep	190	200	210	220	230	240
	ICRFHDLFNPQGAAYVVNFIA	LLELAKEGLVRIVQEDGFGEI	RISLNHEGAHSDGISG			
g993	ICRFHALFNPQGAAYVIVNFIA	LLELAKEGLVIVQEDGFGEI	RISLNHEGAHSDGIFG			
	190	200	210	220	230	240
m993.pep	249					
	TRGGRDVFX					
g993	TRGGRDVFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

1	CTGAAAGTCG	TATTGAGCAG	TTTCAAGGC	CCTTTGGATC	TGCTGCTCTA
51	CCTTATCCGC	AAGCAGAACA	TCGATGTTCT	CGATATTCCG	ATGGTGAAGA
101	TTACCGAACA	GTATCTGCAC	TACATCGCCC	AAATAGAAAC	CTATCAGTTT
151	GATTTGCGCG	CGGAATATCT	TTTGATGGCA	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCCTG	CTGCTGCCGC	GTACCGAAAC	CGTCGAAGAC	GAAGAAGCCG
251	ACCCGCGTGC	CGAGTTGGTG	CGCCGCCTGC	TGGCTTACGA	GCAGATGAAG
301	CTGGCGGCAC	AAGGGTTGGA	TGCGCTTCCT	CGTGC GGCC	GGGATTTGCG
351	ATGGGCATAC	CTGCCACTGG	AAATTGCCGT	CGAAGCCAAG	CTGCCCGAAG
401	TCTATATTAC	CGACTTGACG	CAGGCGTGCG	TGAGTATTTT	GTCTCGGGCA
451	AAACATACGC	GCAGCCACGA	AGTTATCAAA	GAAACCATCT	CCGTGCGCGC
501	GCAAAATGACG	GCAATCCTGC	GCCGTTTGAA	CAAACACGGG	ATATGCAGGT
551	TTCACGACCT	GTTCAATCCC	GAACAGGGCG	CGGCTTACGT	GGTCGTCAAC
601	TTCATCGCAC	TGTTGGAGCT	TGCCAAAGAA	GGTTTGGTCG	GAATCGTACA
651	GGAAGTCGGT	TTCGGAGAAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCGC
701	ATTACAGACG	CATTCCGGC	ACACGGGGCG	GGCGCGATGT	GTTCTAA

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

1	LKVVLSFGQ	PLDLLYLIR	KQNI	DVLDIP	MVKITEQYLH	YIAQIETYQF
51	DLAAEYLLMA	AMLIEIKSRL	LLPRTETVED	EEADPRAELV	RRLLAYEQMK	
101	LAAQGLDALP	RAGRDFAWAY	LPLEIAVEAK	LPEVYITDLT	QAWLSILSRA	
151	KHTRSHEVIK	ETISVRAQMT	AILRLNKGH	ICRFHDLFNP	EQGAAYVVVN	
201	FIALLELAKE	GLVGIVQEVG	FGEIRISLNH	EGAHS	DGISG	TRGGRDVFX*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

a993.pep	10	20	30	40	50	60
	LKVVLSFGQPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQI	ETYQFDLAAEYLLMA			
m993	LKVVLSFGQPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQI	ETYQFDLAAEYLLMA			

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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
	AMLEIEKSRLLLPRTEVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
m993	AMLEIEKSRLLLPRTEVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
	70	80	90	100	110	120
a993.pep	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAWLSILSRKHTRSHEVIKETISVRAQMTAILRRLNKHG					
m993	LPLEIAVEAKLPEVYITDLTQAWLGILSRKHTRSHEVIKETISVRAQMTAILRRLNKHG					
	130	140	150	160	170	180
a993.pep	190	200	210	220	230	240
	ICRFHDLFNPEQGAAYVVVNFIALLELAKEGLVGIVQEVGFGEIRISLNHEGAHSDGISG					
m993	ICRFHDLFNPKQGAAYVVVNFIALLELAKEGLVRIVQEDGFGEIRISLNHEGAHSDGISG					
	190	200	210	220	230	240
a993.pep	249					
	TRGGRDVFX					
m993	TRGGRDVFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1  ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGCG TTCTTACCGC
51  CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCT GAAGGAAGCA
101 CCGTGCTTGC CTTGGGCGAT TCGCTCACCT TCGGCTACGG AGCAAACCCC
151 GCGGAATCCT ACCCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACGTCGCG GCAAGCCCTA TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAAA CCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCAGAAAT TCCCGAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AAAAGGAAAA CATTCGCCGC GTCTCGTCG
401 GCGTGCCGCA CATCACACTG GCGCGTTGTT TCGGGCATTG GAGCGACCAT
451 CCGCTGTATG AGGATTGTGC CGAGGAATAC GGCATTCCGT TGTTCGGCGG
501 CCGTGCGGCG GAAATTTTGG GCAATAATAA TCTGAAATCC GACCAATATC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTCG CCGAAATTTT GAATCAATTT
601 TTGAGAAAAC ATGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1  MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51  GESYPAQLQK LTGWNIVNGG VSGD TSAQAL SRLPALLARK PKLVIVGIGG
101 NDFLRKVPPE QTRANIAKII ETQKENIPA VLVGVPHITL GALTGHLSHDH
151 PLYEDLSEFY GIPLFGGAWA EILGNLNLKS DQIHANGKGY RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1  ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGCG TGCTTACCGC
51  CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCT GAAGGAAGCA
101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCTT
151 GCGGAATCCT ACCCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCTGC CCAAGCCCTG TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAAA CCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCAGAAAT TCCCAAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AGAAGGAAAA CATTCGCCGC GTCTCGTCG
401 GCGTGCCGCA CATCACACTG GGTGCGTTGT TCGGGCATTG GAGCGATCAT
451 CCGCTGTATG AGGATTGTGC CGAGGAATAC GGCATTCCGT TGTTCGGCGG
501 CCGTGCGGCG GAAATTTTGG GCGATAATAA TCTGAAATCC GACCAATATC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTTG CCGAAGATTG GAATCAATTT
601 TTGAGAAAAC AGGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1  MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51  GESYPAQLQK LTGWNIVNGG VSGD TSAQAL SRLPALLARK PKLVIVGIGG

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101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
 151 PLYEDLSEY GIPFPGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF
 201 LRKQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

	10	20	30	40	50	60
m996.pep	MNRR	TFLGAGALLLTACGRKSARTHAKI	PEGSTVLALGDSLTFGYGANPGESYP	QAQLQK		
g996	MNRR	TFLGAGALLLTACGRKSARTHAKI	PEGSTVLALGDSLTFGYGANPGESYP	QAQLQK		
	10	20	30	40	50	60
	70	80	90	100	110	120
m996.pep	LTGWNIVNGGVSGD	TSQAALSRLPALLARKPKLVIVGIGG	NDFLRKVPKEQTRANI	AKII		
g996	LTGWNIVNGGVSGD	TSQAALSRLPALLARKPKLVIVGIGG	NDFLRKVPKEQTRANI	AKII		
	70	80	90	100	110	120
	130	140	150	160	170	180
m996.pep	ETVQKENIPAVLVGVPHITL	GALFGHLSDHPLYEDLSEY	GIPFPGAWAEILGDN	NLKS		
g996	ETVQKENIPAVLVGVPHITL	GALFGHLSDHPLYEDLSEY	GIPFPGAWAEILGDN	NLKS		
	130	140	150	160	170	180
	190	200				
m996.pep	DQIHANGKGYRKFAEDLNQFLRK	QGFR				
g996	DQIHANGKGYRKFAEDLNQFLRK	KGFRX				
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq
 1 ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGC TCCTTACCGC
 51 CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAATTCCTC GAAGGAAGCA
 101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCCC
 151 GCGGAATCCT ACCCGCGCA ACTGCAAAA CTGACGGGT GGAATATTGT
 201 CAACGGCGGC GTATCGGGCG ATACATCCGC CCAAGCCCTG TCGCGCCTGC
 251 CCGCGCTGTT GGCACGCAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
 301 AACGACTTTC TGGCAGAA GTTCCCAAGGAG CAGACCCGCG CCAATATCGC
 351 GAAATCATC GAAACCGTGC AGAAGGAAAA CATCCCGGCC GTCTCTGTCG
 401 GCGTGCCGCA CATTACCTTG GCGCGTTGT TCGGGCATT GAGCGATCAT
 451 CCGCTGTATG AGGATTGTG CGAGGAATAC GGCATTCCGC TGTTCGGCGG
 501 CCGGTGGGCG GAAATTTTGG GCGATAATA TCTGAAATCC GACCAATCC
 551 ACGCCAACGG CAAAGCTAT CGGAAATTG CCGAAGATT GAATCAATT
 601 TTGAGAAAC AGGGGTTAG ATAA

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep
 1 MNRRTFLGGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
 51 GESYPQLQK LTGWNIVNGG VSGDTSQAAL SRLPALLARK PKLVIVGIGG
 101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
 151 PLYEDLSEY GIPFPGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF
 201 LRKQGFR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

	10	20	30	40	50	60
a996.pep	MNRR	TFLGAGALLLTACGRKSARTHAKI	PEGSTVLALGDSLTFGYGANPGESYP	QAQLQK		

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|||||
m996      MNRRFTLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQLOK
           10      20      30      40      50      60
           70      80      90      100     110     120
a996.pep  LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
           |||||||
m996      LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
           70      80      90      100     110     120
           130     140     150     160     170     180
a996.pep  ETVQKENIPAVLVGVPHITLGALFGHLSHDHPLYEDLSEEGYIPLFGGAWAEILGDNNLKS
           |||||||
m996      ETVQKENIPAVLVGVPHITLGALFGHLSHDHPLYEDLSEEGYIPLFGGAWAEILGDNNLKS
           130     140     150     160     170     180
           190     200
a996.pep  DOIHANGKGYRKFAEDLNQFLRKQGF
           |||||||
m996      DOIHANGKGYRKFAEDLNQFLRKQGF
           190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTC TCGGCGCAGG
51  CTGGGCGGCG TTGTCCGCGG CCGTCACCTT GCGCGGCGAC GCCGACGTTA
101 CCCTGTTTGA AGCCGCGCGG CAGGCGGGCG GAAGGGCGCG CACACTGGCC
151 GGAATAACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TCGCCTGTAT GAAAACCATC GGTTCAGACC
251 CCGTGCCCGC CTTTGTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CTGCCCCTGC CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAATGCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCGTAAT
501 GCAGTTTGG CAGCCCTTGG TCTGGGCGCG GCTCAACACG CCTTTGAAA
551 CCACAAGCCT GCGCGTGTG TGCAACGTTT TGTCGCGCG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCGCGA CCCGCCCTGG CGGAGCTTCA ACGGCTCGGC CGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCTCCCGGA CGGAAAAGTC
751 CTCGTCACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCGCGC GCGCTCCTGC CCGAAGGCAC GCCGGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGcCTGc CGCCCGCTG ACCGGCATg CCGAcggcAC
951 ggcaCaatg CTGCTTTg ccgGGGCAGG tccggactgc CcccaaAacg
1001 aagTCTCCG cGTCAAttagc GTTTCGGAcc GCGtcggcgc Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MNNTPHRPRK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILLGAY RGVRLRMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPsAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKORN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSgSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLEPGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTC TCGGCGCAGG
51  CTGGGCGAGG CTGTCCGCGG CCGTCACCTT GCGCGGCGAC GCCGACGTTA
101 CCCTGTTTGA AGCCGCGCGG CAGGCGGGCG GCAGGGCGCG CACACTGGCC
151 GGAATAACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TCGCCTGTAT GAAAACCATC GGTTCGATC
251 CCGTGCCCGC CTTTGTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CTGCCCCTGC CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGTG CACCGACTGC ATTCAAAGCC AAATGCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCGTGAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGAAA

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551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCTACCC AAGCAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCTTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAGC GCGCGTATGC CGTCTGAACA CCTCCCGGA CCGGAAAGTG
751 CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CCACGCCCGC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCCTGCC CGCCCGCTG ACCGCGCTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCGCT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCCG GACTTGTCTG GGTTCACCG GCACCGCATC
1201 TTCCCGCGCG GCGACTACCT CCACCCGGAC TACCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

```

m997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILLAGY RGVRLMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVLT
201 KKSQSDYLLP KQDLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQVW LLCRGRGLP ENEVSAVISV SDRVGAFAFR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPAQDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

g997.pep	10	20	30	40	50	60
m997	10	20	30	40	50	60
g997.pep	70	80	90	100	110	120
m997	70	80	90	100	110	120
g997.pep	130	140	150	160	170	180
m997	130	140	150	160	170	180
g997.pep	190	200	210	220	230	240
m997	190	200	210	220	230	240
g997.pep	250	260	270	280	290	300
m997	250	260	270	280	290	300
g997.pep	310	320	330	340	350	
m997	310	320	330	340	350	

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGCGC TTGTCCGCGC CCGTTACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGGCGCG CGCACTGGCC
151 GGAATAACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGGCGCATAC CGGGCGGTGT TCGCCCTGAT GAAAACCATC GGTTCAGACC
251 CCCATGCCGC CTTTTTGC GC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCCCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCGCGGCGCG TACCGTCCGC ATTCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCGTAAT
501 GCAGTTTTGG CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGTGACG
601 AAAAAATCCG GCAGCGACTA TCTCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCGGCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAGC GCGCATATGC CGTCTGAAAC CCCTCCCGGA CGGGAAGTG
751 CTCGTCAACG GCGAACCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CCGCGCCGCG GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
901 CGCGAACCAG TCCGCTTGCC TGCCCGCGTG ACCGGACTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCGAGCT CGGACTGCCT GAAAACGAAG
1001 TGTCGCCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCCGCATT
1101 GGGCGAACC CGAAGCGTGC GCGTCATCAC CGAAAACGC GCCACAACCG
1151 CAGCCGATGC CCGCGCGCGG GATTTGTCGT GGTGACCCG GCACCGCATC
1201 TTCCCGCGCG GCGACTACCT CCACCCAGAC TACCCGCGCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVRLMKTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVLT
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNPEPFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTVQW LLCRGRLGLP ENEVSAVISV SDRVGAFANR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

	10	20	30	40	50	60
a997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
a997.pep	NGQHILLGAYRGVRLMKTI GSDPHAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVRLMKTI GSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
a997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
a997.pep	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRIC					
	190	200	210	220	230	240
a997.pep	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRIC					

1419

```

m997      PLETASLRVLCNVLS DGVLT KKS GSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

           250      260      270      280      290      300
a997.pep  RLNTLPDGKVLVNGEPFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           |||||
m997      RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           250      260      270      280      290      300

           310      320      330      340      350      360
a997.pep  AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKVHADL
           |||||
m997      AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

           370      380      390      400      410      420
a997.pep  KRILPHLGEPEAVRVITEKRATTAADAPPPDL SWLHRHRIFFAGDYLHPDYPATLEAAVQ
           |||||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDL SWLHRHRIFFAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

           430
a997.pep  SGFASAEACLQSLSDAVX
           |||||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTTCAA TTGTTTTATC
51  AGCCTGCAAC CAACAATCAA AAACGGCACA AGCCGAAGAA CCTGTCCAAA
101 GTATCCAGGC TGCTGATTGT ACCGCCCAA TGGACATCAC AGTTGAACAA
151 TATCTCATCA ATTTGGAGCA AGCATTTAAA ACTCAGAACG TCTCAACAAA
201 AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT
251 TGGTAATGGA TTTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
301 ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
351 ACAAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAGGCAG
401 TTCTGTCTTT AACTACCACA GACAAATTGG GCGAATCGGA AGCAGGAAAA
451 CAACTTTTTA CAGCTTTAAC CGAAGTCGTC AAAGAATCCA ATCAGACAGG
501 AGCAACAGCG CAAAAGACG TTCCGGCAGA TGGTATTTTA TATAGCGTTG
551 TTTTGA AAAA AGAAACAAAC ACCATTGCAA TAATCGGCAG AAAACAACCC
601 TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI CVSIVLSACN QSKTAQAE PVQSIQAADC TAPMDITVEQ
51  YLINLEQAFK TQNVSTKIHN KNIVKDCGY DLTLMDFGA IALKLDEQOK
101 IRAISVGYIL KTDGERGQNL VNNAINGLHS IQAVLSLT TT DKLGESEAGK
151 QLFTALTEVV KESNOTGATA QKDVPADGIL YSVVFEKETN TIAIIGRKQP
*

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

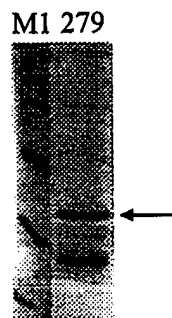
17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

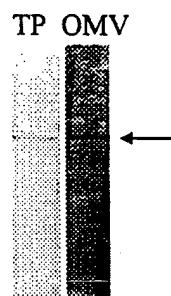
Fig. 2

279 (10.5 kDa)

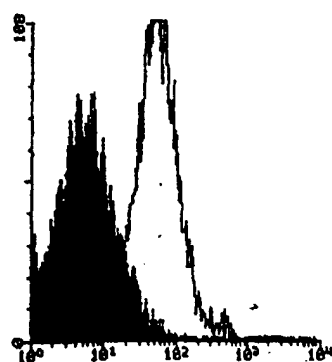
A) PURIFICATION



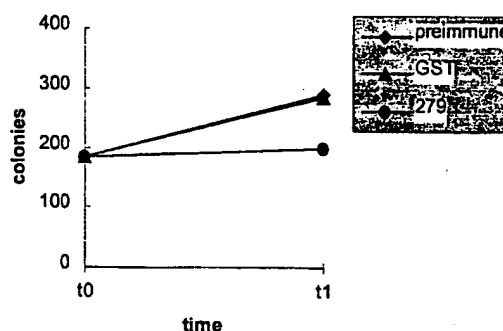
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay: positive

279

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 3

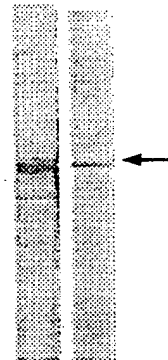
576 (27.8 kDa)

A) PURIFICATION

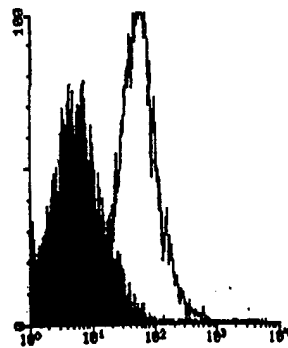


B) WESTERN BLOT

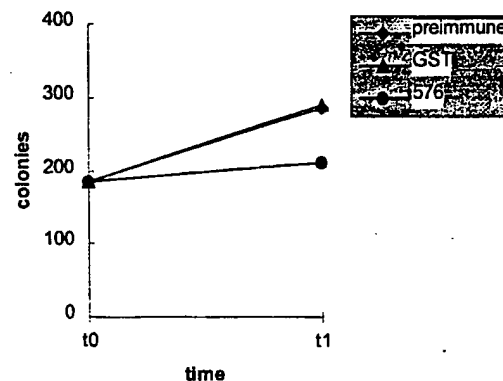
TP OMV



C) FACS



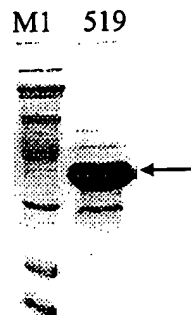
D) BACTERICIDAL ASSAY

E) ELISA assay: positive

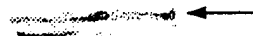
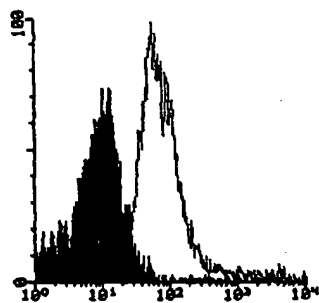
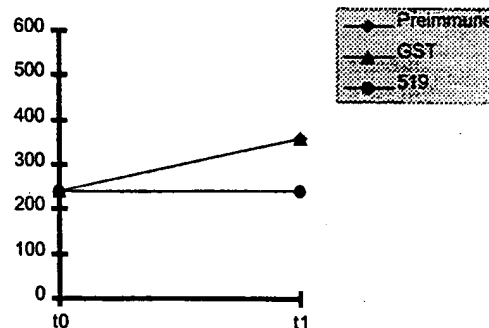
576

The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 4

519 (33 kDa)**A) PURIFICATION****B) WESTERN BLOT**

TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****519**

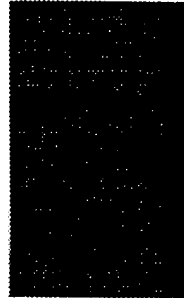
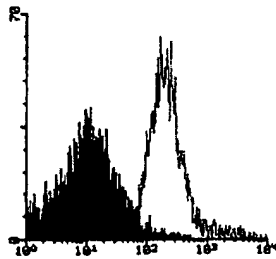
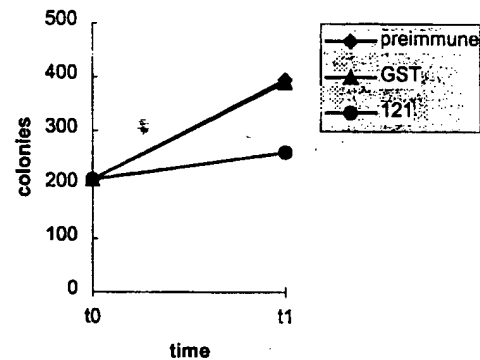
The predicted gene *519* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

121 (40 kDa)**A) PURIFICATION**

M1 121

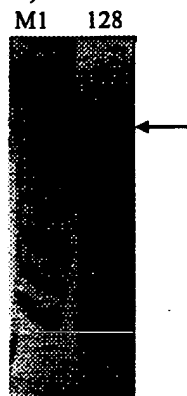
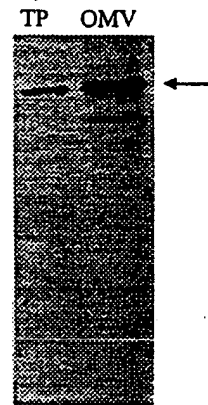
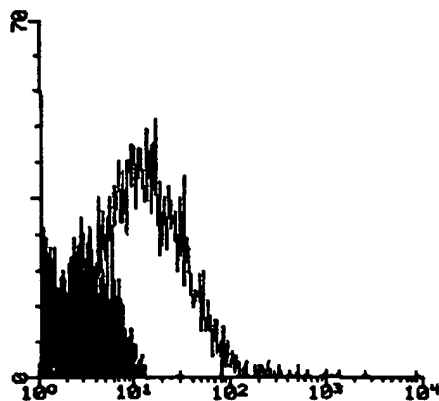
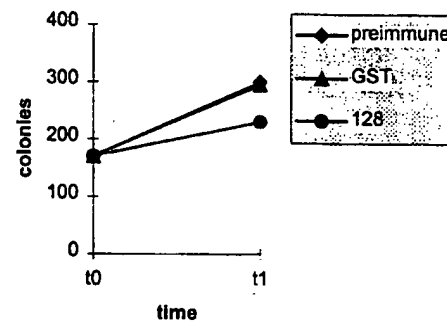
**B) WESTERN BLOT**

TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

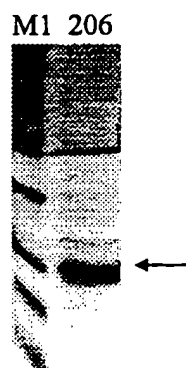
Fig. 5

128 (101 kDa)**Fig. 6****A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****128**

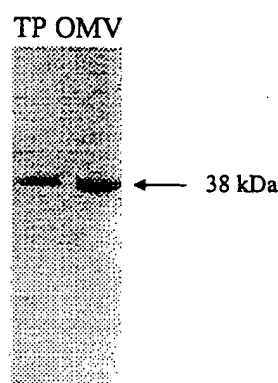
The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

A) PURIFICATION



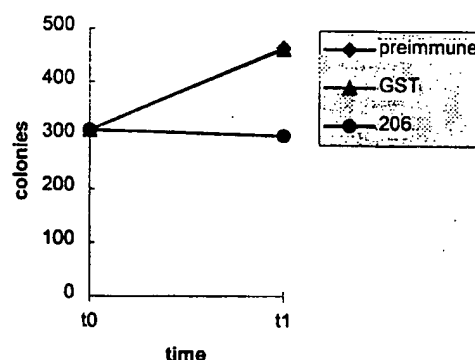
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY



E) ELISA assay: positive

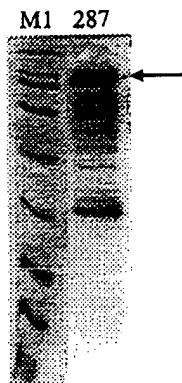
206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worth noting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a reactive band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C) is shown the FACS analysis, in panel D) the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

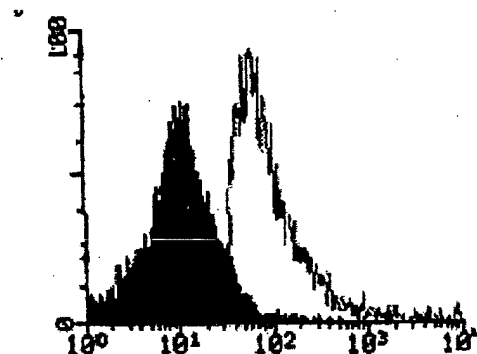
287 (78 kDa)

Fig. 8

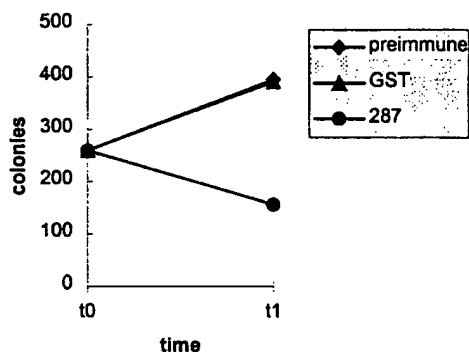
A) PURIFICATION



B) FACS



C) BACTERICIDAL ASSAY

D) ELISA assay : positive

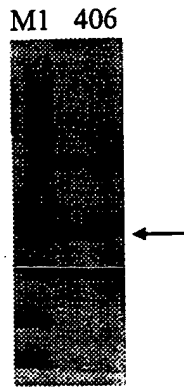
287

The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

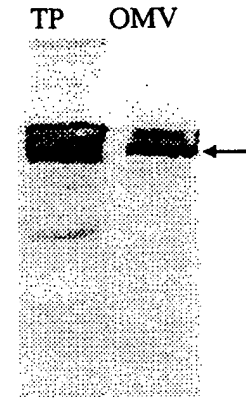
406 (33 kDa)

Fig. 9

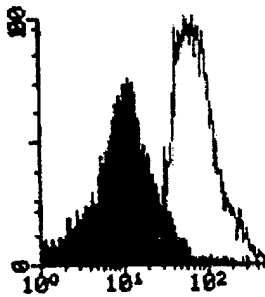
A) PURIFICATION



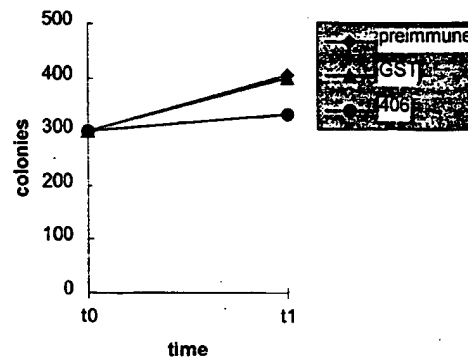
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay : positive

406

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

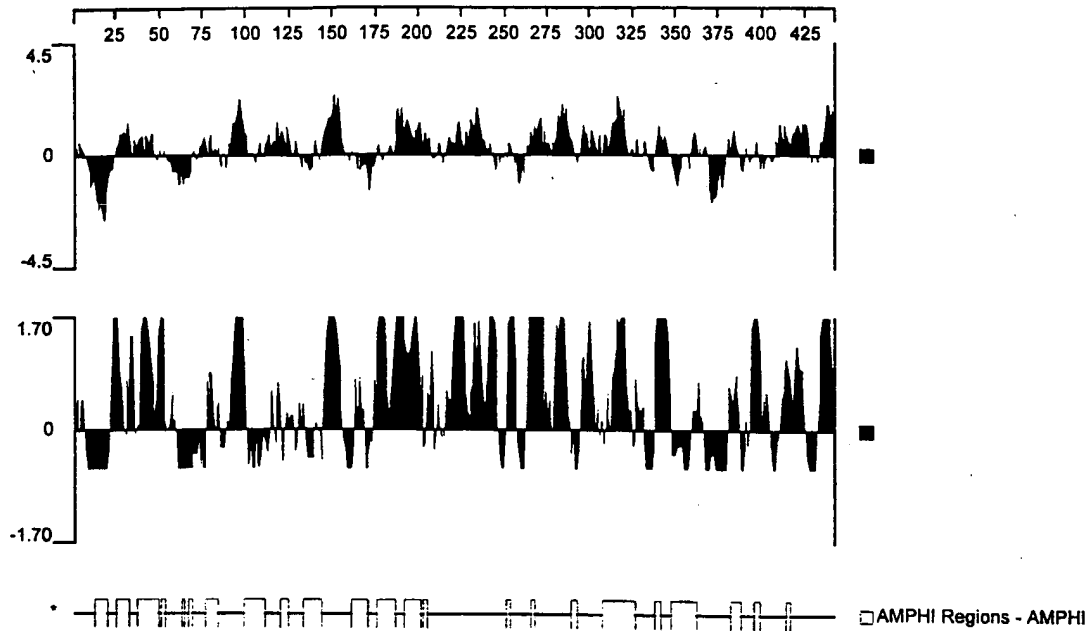
919Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

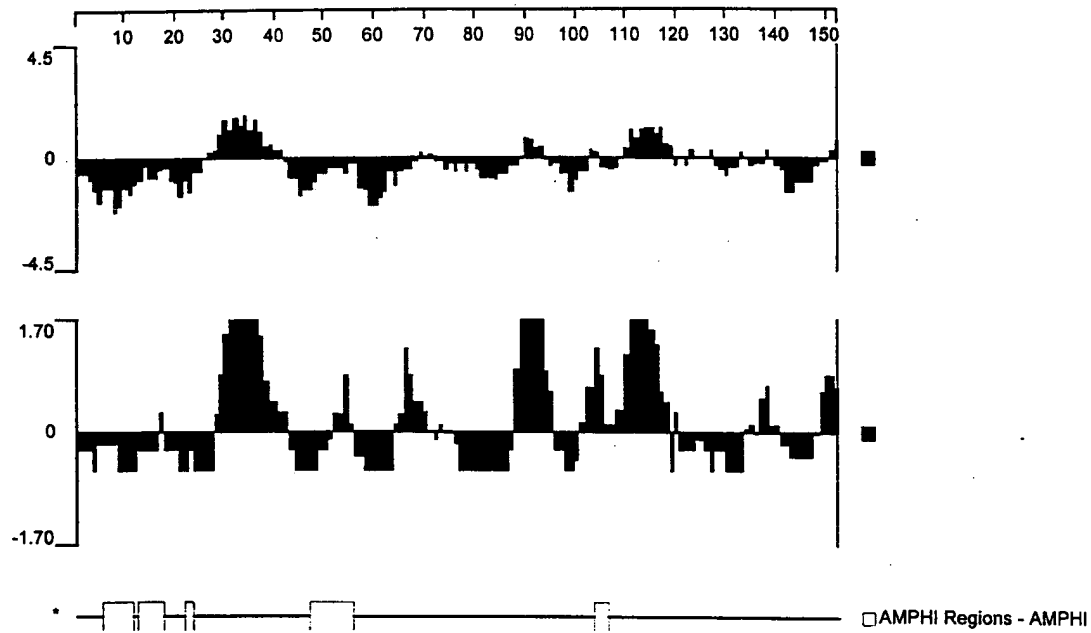
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11

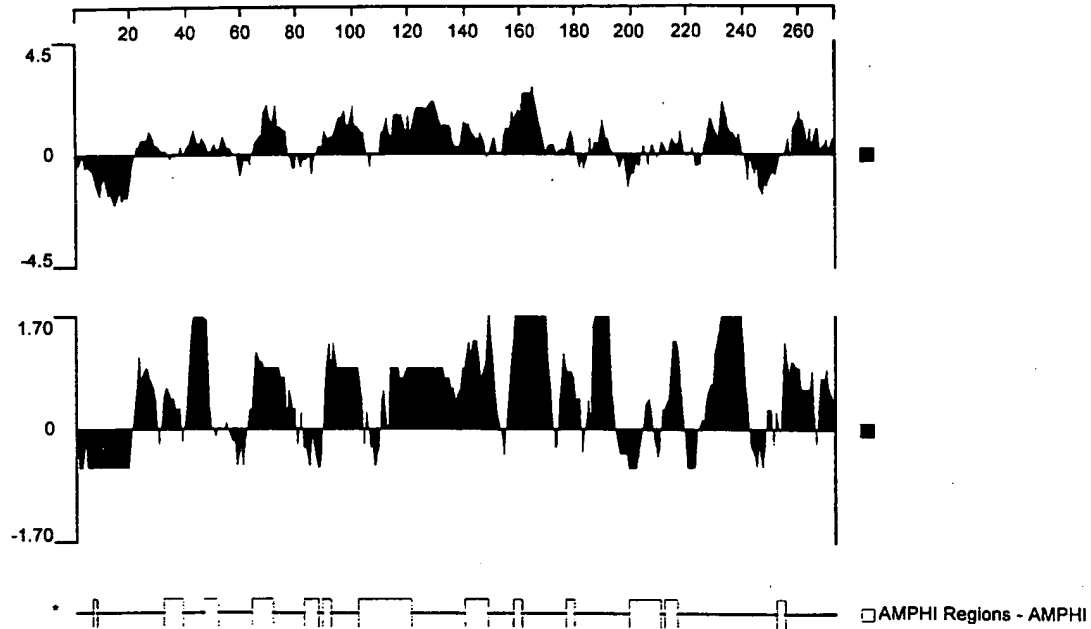
576-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

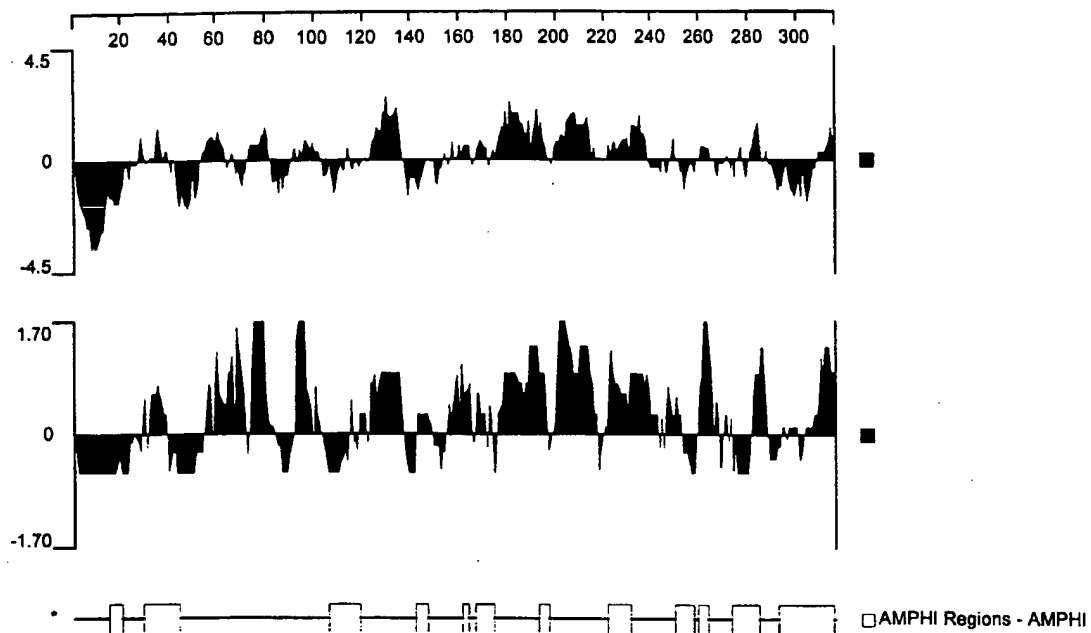
519-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 13

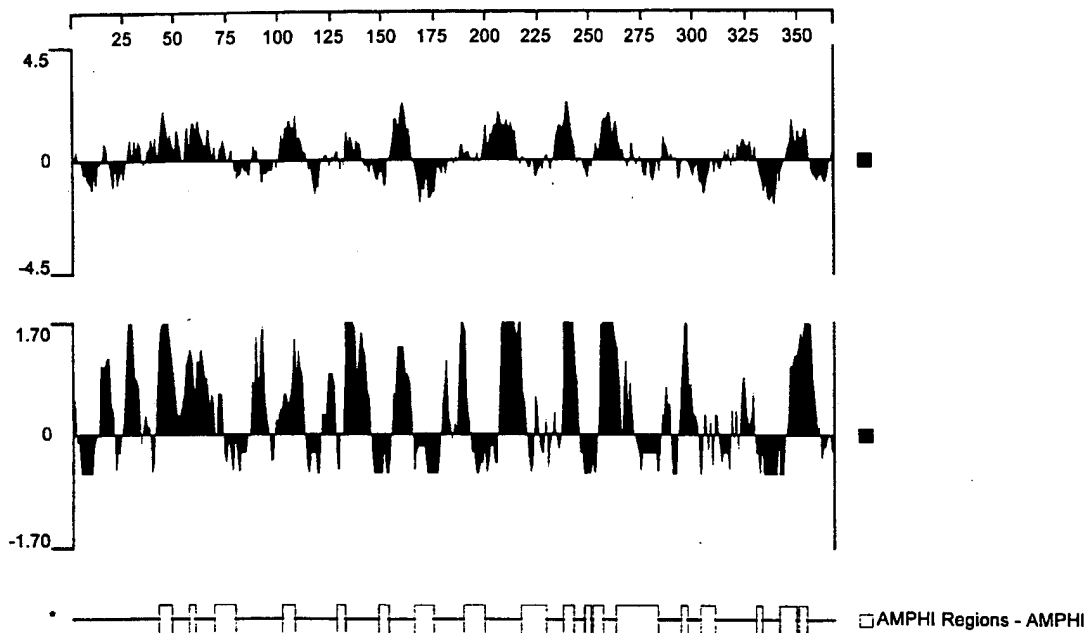
121-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 14

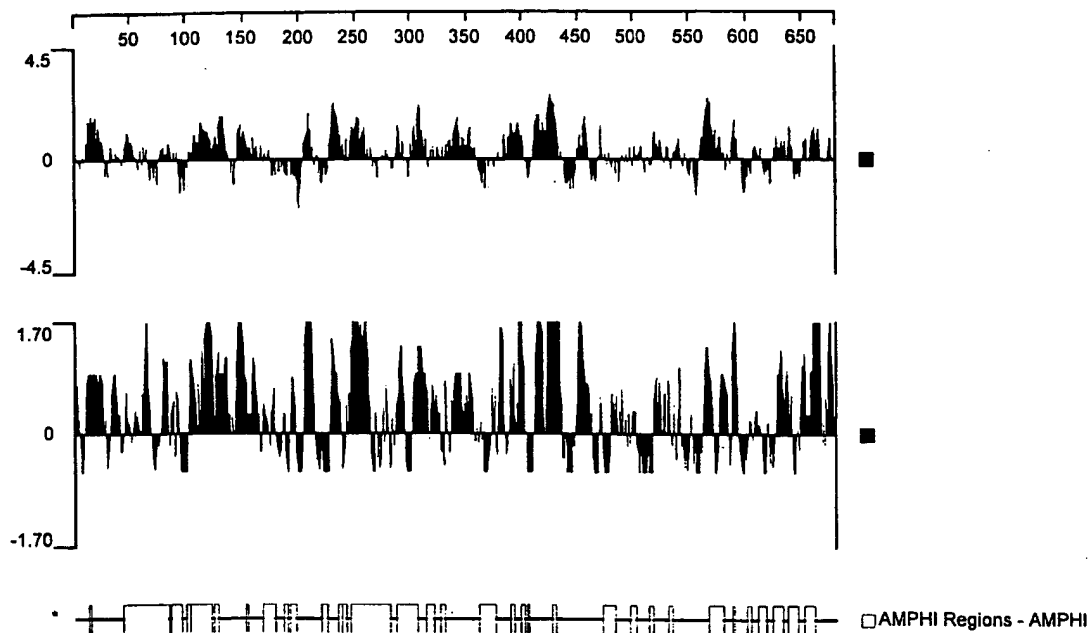
128-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 15

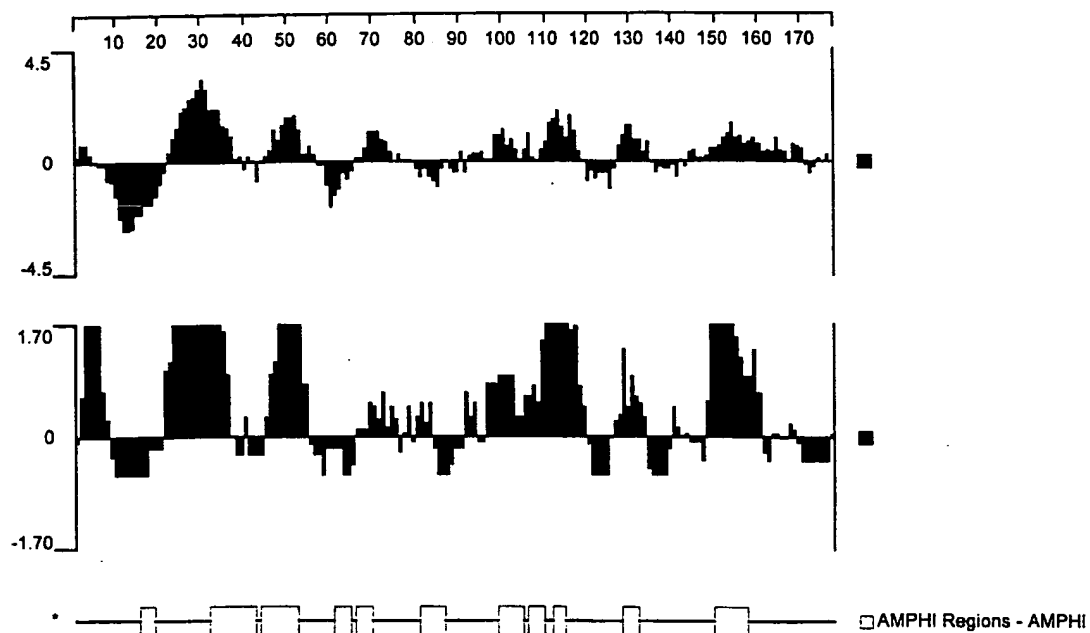
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 16

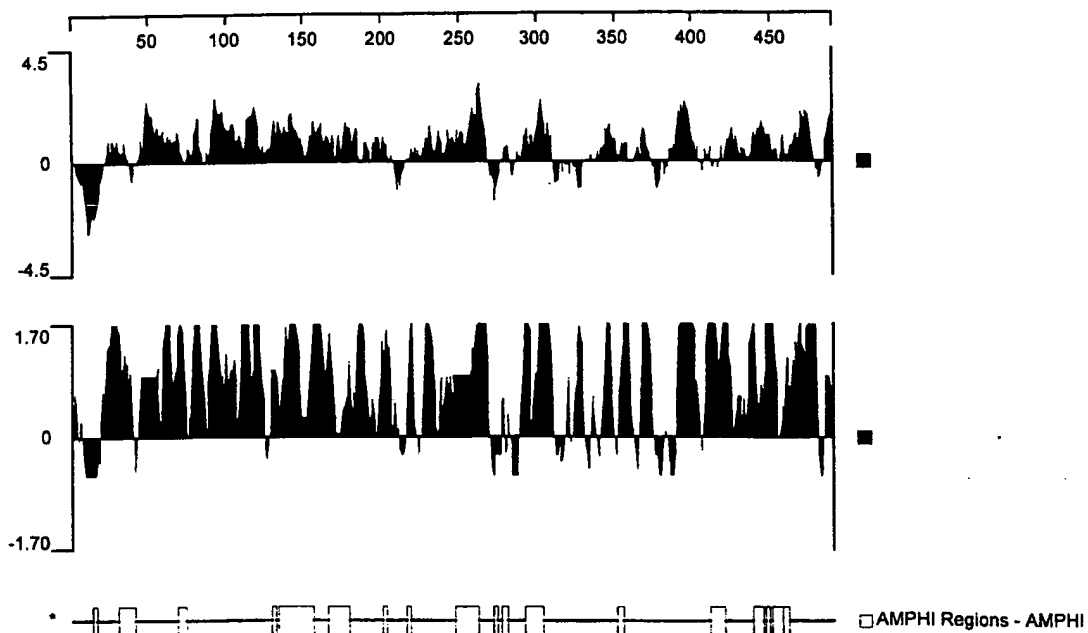
287Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

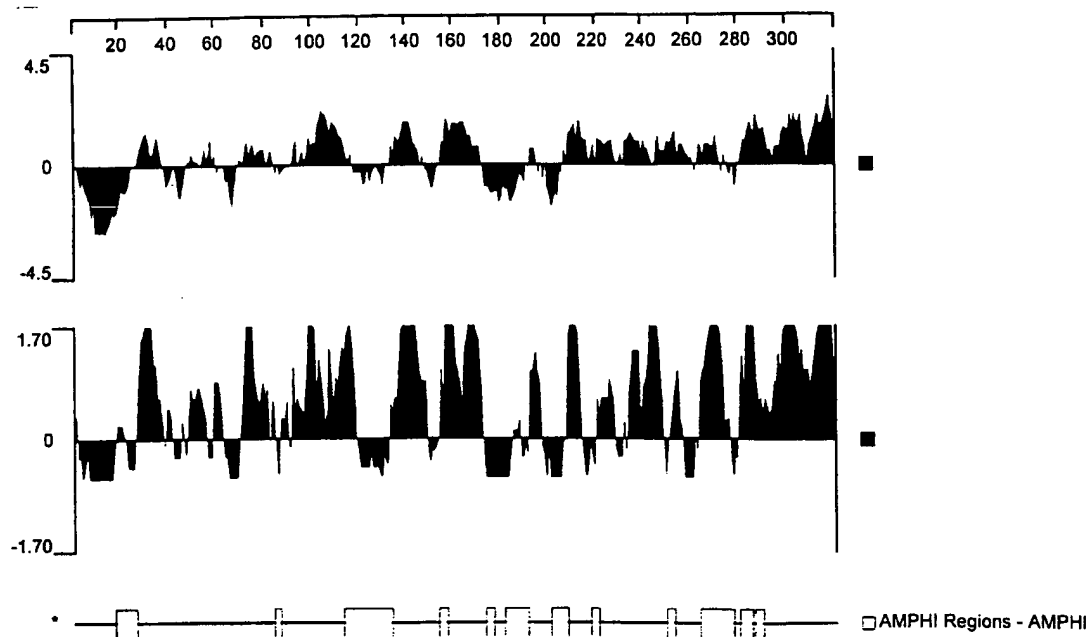
406Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

Fig. 19A

Fig. 19B

zo05_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo08_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
z2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo11_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo20_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo09_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo22_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo24_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo25_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo26_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo27_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo28_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo29_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo13_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Fig. 19C

Fig. 20A

gnmq09	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq31	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
fa1090	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq32	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq33	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq01	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq05	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq08	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq02	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq03	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq04	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq07	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq10	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq11	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq13	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq15	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq16	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq17	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq19	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq21	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq22	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq23	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq24	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq25	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq27	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq28	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq29	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
z2491	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq14	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq18	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq26	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT

gnmq09	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq31	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
fa1090	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq32	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq33	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq01	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq05	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq08	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq02	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq03	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq04	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq07	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq10	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq11	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq13	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq15	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq16	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq17	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq19	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq21	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq22	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq23	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq24	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq25	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq27	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq28	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq29	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
z2491	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq14	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq18	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq26	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK

Fig. 20B


```

287_14 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE.....KETEAE
287_2 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE.....KETEAE
287_21 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE.....KETEAE
z2491 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE.....KETEAE
287_9 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVEEDVGEEVLPKEKKEEAE
fa1090 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVEEDVGEEVLPKEKKEEAE

287_14 50 KEDAPQAGGQGGGAPSNQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT
287_2 50 KEDAPQAGGQGGGAPSNQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT
287_21 50 KEDAPQAGGQGGGAPSNQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT
z2491 50 KEDAPQAGGQGGGAPSNQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT
287_9 61 VSGAPQADT...QDATAGGQGGQDMAAVSAENTGNGGAATTDNPKNEDEGAQNDMPQNAADT
fa1090 61 AGGAPQADT...QDATAGGQGGQDMAAVSAENTGNGGAATTDNPKNEDEGAQNDMPQNAADT

287_14 110 DSLTPNHTPASNMPAGNMCNOAPDAGESEQPANQPDMAANTADGMOGDDPSAGGENAGNTA
287_2 110 DSLTPNHTPASNMPAGNMCNOAPDAGESEQPANQPDMAANTADGMOGDDPSAGGENAGNTA
287_21 110 DSSTPNHTPDNMLAGNMCNOATDAGESEQPANQPDMAANTADGMOGDDPSAGGENAGNTA
z2491 110 DSSTPNHTPDNMLAGNMCNOATDAGESEQPANQPDMAANTADGMOGDDPSAGGENAGNTA
287_9 119 DSSTPNHTPDNMPTRDMCNOAPDAGESEQPANQPDMAANTADGMOGDDPSAGGENAGNTA
fa1090 117 .....

287_14 170 AQSTNOALNNQTAGSQNPASSTNPSTNSGGDEGRITNTNSVVIDGSPQNTLTHCKGDS
287_2 170 AQSTNOALNNQTAGSQNPASSTNPSTNSGGDEGRITNTNSVVIDGSPQNTLTHCKGDS
287_21 170 AQSTNOALNNQTAGSQNPASSTNPSTNSGGDEGRITNTNSVVIDGSPQNTLTHCKGDS
z2491 170 AQSTNOALNNQTAGSQNPASSTNPSTNSGGDEGRITNTNSVVIDGSPQNTLTHCKGDS
287_9 178 DOALNOALNNQVGGSQNPASSTNPSTNSGGDEGRITNTNSVVIDGSPQNTLTHCKGDS
fa1090 117 .ESANQTNNOAGSSDSAPASNPAPANGGSDGGRITNTNSVVIDGSPQNTLTHCKGDS

287_14 230 CSGNNFLDEEVOLKSEFEKLSDAKISNYKKDGGKNDGKNKFFVGLVADSVMKGINOYII
287_2 230 CSGNNFLDEEVOLKSEFEKLSDAKISNYKKDGGKNDGKNKFFVGLVADSVMKGINOYII
287_21 230 CSGNNFLDEEVOLKSEFEKLSDAKISNYKKDGGKNDGKNKFFVGLVADSVMKGINOYII
z2491 230 CSGNNFLDEEVOLKSEFEKLSDAKISNYKKDGGKNDGKNKFFVGLVADSVMKGINOYII
287_9 238 CDRD.FLDEEAPPKSEFEKLSDAKIKRYKK...DEQRNFVGLVADRVKKDGTNRYII
fa1090 176 CNGDNLDEEAPPKSEFEKLSDAKIKRYKK...DEQRNFVGLVADRVKKDGTNRYII

287_14 290 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_2 290 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_21 286 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
z2491 286 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_9 293 IYKDKSAS...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
fa1090 232 FYTDKPT.....RSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG

287_14 348 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPPGRFAA
287_2 348 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPPGRFAA
287_21 344 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPPGRFAA
z2491 344 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPPGRFAA
287_9 353 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPPGRFAA
fa1090 285 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPPGRFAA

287_14 408 KVDFGSKSVDCIIDSDDLHMGTOQKFKAIDGNGFKGTWTENGCGDVSG:FYGPAGEEVA
287_2 408 KVDFGSKSVDCIIDSDDLHMGTOQKFKAIDGNGFKGTWTENGCGDVSG:FYGPAGEEVA
287_21 404 KVDFGSKSVDCIIDSDDLHMGTOQKFKAIDGNGFKGTWTENGCGDVSG:FYGPAGEEVA
z2491 404 KVDFGSKSVDCIIDSDDLHMGTOQKFKAIDGNGFKGTWTENGCGDVSG:FYGPAGEEVA
287_9 413 KVDFGSKSVDCIIDSDDLHMGTOQKFKAIDGNGFKGTWTENGCGDVSG:FYGPAGEEVA
fa1090 345 KVDFGSKSVDCIIDSDDLHMGTOQKFKAIDGNGFKGTWTENGCGDVSG:FYGPAGEEVA

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FIG. 21A

287_14	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_2	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_21	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
z2491	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_9	473	GKYSYRPTDAEKGGFGVFAGKKEQD*
fa1090	405	GKYSYRPTDAEKGGFGVFAGKKEQD*

FIG. 21B

x2491_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv26_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv22_519aaa	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
fa1090_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv32_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv11_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv28_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv96_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv02_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv03_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv04_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv05_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv01_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv07_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv12_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv18_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv19_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv21_519aaa	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv27_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv20_519aaa	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv06_519aaa	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
xv29_519aaa	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE

FIG. 22A

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z2491_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR

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z2491_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv26_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv22_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
fa1090_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv32_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv11_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv28_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv96_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv02_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv03_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv04_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv05_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv01_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv07_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv12_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv18_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv19_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv21_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv27_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv20_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv06_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv29_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL

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z2491_519 301 ISAGMKIIDSSKTAK*
zv26_519 301 ISAGMKIIDSSKTAK*
zv22_519ass 301 ISAGMKIIDSSKTAK*
fa1090_519 301 ISAGMKIIDSSKTAK*
zv32_519 301 ISAGMKIIDSSKTAK*
zv11_519 301 ISAGMKIIDSSKTAK*
zv28_519 301 ISAGMKIIDSSKTAK*
zv96_519 301 ISAGMKIIDSSKTAK*
zv02_519 301 ISAGMKIIDSSKTAK*
zv03_519 301 ISAGMKIIDSSKTAK*
zv04_519 301 ISAGMKIIDSSKTAK*
zv05_519 301 ISAGMKIIDSSKTAK*
zv01_519 301 ISAGMKIIDSSKTAK*
zv07_519 301 ISAGMKIIDSSKTAK*
zv12_519 301 ISAGMKIIDSSKTAK*
zv18_519 301 ISAGMKIIDSSKTAK*
zv19_519 301 ISAGMKIIDSSKTAK*
zv21_519ass 301 ISAGMKIIDSSKTAK*
zv27_519 301 ISAGMKIIDSSKTAK*
zv20_519ass 301 ISAGMKIIDSSKTAK*
zv06_519ass 301 ISAGMKIIDSSKTAK*
zv29_519ass 301 ISAGMKIIDSSKTAK*

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Fig. 22B

Fig. 23A

Fig. 23B

Fig. 23C

fa1090	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm33asbc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm32asbc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm23asbc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm27bc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm09	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm10	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm24	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm25	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm14	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm04	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm11asbc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm08n	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm96	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm01	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm02	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm03	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm07	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm12	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm18	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm19	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm20	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm21	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm06	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm17	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm13	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm05	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
z2491	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm22	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm26	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm28	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm29asbc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm16	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm15	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm31asbc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
fa1090	421	QKTTGYVWQLLPNGMKPEYRP
zm33asbc	421	QKTTGYVWQLLPNGMKPEYRP
zm32asbc	421	QKTTGYVWQLLPNGMKPEYRP
zm23asbc	421	QKTTGYVWQLLPNGMKPEYRP
zm27bc	421	QKTTGYVWQLLPNGMKPEYRP
zm09	421	QKTTGYVWQLLPNGMKPEYRP
zm10	421	QKTTGYVWQLLPNGMKPEYRP
zm24	421	QKTTGYVWQLLPNGMKPEYRP
zm25	421	QKTTGYVWQLLPNGMKPEYRP
zm14	421	QKTTGYVWQLLPNGMKPEYRP
zm04	421	QKTTGYVWQLLPNGMKPEYRP
zm11asbc	421	QKTTGYVWQLLPNGMKPEYRP
zm08n	421	QKTTGYVWQLLPNGMKPEYRP
zm96	421	QKTTGYVWQLLPNGMKPEYRP
zm01	421	QKTTGYVWQLLPNGMKPEYRP
zm02	421	QKTTGYVWQLLPNGMKPEYRP
zm03	421	QKTTGYVWQLLPNGMKPEYRP
zm07	421	QKTTGYVWQLLPNGMKPEYRP
zm12	421	QKTTGYVWQLLPNGMKPEYRP
zm18	421	QKTTGYVWQLLPNGMKPEYRP
zm19	421	QKTTGYVWQLLPNGMKPEYRP
zm20	421	QKTTGYVWQLLPNGMKPEYRP
zm21	421	QKTTGYVWQLLPNGMKPEYRP
zm06	421	QKTTGYVWQLLPNGMKPEYRP
zm17	421	QKTTGYVWQLLPNGMKPEYRP
zm13	421	QKTTGYVWQLLPNGMKPEYRP
zm05	421	QKTTGYVWQLLPNGMKPEYRP
z2491	421	QKTTGYVWQLLPNGMKPEYRP
zm22	421	QKTTGYVWQLLPNGMKPEYRP
zm26	421	QKTTGYVWQLLPNGMKPEYRP
zm28	421	QKTTGYVWQLLPNGMKPEYRP
zm29asbc	421	QKTTGYVWQLLPNGMKPEYRP
zm16	421	QKTTGYVWQLLPNGMKPEYRP
zm15	421	QKTTGYVWQLLPNGMKPEYRP
zm31asbc	421	QKTTGYVWQLLPNGMKPEYRP

Fig. 23D